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S.001. MERGING EVOLUTIONARY APPROACHES WITH ETHNOBOTANICAL KNOWLEDGE

P.0001 Human and ant-domesticated plants harbour significantly different disease resistance gene repertoires compared to their wild relatives.

Noah G. Bourne[1]

1 Durham University, Durham, UK

Plant domestication is a pivotal innovation driving the success of human civilizations; however, the domestication process often includes unintended phenotypic and or genomic consequences for the plants involved. These include susceptibility to diseases in which their wild relatives are resistant. Convergently ant-domesticated epiphytes are susceptible to disease upon ant-exclusion compared to their non-farmed (wild analogues) relatives. The genomic basis of this apparent discrepancy is linked to domesticated plants having differing resistance gene (R-gene) repertoires to their respective wild relatives. Although due to the lack of consistent annotations in previous studies it is unclear whether domestication repeatedly leads to reduced R-gene repertoires and thus unequal disease resistance capability across the phylogeny of domesticated plants. Pan-genome approaches highlight that many R-genes in plants exist in the auxiliary portion of the genome with their diversity being maintained in a population by strong balancing selection which is often negated during domestication. This provides an evolutionary explanation to why reduced R-gene repertoires persist in crop plants. Using high quality genomes of crop plants and their wild relatives, including ant-domesticated Squamellaria and their non-farmed relatives, we use state of the art deep learning approaches to provide consistent annotations of R-gene repertoires. Among the 16 crop/wild relative pairs we see significant reductions in the repertoire of R-genes in crops across the plant phylogeny. Additionally, the inclusion of ant-domesticated Squamellaria provides an exceptionally unique insight into the evolution of domesticated plants over a larger timescale.

P.0002 Survey on the usage status of tatami in historical cultural properties in Japan

Kumiko Kihara[1]

1 National Institute of Technology, Kumamoto college, Kumamoto, Japan.

Tatami, which gave rise to Japanese-style rooms, is now a rare flooring material that is only used in Japan. These tatami mats are made by wrapping a core material such as straw in "goza", mat sheet made from woven rushes, and have a long history as documented in literature. One way to elucidate the origin of tatami, where it originated and how it came to its current state, is to comprehensively collect information on the usage of tatami from existing buildings and there is one possible method to analyze it in conjunction with the historical background. Therefore, in this study, we focused on historical buildings and attempted to find out where, how much, and for what purpose tatami were used at the time of construction or in the present day. As a result, it was estimated that about 70% of Japan's nationally and prefecture-designated Important Cultural Properties have tatami mats. Among these buildings, temples and shrines accounted for a high proportion. Tatami mats were used by 59.7% of temples and 9.0% of shrines. A more detailed look at the location of use, tatami was in approximately 13% of Buddhist temples, 26% of worship halls of shrine, 6% of main shrines, 81% of main halls of temple. Tatami mats might be found in the temple main hall because it was suitable for indoor worship. If there are any historical cultural properties that have tatami mats preserved from the time of their construction, it is possible to elucidate the origin of tatami mats by scientifically analyzing that tatami. However, tatami mats deteriorate easily, and there are extremely limited cases in which actual old tatami mats can be seen. The future challenge is to acquire old tatami mats.

P.0003 Multi-omic analysis analyses reveal divergent responses to nitrogen limitation in tomato cultivars and the wild relatives

Sergio G. Nebauer[1], Gara Romero-Hernandez[2], Begoña Renau-Morata[3], Daniel Gil-Villar[1], Laura Carrillo[2], Rosendo Hijar-Jiménez[2], Eva Jiménez-Benavente[1], Purificación Martinez-Melgarejo[4], Francisco Perez-Alfocea[4], Javier Canales[5], Jaime Cebolla-Cornejo[6], Rosa Victoria Molina[1], Jaume Prohens[7], Joaquin Medina[2].

1 Departamento de Producción Vegetal, Universitat Politècnica de València, València, Spain. 2 Centro de Biotecnología y Genómica de Plantas, INIA-CSIC-Universidad Politécnica de Madrid, Madrid, Spain. 3 Biotecmed, Universitat de València, Burjassot, Spain. 4 Centro de Edafología y Biología Aplicada del Segura, Spanish National Research Council (CEBAS-CSIC), Murcia, Spain. 5 Institute of Biochemistry and Microbiology, Faculty of Sciences, Universidad Austral de Chile, Valdivia, Chile. 6 Joint Research Unit, UJI-UPV, Universitat Politècnica de València, Valencia, Spain. 7 Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Valencia, Spain.

Nitrogen (N) is an essential macronutrient for plants, and a major limiting factor for plant growth and crop production. Nitrate is the main source of N available for plants in agricultural soils and in many natural environments. In addition, NO_3^- plays a key function as a signaling molecule in many aspects of plant metabolism and developmental processes like the ones involved in seed germination, root, and shoot development and senescence. In previous studies we have identified a significant variability in plant growth, fruit quality and NUE traits among a tomato (*Solanum lycopersicum* L.) panel of varieties under low N supply. However, the relevance of its wild relatives has not been detailed assessed. In this study, we examined the effects of limiting N conditions on the transcriptome and metabolome of a tomato cultivar, cv moneymaker (MM), and the closest wild relative *S. pimpinellifolium*, accession To-937 (SP), to identify specific molecular processes and key regulators at the organ scale. Physiological and metabolic analysis revealed that both genotypes display significant differences in performance of the nitrogen assimilation efficiency (NAE). The wild relative SP displays physiological characters related to biomass production and use, showing tolerance to the limitation in N supply. Moreover, it was highlighted the ability of SP to maintain the flux of photoassimilates to the fruit even under N deficiency conditions, which is strongly inhibited in the domesticated MM cultivar. Consistently, the transcriptomic analyses allowed us to identify common and specific set of genes in root, leaf, and fruit of both genotypes whose expression depends on N availability. All these data together provide a set of metabolic pathways and nitrogen-responsive genes that are new putative targets for tomato NUE and fruit quality improvement under N limiting conditions as well new insights on the domestication process.

S.002. A CONTINENTAL SCALE CONSORTIUM APPROACH TO BUILDING GENOMICS CAPACITY AND RESOURCES: GENOMICS FOR AUSTRALIAN PLANTS

P.0004 Phylogenomic reconstruction of Australian carnivorous Drosera L. (Droseraceae) using a hybrid capture approach

Luis T. Williamson[1], Ed Biffin[2], Kor-Jent van Dijk[1], John G. Conran[1], Michelle Waycott[1,2]

1 The University of Adelaide, Adelaide, Australia 2 State Herbarium of South Australia, Adelaide, Australia.

Drosera L. is a cosmopolitan genus of carnivorous plants that are most diverse in the southern hemisphere. Approximately half of the global species diversity occurs in Australia, however the evolutionary relationships between Australian taxa remain poorly resolved. Previous studies show conflict between phylogenetic tree topologies and traditional morphological classifications; however, these earlier studies were limited to two genetic marker loci (*rbcL* and 18S) and include comparatively few Australian *Drosera*. To fill this knowledge gap, we partnered with the Genomics for Australian Plants Initiative (GAP), aiming to sequence representatives of all *Drosera* clades occurring in Australia. Additional samples were included from species occurring outside of Australia, to place our results in a global context. Using a targeted sequence capture approach with the OzBaits and Angiosperms353 bait sets, we recovered genomic data from hundreds of nuclear loci for 96 Drosera samples, representing approximately half of the *Drosera* species diversity in Australia. As higher classification concepts differ among authors, we aimed to include sequence data from the type species for each subgenus and section, where possible. While the broad tree topology is congruent with other molecular studies, novel relationships are found between taxa within multiple clades. Particularly novel relationships are found among the tuberous *Drosera* (subg. *Ergaleium* sect. *Ergaleium*), including multiple suspected instances of convergent evolution. This robust, broad scale phylogenetic framework provides the most comprehensive view of the evolution of Australian *Drosera* to date and is the first of several ongoing molecular studies into the genus.

P.0005 Another forking sundew: Biogeography of the Drosera binata Labill. (Droseraceae) species complex in Australia and New Zealand

Luis T. Williamson[1], Ed Biffin[2], Kor-Jent van Dijk[1], John G. Conran[1], Michelle Waycott[1,2]

1 The University of Adelaide, Adelaide, Australia. 2 State Herbarium of South Australia, Adelaide, Australia.

Drosera binata Labill. (Droseraceae) are widely distributed flypaper trap carnivorous plants, occurring in temperate and subtropical environments in Australia and New Zealand. Across its distribution, *D. binata* displays highly variable leaf morphology, with four morphotypes ('T-form', var. *dichotoma*, var. *multifida* and var. *multifida* f. *extrema*) that are considered indicative of evolutionary affinities. To resolve the relationships between morphs, population and singleton sampling was conducted for all morphs across the full extent of the distribution. Next generation sequencing was conducted using a target enrichment hybrid capture method with a custom bait set (OzBaits). Sequence data recovered from numerous chloroplast and nuclear loci was processed with the CAPTUS pipeline and analysed using IQ-TREE. Three well supported clades were found; a polymorphic 'southern' clade that extends across south and south-eastern Australia, extending to New Zealand; a closely affiliated polymorphic 'eastern' clade, occurring in New South Wales and south-eastern Queensland; and a geographically isolated, morphologically stable Western Australian 'T-form' clade that is highly divergent from all other populations. Multiple morphs occur within the 'southern' and 'eastern' clades, with populations showing strong geographic patterns regardless of differences in leaf morphology and growth habit. The results of these analyses challenge the proposed morphological classification of the species based on lamina morphology. All populations, except those in South Australia, feature high levels of within- and between-population variation; the potential origin of South Australian polymorphic but genetically homogenous populations are discussed. Close affiliations between 'southern' *D. binata* populations in south-east Australia and in New Zealand are considered evidence of at least one long distance dispersal event from Australia to New Zealand. The conservation and taxonomic issues raised by this study are discussed in detail, with a focus on the highly divergent Western Australian clade, dispersal, morphology and population diversity.

P.0006 Integrating phenotypic, genomic, and spatial analyses to identify the role of plasticity and local adaptation in climate responses

Joshua A. Zimmerman[1], Rhiannon smith[1], Paul D. Rymer[2], Justin Borevitz[3], Rose L. Andrew[1]

1 School of Environmental and rural Sciences, University of New England, Armidale, New South Wales, Australia. 2 Hawkesbury Institute for the environment, Western Sydney university, Sydney, New South Wales, Australia. 3 Research School of Biology, Australian National university, Canberra, Australia.

With global climate change leading to increasing environmental pressures across ecosystems, understanding the interactions between these novel pressures, genomic capacity, and existing ecosystem pressures is of crucial importance. Combining multiple data points to gauge species, and population level resilience to change is valuable for maintaining conservation targets and improving outcomes. To this effect, we seek to combine temporal condition measurements, phenotypic trait measurements, and whole genome sequence data from across the range of our target species: *Eucalyptus nova-anglica. This* is a species of *Eucalyptus* endemic to the New England Tablelands region of New South Wales Australia, in the past this species has been under immense stress due to herbivory related dieback and was the most severely affected species by 'New England Dieback' a defoliation related die-off of trees. As drought related dieback increases across the world there are fears that this species, and others typically affected by herbivory dieback may be irrevocably impacted due to the changing patterns of herbivores, the increased climatic stressors on trees, and possibly due to a trade-off between drought, and herbivory related physiological defences. By including condition assessments, and morphological traits, with temporal climatic variables, we aim to identify signatures of local adaptation and determine whether differences in phenotype relate to identifiable outlying loci or are examples of phenotypic plasticity. The identification of outlying loci will allow for gene ontology annotation, to further identify the pathways of this local adaptation. The data we have collected will also inform gene environment association, and genome-wide association studies, with the overall goal of creating genetic offset maps sing climate predictions over the next 50 years. These offset maps will inform conservation goals via the identification of 'stable' and 'vulnerable' populations for conservation prioritisation, and the selection of specific seed-stock provenances for revegetation and conservation efforts.

P.0007 Drought and its effects on biochemical pathways, trade-offs for herbivory defence, and implications on herbivory related dieback

Joshua A. Zimmerman[1], Paul D. Rymer[2], Rose L. Andrew[1], Rhiannon Smith[1]

1 School of Environmental and rural Sciences, University of New England, Armidale, New South Wales, Australia. 2 Hawkesbury Institute for the environment, Western Sydney university, Sydney, New South Wales, Australia.

The impacts of climate change on ecosystems extend further than simply drought or water related stressors and encompass all ecosystem related functions. Changing food webs, and herbivore-plant interactions are an important factor to consider in the question of climate related impact on plant species. *Eucalyptus nova-anglica* is a species of Eucalyptus endemic to the New England Tablelands region of New South Wales, Australia. In the past this species has been severely impacted by herbivory related dieback on multiple occasions. The worst such, saw over 50% of all individuals of this species die-off due to defoliation rates up to 300% of canopy coverage annually. This species is one of many species worldwide that are heavily affected by cyclical herbivory causing stress and dieback. It is therefore important, not only to determine a species' response to climate stress, but also how this response affects a species ability to defend against herbivory, and other stressors in the environment. In a 6-month greenhouse study *E. nova-anglica* seedlings from across the species range were subjected to 3 months of graduating severe water stress. Half of the plants were water stressed past a permanent wilting point (1500kpa). Physiological, phytochemical, and morphological measurements were taken, and RNA extracted for transcriptomics. Differences in growth, and water stress tolerance, as well as phytochemical differences among populations will be compared with differential gene expression from 96 individuals across populations to help disentangle intraspecific differences in water-stress tolerance, as well as identifying the biochemical pathways that are most important in this response. In addition, phytochemical analysis of key anti-herbivory mono- and sesquiterpenes will provide evidence as to whether a trade-off between water stress response and herbivory defences exists, elucidating whether there is a deleterious interaction between drought tolerance and future herbivore defence at a biochemical level in plants.

S.003. ACROSS LAND AND WATER: UNDERSTANDING PLANT GENE FLOW AT A LANDSCAPE SCALE

P.0008 Patterns of genetic variation in the riparian plant species, Carex aquatilis Wahlenb.

Jennifer Clayton Brown[1], Paul Ashton[1]

1 Biosciences, Edge Hill University, Lancashire, UK.

Riparian systems are diverse and widespread. Water borne seed dispersal (hydrochory) within a river system helps shape the genetic diversity of the associated flora whilst the extent of gene flow between river systems is determined the pattern of genetic differentiation between systems. The role of hydrochory and other methods of gene flow in genetically structuring populations has not been fully explored. *Carex aquatilis*is a riparian sedge species restricted to a few rivers systems in the UK with some outlying populations. This study focuses upon the genetic structure of the species in three rivers plus isolated populations within the UK. River systems allow consideration of gene flow by hydrochory and other methods of gene flow, while isolated populations lack hydrochore dispersal. Genetic analysis utilising SSRs was used to determine the genetic diversity and isolation by distance (IBD) in populations downstream vs upstream within the same river system and between adjacent catchments. Isolated populations were incorporated both within the mainland and on adjacent isles. IBD is evident, with unique gene pools present in isolated sites and a distinction between genetic portfolios present in the different regions. However, no significant difference in genetic variation was observed between upstream and downstream populations or between the adjacent river systems. These findings indicate dispersal methods outside of hydrochory are being utilised bypassing geographical barriers between catchments. This has implications for broader connectivity within the landscape.

P.0009 Modes of reproduction affects genetic diversity and population maintenance in three Japanese Dioscorea species

Kazuki Okamoto[1], Satoshi Nanami[1], Hayato Tokumoto[1], Shizue Yoshihara[1], Akira Itoh[1]

1 Osaka Metropolitan University, Osaka, Japan.

Plants have three modes of reproduction: sexual, asexual, and both. To understand the effectiveness of each mode and the significance of reproductive diversity, it is important to compare genetic diversity and population structure among species with different modes of reproduction and elucidate the mechanisms of population maintenance. This study extensively sampled three dioecious Dioscorea plants in Japan and examined their genetic diversity and geographic genetic structure. *D. quinquelobata* reproduced solely through sexual reproduction via seed. *D. japonica* reproduced through both sexual reproduction via seed and asexual reproduction via bulbil. Male plants of *D. bulbifera* reproduced only asexually by producing bulbils, as female plants are rare in Japan. In *D. quinquelobata* populations, most individuals exhibited distinct genotypes. The population of *D. japonica* consisted of numerous clones, all of which were limited to local distribution. In contrast, the majority of *D. bulbifera* individuals were limited to three clones. Two of these clones were distributed over a large geographical area, while the third was only found in a single local population. The genetic diversity and structure of the three species may reflect their unique population maintenance mechanisms. *D. quinquelobata's* population is maintained through crossbreeding male and female plants to produce diverse offspring. *D. japonica* combines sexual reproduction to ensure genetic diversity with asexual reproduction which requires only one individual. *D. bulbifera* maintained its population through the production of bulbils, even though it grows almost exclusively on male plants. The narrow distribution of each *D. japonica* clone suggests that the dispersal range of *D. japonica* bulbils is limited. In contrast, *D. bulbifera* bulbils have a wide enough dispersal range to form a geographically widespread distribution.

P.0010 Gene flow and genetic divergence in insular populations: a case study from Andaman and Nicobar archipelago

Sarath Paremmal[1,3], Muneera Parveen AB[2], Ghosh Dasgupta M[2], Sreekumar VB[1], Dev SA[1*]

*1 Kerala Forest Research Institute, Thrissur, Kerala, India. 2 Institute for Forest Genetics and Tree Breeding, Coimbatore, India. 3 Forest Research Institute Deemed University, Dehradun, India. *sumadev@rediffmail.com.*

Islands provide unique platform for studying the roles of geography and ecology in driving population divergence and speciation. Geographically isolated populations of pan-archipelagic species often diverge via accumulation of genetic and phenotypic variations. We intended to investigate this phenomenon in morphologically diverged island populations of *Korthalsia laciniosa,* a threatened climbing palm distributed in wet evergreen forest patches of the Andaman and Nicobar Archipelago, in the Bay of Bengal. Draft genome of *K. laciniosa* (592Mbp) was developed and explored to mine out genome-wide microsatellite markers. A subset of identified neutral, genic and chloroplast microsatellite markers were then utilized to address how gene flow, seed dispersal, local environmental variation, landscape and geography could influence population divergence. Further, Ecological Niche Modelling (ENM) in different climate regimes were also explored. The genotyped thirteen populations of *K. laciniosa* across the archipelago have shown high genetic divergence among islands and increased number of private alleles in most isolated populations. Nuclear and chloroplast genetic data has provided evidence of distinct genetic clusters, and discrete population structure. Genetic admixture among isolated but geographically closer populations with exceptions were also observed. The profound influence of IBD and IBE on genetic distance was identified along with putative loci under selection. Approximate Bayesian Computation analysis was utilized to test different demographic scenarios to draw inferences on the population history of the species. The analysis supported past admixture and subsequent reduction and isolation of populations. Furthermore, estimates on historical and contemporary gene flow using Migrate-n and BAYESASS concord with this observation. ENM identified wider potential ecological niches suitable for the species in the paleo/Pleistocene climate scenario which reduced subsequently in the present. Additionally, it implies that these islands had a larger distribution of moist evergreen forests in the past. The information generated could be used to implement tailor-designed conservation strategies.

S.004. ADVANCES IN FERN ECOLOGY: RESPONSES TO ENVIRONMENTAL AND BIOTIC STRESS FACTORS

P.0011 Tropospheric ozone compromises plant performance throughout their ontogeny

S. Prieto-Benítez[1], I. Gónzalez-Fernandez[1], R. Ruiz-Checa[1], E. Torres[2], R. Alonso[1], V. Bermejo-Bermejo[1]

1 Centro de Investigaciones Energéticas, Medioambientales y Tecnológicas, Madrid, Spain. 2 Universidad Politécnica de Madrid, Madrid, Spain.

Due to the high plant toxicity, wide distribution in rural and natural areas, and its greenhouse effect, tropospheric ozone (O_3) is one of the most relevant air pollutants in the Northern hemisphere. The Mediterranean climatic conditions facilitate photochemical formation and persistence of O_3, leading in the Iberian Peninsula to a chronic exceedance of the threshold levels for plant protection established by the UNECE Air Convention and the EU Air Quality Directive (2008/50/EC). The high levels of O_3 in forested and rural areas, far away from precursor emission areas, are negatively affecting natural ecosystems, such as those of the Mediterranean mountains considered hot spots for plant biodiversity on a global scale. This is the case of the "Sierra de Guadarrama (SG)" mountains belonging to the Spanish Central system. The high oxidative capacity of O_3 may cause vegetative growth loss, nutrient imbalance and reproductive success reduction, weakening plants to tolerate other environmental stresses like water stress. Different experimental OTC assays under semi-natural conditions have been developed to analyze the O_3 tolerance of different species belonging to the perennial pasture communities in the SG. Plants were submitted to four different O_3 exposures, from background pre-industrial levels till future expected levels in the present century. Vegetative growth, flower traits, number of seeds, seed weight and seed germination were measured to figure out the impact of O_3 through the ontogeny of the plants. Species from different altitudes were assayed, from the summits (e.g., *Silene ciliata*) to the base of the mountains (e.g., the endemic *Erodium paularense*). From this research, new O_3 risk indicators will come and the development of new critical levels (O_3 thresholds for plant protection) for Mediterranean mountain pastures ecosystems following the UNECE Air Convention.

P.0012 Catalog of Lycophyta from Chile

Fernanda Céspedes[1], Paulette I. Naulin[1]

1 Laboratorio Biología de Plantas, Universidad de Chile, Santiago, Chile.

Lycophyta, the first lineage of plants with secondary growth, includes arborescent specimens. Reproducing through spores, they lack seeds and exhibit dichotomous apical growth in stems and roots. *Lycophyta* have sterile and fertile lycophylls with a single central vascular bundle. Thriving in humid environments, they serve as bioindicators of environmental changes. Besides, they have medicinal and cultural value. Although this clade holds evolutionary importance, there is a lack of studies in Chile that organize the taxonomic understanding and assess the risk of extinction within it. Therefore, this study proposes an updated catalog for the lycophytes present in Chile. The taxonomy, distribution, morphological description, conservation status, and taxonomic history of Chilean lycophytes were systematized through an exhaustive revision of literature, herbarium specimens, and internationally recognized web pages. Chile presents 12 species across three families: *Lycopodiaceae* (seven species), *Isoetaceae* (four species), and *Selaginellaceae* (one species). *Lycopodiaceae* is the richest family in the country, with seven species belonging to three genera (*Austrolycopodium, Diphasium, and Huperzia*). *Isoetaceae* follows with four species of the genus Isoetes, and finally, the only species of Selaginellaceae in Chile is *Selaginella apoda* (L.) Fernald, an introduced species native to North America. Distribution spans from the Coquimbo Region to the Magallanes and the Chilean Antarctic Region, excluding the Metropolitan and O'Higgins regions. The Archipiélago de Juan Fernández hosts three *Lycopodiaceae* species. Concerning conservation, seven species are Least Concern (LC), one is Endangered (EN), one is Critically Endangered (CR), one is Vulnerable (VU), and one lacks information. *Selaginella apoda* is an introduced species, so its conservation status was defined by NatureServeExplorer, rating it as G5, indicating that the species is "at very low risk or extinction or collapse due to a very extensive range, abundant populations or occurrences, and little to no concern from declines or threats.

P.0013 The compensation of the costs of heterospory

Lucía De Soto[1], John R. Pannell[2], Sonia Molino[3], Susana Vega[4], Marcos Méndez[5]

1 Complutense University of Madrid, Madrid, Spain. 2 University of Lausanne, Lausanne, Switzerland. 3 Universidad Europea de Madrid, Madrid, Spain. 4 Universidad de Antioquia, Medellín, Colombia. 5 King Juan Carlos University, Madrid, Spain.

Heterospory, the production of spores of two different sizes (microspores which develop into male gametophytes and megaspores into female gametophytes), has evolved independently at least eight times in land plants, one of them in lycophytes. Heterospory entails a potential cost in fecundity derived from the sex specialisation of spores. The development of unisexual gametophytes reduces the number of young sporophytes returned per spore, usually only one per megaspore and several per microspore, and therefore the number of spores produced by a heterosporous sporophyte should increase to compensate this reduction. Here, we will use two sister clades, the homosporous Lycopodiales and the heterosporous Selaginellales, as a model system to test the hypothesis that the number of spores produced per unit of sporophyte biomass of heterosporous lycophytes is greater than the number of isospores produced per unit of sporophyte biomass of homosporous ones. To this end, we are asking for the scientific collaboration of pteridologists specialised in lycophytes to participate in our study by contributing samples of several populations of relevant species. Overall, we aim to bring the empirical study of heterospory in pteridophytes to a more prominent position in plant evolutionary ecology.

P.0014 Winter is coming: potential desiccation and freezing cross-tolerance in ferns

Beatriz Fernández-Marín[1], Lucía Herrero-Quintanilla[1], Miren Irati Arzac[1], Alicia Victoria Perera-Castro[1], José Manuel Laza[2], Jose Luis Vilas[2], Aitor Laza[1], José Ignacio García-Plazaola[1]

1 Department of Plant Biology and Ecology, University of the Basque Country, Leioa, Spain. 2 Department of Physical Chemistry, University of the Basque Country, Leioa, Spain.

Among temperate and boreoalpine ferns, some species retain their fronds during wintertime. Evergreen fronds must then be able to tolerate repeated freezing/thawing events throughout the wintertime that have down-stream consequences. These include risks such as: photooxidative stress, xylem embolism and mechanical damage derived from freeze-induced cell-dehydration. Most of these risks have been successfully prevented/solved by desiccation-tolerant species: i.e. those able to equilibrate the water potential of their fronds with that of the atmosphere and then recover normal metabolic functions after rehydration. Thus, we hypothesise that anatomical and physiological mechanisms enabling desiccation tolerance in ferns may provide ecophysiological advantages to face freezing stress too. To test this hypothesis we selected few species naturally growing in the North of the Iberian Peninsula and with different tolerances to dehydration. After evaluating their tolerance to different subzero temperatures, we assessed their ice nucleation temperature through differential scanning calorimetry, their gas exchange through infra-red gas analyser, xylem anatomy through fluorescence microscopy, glass transition temperature through dynamic thermal analyses, and photoprotective responses through chlorophyll fluorescence and high performance liquid chromatography. Our results reveal significant interspecific differences in freezing tolerance, maximal photosynthetic capacity, xylem properties and ice nucleation temperature. Data also reflect some common mechanisms particularly related to photoprotection. All things considered, data support a side-effect protection against freezing/thawing damage in desiccation-tolerant species, although some specific physiological adaptations are also needed.

P.0015 Ferns on ferns: an exploration of epiphytic fern gametophytes growing on low trunks of tree ferns

Alexandria Quinlan[1], Li-Yaung Kuo[2]

1 Institute of Ecology and Evolutionary Biology, National Taiwan University, Taipei, Taiwan. 2 Institute of Molecular & Cellular Biology, National Tsing Hua University, Hsinchu City, Taiwan.

Tree ferns have been documented as significant hosts for epiphytes, often composed of distinct communities that are considerably different from other hosts. Particularly, exclusive growth of epiphytic fern species has been exhibited on tree ferns, however, this fern-on-tree-fern epiphytism has yet to be explored for the gametophyte generation. In June and October of 2022, in a subtropical forest in Taiwan, low trunks of two tree fern species, *Alsophila spinulosa* and *A. podophylla* (Cyatheaceae), and nearby angiosperm tree hosts were surveyed for epiphytic fern gametophytes. The surveys aimed to identify differences in fern gametophyte communities between tree ferns and other hosts, and whether stable humidity is a key factor associated with such differences. Gametophytes were identified using a metabarcoding approach that involved sequencing multiplexed amplicons from the trnL-F DNA barcode region, which were derived from tissue-direct PCRs. Overall, tree ferns harbored a significantly higher abundance and species richness of gametophytes than angiosperm hosts, and hosted more cordiform gametophytes that were mostly from accidental and facultative fern species. In comparison, angiosperms hosted a higher abundance of non-cordiform individuals. In addition, two independent fern gametophytes were found on the surveyed hosts, *Callistopteris apiifolia* (Hymenophyllaceae) and *Haplopteris yakushimensis* (Pteridaceae). Results from a relative humidity (RH) survey showed that the RH of all surveyed hosts was most frequently over 95%, however, the angiosperm host spent a longer duration below 95% and 85% RH compared to the tree ferns. The stable RH of the tree fern trunks, presumably resulting from the moist root mantle, allowed for a high diversity of fern gametophytes. Additionally, the webbed structure and humus accumulation in the root mantle simulate a terrestrial-like environment, offering a habitat for fern species that typically establish on the ground. Importantly, this study is among the first insights into epiphytic fern gametophyte communities on tree ferns.

P.0016 Exploring the isotopic composition of club mosses (Lycopodiaceae) and their juvenile population structure in natural ecosystems

Radvile Rimgaile-Voicik[1], Anita Elizabeth Clarke[1], Jonas Remigijus Naujalis[1], Andrius Garbaras[2]

1 Vilnius University, Life Sciences Center, Institute of BiosciencesVilnius, Lithuania. 2 State Research Institute Center for Physical Sciences and Technology Vilnius, Lithuania.

Homosporous club mosses have an archaic life cycle, alternating two locationally, nutritionally, and physiologically independent generations. The sexual generation of club mosses – the gametophytes (or prothalli) – are among the least researched botanical objects. Little is known about the life cycle, population structure, and fitness of club mosses and their role in nutrient cycling. Forty years ago, one of the rarest botanical objects – club moss gametophytes and juvenile sporophytes – were discovered for the first time in forests of Lithuania. We were the first to collect spatial data on gametophyte distribution and their diversity in soil. We applied Nearest Neighbour Analysis (NNA) to evaluate the spatial distribution of juvenile sporophytes and gametophytes of genera *Lycopodium* L. and *Diphasiastrum* Holub. Our results suggest that initial populations of club mosses in pine forests are multi-aged and display a relatively stable degree of spatial aggregation. In recent years, efforts have been put into employing stable isotopes to investigate plants that are otherwise difficult to study due to their peculiar biology and ecology. The ratios of stable carbon ($^{13}C/^{12}C$) and nitrogen ($^{15}N/^{14}N$) isotopes are applied in quantitative assessments of ecophysiological processes in plants. Stable isotopes can reveal carbon and nitrogen sequestration trends across different levels spanning from individuals to entire ecosystems. We analyzed the distribution of ^{13}C and ^{15}N by Isotope Ratio Mass Spectrometry (IRMS). We determined the carbon (C%) and nitrogen (N%) content in different organs of *Lycopodium annotinum* L. (interrupted clubmoss, syn. *Spinulum annotinum* (L.) A.Haines) sporophytes. We found a seasonal gradient and linked isotope distribution with neighboring plant diversity. Our findings are crucial to better understanding lycophyte ecophysiology and their function in hemi-boreal forests.

P.0017 Water stress effects on germination and gametophyte growth in four ferns from contrasting habitats

Sarghini L.[1], Ruiz-Cano S.[2], Medina N.G.[2], Gago J.[3], Quintanilla L.G.[1]

1 Global Change Research Institute, Rey Juan Carlos University, Móstoles, Spain. 2 Biodiversity and Global Change Research Centre, Autonomous University of Madrid, Madrid, Spain. 3 Agro-Environmental and Water Economics Institute, University of the Balearic Islands, Palma, Spain.

Climate change is posing a threat to plant biodiversity, especially in Southern Europe, where adverse abiotic stress factors like water deficit are prevalent. Although spore germination and gametophyte establishment are indispensable for effective fern dispersal and sporophyte recruitment, the effects of water limitation on these stages have been poorly investigated. In this study cultivation and desiccation tolerance experiments were conducted to test the hypothesis that xerophytic species have adaptations in spore germination and gametophyte growth that allow them to establish in environments with lower water availability than hygrophytic species. To do so, two hygrophyte ferns (*Culcita macrocarpa* and *Woodwardia radicans*) and two xerophyte ferns (*Asplenium ceterach* and *Cosentinia vellea*) were compared. Interestingly, *C. vellea*, the most xerophytic species, exhibited a sharp germination decline with decreasing water potential (ψ) contrasting with *W. radicans*, which maintained germination at lower ψ, and *A. ceterach* and *C. macrocarpa* showed intermediate responses to ψ. This germination inhibition of *C. vellea* at low ψ can be an adaption preventing germination during transient wet conditions, which would lead to subsequent gametophyte death through desiccation. Water limitation reduced gametophyte survival, especially in *C. macrocarpa* but gametophyte growth was not significantly affected. Gametophytes of all species showed low recovery of physiological status after desiccation treatments suggesting that they are desiccation sensitive. The higher leaf mass per area obtained in xerophytes is consistent with their sporophyte desiccation tolerance. However, the also higher gametophyte mass per area of xerophytes did not translate into a greater desiccation tolerance at the gametophyte stage. All these findings suggest that climate change-related increases in drought events may reduce spore germination and gametophyte survival, and thus sporophyte recruitment of both hygrophyte and xerophyte ferns.

P.0018 Photosynthetic responses of Pinus brutia trees to defoliation by pine processionary moth (Thaumetopoea wilkinsoni Tams.)

Gürkan Semiz[1], Ayşe Deligöz[2], Esra Bayar[2], Gürçay Kıvanç Akyildiz[1], Batıkan Günal[1]

1 Department of Biology, Pamukkale University, Denizli, Turkey. 2 Department of Forest Engineering, Isparta University of Applied Sciences, Isparta, Turkey.

Insect damage, which is predicted to increase with global climate change, can adversely affect the growth and survival of trees. *Pinus brutia* Ten. is the species with the widest distribution range among coniferous forests in Turkey. *Pinus brutia* is of great importance both ecologically and economically, as it can grow rapidly and is suitable for afforestation over large areas. The major biological pest of *P. brutia* in both natural and afforestation areas is the pine processionary moth (*Thaumetopoea wilkinsoni* Tams.) defoliation. This pest causes significant damage, especially in the pine forests of the Mediterranean, Aegean and Marmara regions of Turkey. In this study, we investigated the changes in photosynthetic responses (net photosynthesis rate, stomatal conductance, and transpiration rate) in pine samples both resistant and susceptible clones against *T. wilkinsoni* over a year in a clonal seed orchard, near Antalya, Turkey. The photosynthetic responses of *P. brutia* needles were investigated using one-year-old shoots using a portable photosynthesis system (LI-6400XT, LI-COR) with an LED light source (6400-02B, LI-COR). Our results showed that the net photosynthetic rate, stomatal conductance and transpiration rate were lower in the dry period (July and September) than in the rainy period (April and January). There were statistically significant differences between resistant and susceptible clones in the sampling periods. Susceptible clones exhibited a higher net photosynthetic rate, stomatal conductance and transpiration rate in some sampling periods. Overall, this study shows that susceptible and resistant clones of *P. brutia* show differences in their photosynthetic and defensive responses to pine processionary moth herbivory.

P.0019 Microphylls are diverse too: evidence from a structural study of Selaginellaceae

Shau-Fu Li[1, 2], Jian-Wei Liu[1], Iván A. Valdespino[3], Chun-Lin Huang[2], Peter Chesson[1,4], Chiou-Rong Sheue[1]

1 National Chung Hsing University, Taichung City, Taiwan. 2 National Museum of Natural Science, Taichung City, Taiwan. 3 Universidad de Panamá, Panama, Panama. 4 University of Arizona, Tucson, USA.

Selaginellaceae (Lycophyta) is monogeneric and cosmopolitan, having highly diverse species. Generally, the leaves of *Selaginella* are tiny and single vein, recognized as microphylls, occurring in two major forms, isophylls and anisophylls, named for their morphological variation and arrangements on the plant. In contrast to multivein leaves (megaphylls), the study of microphylls is greatly under reported. The aim of this study is to explore the diversity of microphyll structure of Selaginellaceae and associate with chloroplast traits and habitats. Seventy-six species from seven subgenera of *Selaginella* collected from the Old- and New- World were studied with light microscopy, scanning electron microscopy and confocal scanning light microscopy for understanding leaf structures and chloroplast traits. Based on the vein and leaf structures, eight microphyll types were delineated in this study: Epidermis-spongy type (ES); Epidermis-funneled subepidermal cell-spongy type (EfSeS); Epidermis-palisade-spongy type (EPS); Funneled epidermal cell type (fE(S)); Funneled epidermal cell-spongy type (fES); Funneled epidermal cell-funneled subepidermal cell-spongy type (fEfSeS); Funneled epidermal cell-palisade-spongy type (fEPS) and multivein palisade-spongy type (mPS). The presence of giant chloroplasts (monoplastid) is strongly associated with the funnel-shaped epidermal or subepidermal cells on the dorsal surface cell, and tend to be found in humid shady environments. Open and arid environments show diverse leaf forms, including a multiveined form (*S. schaffneri*), often with thick epidermal cell walls, and may have a resurrection ability. The differentiation of leaf structure of anisophyllous species can be higher than the isophyllous species. The evidence points to increasing diversity of *Selaginella* microphylls with time. Even though small and simple leaves, the microphylls of *Selaginella* show structural flexibility adapted to a wide variety of environments.

P.0020 Bioactive compounds and neuroprotective effects of the fern Lophosoria quadripinnata (Dicksoniaceae): UHPLC-MS and in silico approach

Alfredo Torres-Benítez[1,2*], Mario J. Simirgiotis José Erick Ortega-Valencia[3], Jaqueline S. Ley-Martínez[3], Javian Gallardo-Valdivia[4], Marta Sanchez[5], María Pilar Goméz-Serranillos[5, 1]

*1 Universidad Austral de Chile, Valdivia, Chile. 2 Universidad San Sebastián, Valdivia, Chile. 3 Instituto Tecnológico de Tlalnepantla, Estado de México, Mexico. 4 Universidad de Chile, Santiago de Chile, Chile. 5 Universidad Complutense de Madrid, Madrid, Spain. *aljotobe19@hotmail.com*

Lophosoria quadripinnata is a fern species of the family Dicksoniaceae, widely distributed in the American tropics and ranges between humid and temperate regions from Veracruz and Hidalgo in Mexico to southern Chile and Argentina. Has ornamental value in gardens, as a cut leaf for florists, and in traditional medicine as homeostatic and to stop bleeding. The objective of this work was to identify the bioactive compounds of the lyophilized extract of *L. quadripinnata* and evaluated the neuroprotective effects by the action of major compounds through *in silico* analysis. From 20 g of fronds of *L. quadripinnata* collected in an area adjacent to the botanical garden of the Universidad Austral de Chile (Valdivia, Los Ríos region, Chile) a lyophilized extract with a final yield of 9% was obtained. Thirteen compounds were identified by liquid chromatography coupled with quadrupole-time-of-flight mass spectrometry (UHPLC-ESI-QTOF-MS). The pharmacokinetic properties and toxicological behavior (mutagenicity, tumorigenicity, reproductive effect, and irritation) of the phytochemicals were calculated using the computational tool Osiris Data Warrior (v 5.5.0); according to the results of violation of Lipinski's rules and the absence of toxicity risks, the compounds 5GDC (5-glucosyloxy-6,7-dimethoxy coumarin), 5C3M (5-O-caffeoyl-3-O-malonylquinic acid), and irifloside were selected as possible inhibitors of the enzyme and protein complexes of interest. The two-dimensional structures of the selected compounds were prepared with the ChemDraw program 8.0, and the crystal structures of Acetylcholinesterase (TcAChE) (PDB:1DX6), Butyrylcholinesterase (hBuChE) (PDB: 4BDS), Tyrosinase (PDB: 2Y9X) and human Nrf2-Keap1 (PDB: 4L7B) were downloaded from the PDB database (http://www.rcsb.org/pdb). The strongest binding affinities with Acetylcholinesterase, Butyrylcholinesterase, Tyrosinase, and Nrf2-Keap1 were presented by the compound 5C3M (-9.90 kcal/mol, -8.90 kcal/mol, -7.50 kcal/mol, and -10.70 kcal/mol, respectively). This fern constitutes a potential source of bioactive compounds that can be widely studied in different disease models related to oxidative stress.

P.0021 Finding a bug in fern sori: host range dynamics in fern-spore-feeding moth Cuprininae (Stathmopodidae)

Yu-Chia Wang[1], Yan-Zhen Chen[2], Zong-Yu Shen[3,4], Yu-Feng Hsu[3], Jen-Pan Huang[4], Li-Yaung Kuo[1,2]

1 Institute of Molecular & Cellular Biology, National Tsing Hua University, Hsinchu, Taiwan. 2 Department of Life Science, National Tsing Hua University, Hsinchu, Taiwan. 3 Department of Life Science, National Taiwan Normal University, Taipei, Taiwan. 4 Biodiversity Research Center, Academic Sinica, Taipei, Taiwan.

Lepidoptera is the primary invertebrate herbivore of ferns. Among these fern herbivores, 6.1% exhibit a feeding habit specific to spores (i.e., fern-spore-feeding, FSF). In particular, Stathmopodidae is the most diversified family with FSF taxa, and the larvae of the subfamily Cuprininae exclusively specialize in FSF. Cuprininae is, therefore, an ideal group for understanding the evolutionary and ecological dynamics between fern plants and insect herbivores. To study host-herbivore relationships widely in Cuprininae species, we conducted a one-year phenological survey in Taiwan and investigated the spore-feeding larval diversity on 30 fern species across 13 families. Notably, we applied a new approach to DNA-identify these moth larvae that was cost-effective and leveraged by tissue-direct PCR and NGS metabarcoding. After assessing various PCR conditions for COI barcodes, our optimized protocol achieved a final success rate of 98% for the DNA identification of Cuprininae larvae. Importantly, these identification results revealed some previously unknown fern-moth links but also identified new Cuprininae species. Additionally, by updating the host records, we traced the evolutionary trends of (sub)order-level host ranges of Cuprininae species along their dated phylogeny. Our phylogenetic findings suggest that Cuprininae were ancestrally oligophagous, feeding on eupolypod ferns (suborders Polypodiineae + Aspleniineae), and subsequently switched to host on other fern lineages, including other polypod suborders and the order Cyatheales. These host transitions also revealed a significant trend from oligophagous feeders to specialists, implying a co-evolutionary link between recent diversifications of Cuprininae and polypod fern hosts.

P.0022 An exploration of the ant:plant mutualism in the rare fern Microgramma (Solanopteris) brunei.

James E. Watkins, Jr.[1], Juliana Cardona-Duque[2], Mileidy Idárraga[2], Xiomara Rojo Piñeres[3], Catherine Cardelus[1]

1 Colgate University, Department of Biology, Hamilton, USA. 2 Colecciones Biológicas Universidad CES (CBUCES), Facultad de Ciencias y Biotecnología, Universidad CES, Medellín, Colombia. 3 Ecology Program, Facultad de Ciencias y Biotecnología, Universidad CES, Medellín, Colombia.

Fern-insect interactions are poorly explored yet one of the more notable of these is the relationship of *Azteca* ants and the fern *Microgramma* (*Solanopteris*) *brunei.* This is a rare and unusual epiphytic fern species known from a small number of collections from Mexico south to Colombia. While exceptionally poorly studied, the species is unusual in that it forms an apparently mutualistic association with ants primarily mediated through the production of enlarged stem domatia produced on long creeping rhizomes. The goal of this work was to understand the ecology and natural history of this fern and to explore the costs and benefits of this mutualistic interaction. The fern showed a strong affinity to guava trees *Psidium guajava* (Myrtaceae) in open pastures near humid forests in the eastern slope of the Western Cordillera in Colombia. Hollow stem domatia provided housing/shelter for the ants and often produced roots in the walls and inside the domatia cavity. Ants showed aggressive behavior when disturbed, and were also observed predating various insect species, including the rizophagous weevil *Exophtalmus parentheticus* (Curculionidae: Entiminae). We discovered that the fern produces massive ant gardens composed of hundreds of domatia in various stages of development and decay and ant-constructed internal structures. These gardens hosted one or more queens and were full of ants at varying developmental stages. We examined stable isotopes ^{15}N and ^{13}C and a two-pool mixing model to calculate the percentage of both N and C that is transferred in this system. We hypothesized that the ferns would receive significant inputs of N and C from ant wastes. We also collected a suite of plant functional trait data in this species and four others with similar ecology but lacking ant domatia. The project is ongoing and revealing novel insights into this unique relationship.

P.0023 Genome-wide identification of BAHD gene family and expression analysis in tobacco (Nicotiana tabacum L.)

Lin Xia[1], Zefeng Li[1], Yijun Li[1], Zhong Wang[1], Xiaodong Xie[1], JunYang[1], Mingzhu Wu[1]

1 China Tobacco Gene Research Center, Zhengzhou, Tobacco Research Institute of China National Tobacco Corporation, China.

Plant BAHD acyltransferases constitute a large family of enzymes that utilize acyl CoA as a substrate and play diverse biological roles, including catalyzing thesynthesis ofphenolics, terpenes, small volatile esters, as well as defense compounds. In this study, a total of 87 *NtBAHD* genes were identifed from the genome of tobacco (*Nicotiana tabacum* L.), and we found that*NtBAHD*genes are diverse based on gene structure, physiochemical properties, and function. The NtBAHD genes were found to be located on 20 tobacco chromosomes. Two pairs of tandem duplication genes and 27 pairs of segmental duplication genes were obtained by analysis of gene duplication events, indicating that both tandem and segmental duplications have contributed to the expansion of the NtBAHD gene family in tobacco. The cis-regulatory elements present in the promoters of NtBAHD genes were involved in phytohormones, abiotic stresses, and photoresponsive. Expression profile analysis revealed that the expression patterns of different members of NtBAHD were found to be diverse in different developmental stages of the same tissue or in different tissues.

P.0024 Transcription factor NtMYB59 positively regulates the synthesis of tobacco chlorogenic acid

MingzhuWu[1], XiaLin[1], ZhongWang[1], Yalong Xu[1], Zefeng Li[1], Chen Wang[1], JunYang[1]

1 China Tobacco Gene Research Center, Zhengzhou Tobacco Research Institute of China National Tobacco Corporation, China.

Chlorogenic acid is one of the most abundant soluble polyphenol in solanaceae plants, which possess many biological and pharmaceutical properties, including anti-inflammatory, antiviral and anti-tumor, and it has important economic value. MYB transcription factors play an important role in plant growth and development, protect against biological and abiotic stresses. We mapped the co-expression network of genes related to chlorogenic acid synthesis using the whole-genome and whole-growth expression profile data of tobacco, and found that NtMYB59 gene may interact with NtHQT1. Through cloning and bioinformatics analysis of NtMYB59 gene, we found that it has the typical R2 and R3 domains of R2R3-MYB transcription factors. Phylogenetic analysis shows that NtMYB59 and AtMYB59 belong to the same clade in evolution. By analyzing the chlorogenic acid content in the leaves of NtMYB59 overexpression and RNAi transgenic plants, it was found that the chlorogenic acid content in the leaves of overexpression plants was significantly increased, while in RNAi plants was significantly decreased. Meanwhile, we found that the expression of NtMYB59 and NtHQT1 in overexpression and RNAi plants showed a similar rule with the change of chlorogenic acid content. We also found that NtMYB59 could directly bind to the promoter of NtHQT1, so as to regulate the expression of NtHQT1. Our study provides genetic resources and technical support for the analysis of plant chlorogenic acid synthesis regulatory network, gene regulation and genetic improvement of tobacco quality traits.

P.0025 The independent gametophytes of Hymenasplenium murakami-hatanakae (Aspleniaceae)

Katsuhiro Yoneoka[1], Tao Fujiwara[2], Toshifumi Kataoka[1], Kiyotaka Hori[3], Atsushi Ebihara[4], Noriaki Murakami[1]

1 Makino Herbarium, Tokyo Metro Plan University, Tokyo, Japan. 2 The Center for Molecular Biodiversity Research, National Museum of Nature and Science, Ibaraki, Japan. 3 The Kochi Prefectural Makino Botanical Garden, Kochi, Japan. 4 Department of Botany, National Museum of Nature and Science, Ibaraki, Japan.

All land plants alternate between the diploid sporophyte and haploid gametophyte stages. In ferns, life cycles are characterized by a separation of generations. In general, most of the life cycle is thought to be dominated by the sporophyte. However, there are exceptions, as fern independent gametophytes capable of maintaining a long-term population through vegetative reproduction have been observed in certain lineages, namely Hymenophyllaceae, Pteridaceae, Lomariopsidaceae, and Polypodiaceae. This phenomenon is particularly observed in the non-cordate gametophytes of epiphytic or epilithic ferns. Surprisingly, the discovery of mysterious strap-like gametophytes on Izu-Oshima Island, Japan, has led to the hypothesis that *Hymenasplenium murakami-hatanakae*, a fern species belonging to Aspleniaceae, can also form independent gametophytes. In this study, we focused on three key questions to test this hypothesis: 1) Can the gametophyte population be maintained by vegetative reproduction via gemmae? 2) Can they clearly exist independently of neighboring conspecific sporophytes? 3) What are the differences between the sites where gametophyte populations and conspecific sporophytes grow? Our investigation revealed that gametophyte populations of *H. murakami-hatanakae* on three islands in the Izu Islands. Based on cpDNA analysis between the gametophyte and sporophyte populations, the gametophytes were found to be maintained by gemmae reproduction without new supplies of spores. Finally, a comparison of the surrounding vegetation at the collection sites suggested that environmental factors such as light and humidity may influence the maintenance of gametophyte populations. These results clearly demonstrate that *H. murakami-hatanakae* is one of the ferns capable of forming independent gametophytes. To our knowledge, this is the first report of independent gametophytes from the suborder Aspleniineae (Eupolypod II). The discovery of the independent gametophyte within a phylogenetic lineage previously thought not to form such gametophytes will provide important insights into the morphological and functional evolution of gametophytes in ferns.

P.0026 Genomic variation landscape of the model salt cress Eutrema salsugineum

Xiaojuan Wang Guifang Zhao[1]

1 Key Laboratory of Resource Biology and Biotechnology in Western China, Ministry of Education, College of Life Sciences, Northwest University, Xi'an, China

Eutrema salsugineum has long been used as the model for examining salt and other abiotic stress in plants. In addition to the forward genetics approaches widely used in the lab, natural variations undoubtedly will provide a rich genetic resource for studying molecular mechanisms underlying the stress tolerance and local adaptation of this species. We used 90 resequencing whole genomes of natural populations of this species across its Asian and North American distributions to detect the selection signals for genes involved in salt and other stresses at the species-range level and local distribution. We detected selection signals for genes involved in salt and other abiotic tolerance at the species level. In addition, several cold-induced and defense genes showed selection signals due to local adaptation in North America-NE Russia or northern China, respectively. These variations and findings provide valuable resources for further deciphering genetic mechanisms underlying the stress tolerance and local adaptations of this model species.

S.006. ADVANCES IN MICROCLIMATE RESEARCH FOR CRYPTOGAM ECOLOGY.

P.0027 A novel allometric model for the assessment of non-vascular epiphyte (bryophyte) biomass within the Brazilian Atlantic Rainforest

Gabriela B. Berro[1], Carlos A. Joly[1], Simone A. Vieira[1]

1 University of Campinas, Campinas, Brazil.

Non-vascular epiphytes (bryophytes) are very common and highly biodiverse in tropical forests. They play multiple roles in ecosystem functioning, harboring nitrogen-fixing organisms and contributing to primary productivity. Known as biological indicators due to their sensitivity to environmental conditions, they are among the first groups affected by climate change. However, their importance in carbon stocks is still unclear. This study, conducted within the Serra do Mar State Park in southeastern Brazil, focuses on quantifying the biomass of non-vascular epiphytes in the Brazilian Atlantic Forest. Samples were collected in five permanent plots (1ha) of Montane Atlantic Forest with different anthropic disturbances history (three old-growth forests, one subjected to selective logging, and one late-successional forest). A new index was created and implemented to classify the areas' phorophytes (support trees) according to the coverage of their trunk and branches by non-vascular epiphytes (ICEav). We collected samples of non-vascular epiphytes from 10 phorophytes belonging to each ICEav class, in all their faces (N, S, E, W) and at four heights, including trunk and branches (n=480). The carbon and nitrogen content of the samples was measured and a new allometric model was developed to estimate the total biomass of non-vascular epiphytes in the areas. We classified 8.149 living phorophytes in the ICEav classes, and we didn´t find any differences between epiphytes biomass of faces (p=0.55) or heights (p=P.8). The carbon content of the non-vascular epiphytes was 43.93 ± 3.30%, and the nitrogen was 2.07 ± 0.63%. The allometric model, using ICEav and phorophyte diameter as variables, resulted in estimated non-vascular epiphyte biomass averages of 255.9 kg.ha^{-1} in the old-growth forest, 229.3 kg.ha^{-1} in the selectively logged area, and 208.4 kg.ha^{-1}in the late-successional plot.

P.0028 Ecological impacts on bryophyte microhabitats in Barail Wildlife Sanctuary, Assam, India

Sudipa Das[1]

1 Department of Botany, Sundarban Hazi Desarat College, West Bengal, India.

Microhabitat components play a vital role on the diversity and distribution of bryophytes. Barail Wildlife Sanctuary (BWS), situated in Southern Assam of Northeastern India was explored for its bryophyte wealth and an investigation was done on the influence of various ecological parameters on their microhabitats. A total of about 120 taxa (76 liverworts, 1 hornwort and 43 mosses) were identified from the sanctuary from six different microhabitats viz. forest floor, rocky surface, stem bark of higher plants, leaf of higher plants, streamside and decomposing wood. Ecological parameters like substrate pH, light intensity, moisture content, etc. were investigated. Canopy height, host leaf and stem architechture, etc. were also examined for the epiphytic (both corticolous and foliicolous) communities. It was found that bryophyte communities were most abundant on rocky surface and stem bark of higher plants followed by forest floor and leaf of higher plants. Genera like *Marchantia*, *Dumortiera*, *Conocephalum*, etc. were found to form the main components of rocky surface communities. Liverwort families like Lejeuneaceae, Plagiochilaceae and moss families like Fissidentaceae, Hypnaceae, Pottiaceae, etc. were found growing dominantly as epiphytes. *Cololejeune* a was reported as the most prolific liverwort genus growing as epiphyllous member. Bryophyte composition along streamside differed from rest of the microhabitats probably due to the submergence of the substrates during rainy seasons. It was observed that low pH of host bark is negatively associated with bryophyte richness. Hosts with corky rough barks retaining moisture and nutrients for the bryophytes were found to harbour large percentage of epiphytic bryophytes. Canopy height of hosts was also found to play significant role on growth of epiphytic bryophytes as higher light intensity and temperature near the canopy restrict the drought-intolerant and shade loving epiphytes to grow there. These findings can serve as a benchmark for future studies onbryophytes.

P.0029 Understanding bryophyte communities in the South Brazilian Atlantic Forest: a spatial and ecological distribution approach

Talita S. Dewes[1], Wanessa V. S. M. Batista[2], Juçara Bordin[3], Jorge L. Waechter[1]

1 Federal University of Rio Grande do Sul, Porto Alegre, Brazil. 2 University of Pernambuco, Petrolina, Brazil. 3 State University of Rio Grande do Sul, Osório, Brazil.

The Brazilian Atlantic Forest shows several vegetation types influenced by distinct climatic and soil conditions. One of these vegetation formations is the Hill Forests, occurring on shallow soils of hill slopes and tops. The spatial structure and floristic composition of woody vegetation is already known, unlike bryophytes. The aim of this study was to provide a first approach towards understanding bryophyte composition, richness, and distribution on Hill Forests. Three random plots (10m²) were sampled on each of three distinct hills (H1, H2, H3) located in northern coastal Rio Grande do Sul. All bryophytes were collected from subplots (20×20cm) on eight substrates: soil, rock, decomposing log, tree base, tree trunk, tree root, leaf, and branch. Spatial variables were derived from satellite image, whereas climatic and forest structure variables were recorded in situ. Multivariate analyses of clustering, ordinations, and statistical tests were performed with the software R 4.3.2. A total of 101 bryophyte species were recorded, belonging to the Marchantiophyta (60) and Bryophyta (41), distributed within 26 families, and 54 genera. The richest family was by far Lejeuneaceae (35). The highest species richness was found at H1 (70), followed by H3 (60), and H2 (44). The cumulative variance in the first two ordination-axes was quite explanatory (82.74%). The distance from the coastline (lower at H1) and the cover of the herbaceous layer (higher at H2) were variables that showed the strongest correlation with the sample sites. Floristic composition differed among sites (D = 0.48), but similarity analysis at the subplot scale pointed to higher floristic affinity between substrates ($p = P.01$, $r^2 = 0.39$). Our results highlight that environmental heterogeneity at both the regional and local scales influence bryophyte composition and distribution on Hill Forests. The advancement of this knowledge is essential to elucidate the effects of environmental changes on ecosystem processes.

P.0030 Redox capacity in Brittonodoxa subpinnata (Sematophyllaceae): insights from Brazilian rainforest and savannah environments

Adriana dos Santos Lopes[1], Cláudia M. Furlan[1]

1 Department of Botany, Institute of Bioscience, University of São Paulo, Brazil.

This study highlights the seasonal changes in the redox system of the tropical moss naturally occurring in two different forest ecosystems. The Tropical Atlantic Rainforest and the Brazilian Savannah are characterized by different seasonal fluctuations, imposing different environmental challenges for this avascular poikilohydric species. The research aims to learn how *B. subpinnata*'s redox system responds to seasonal changes through the investigation of key antioxidant enzyme activities (CAT and APX), contents of non-enzymatic antioxidants (AsA), and contents of the oxidative stress indicators (H_2O_2 and MDA). The statistical analysis was conducted using the R project (version 4.P.) with a Linear Mixed Model (LMM) and a non-parametric analysis (Kruskal-Wallis test) when data normality was not observed. The LMM revealed significant seasonal effects on CAT ($p<P.01$) and APX ($p<P.5$) activities, and on contents of reduced ascorbic acid ($p<P.00001$). Higher enzyme activities were observed during the dry period, especially in the Trpical Atlantic Rainforest, over 300% more activity compared to the Savannah. Higher concentrations of reduced ascorbic acid were also observed during the dry season, exhibiting a 108% increase in the Savannah and a 76% increase in the Tropical Atlantic Rainforest. A reduction in the reduced form of AsA levels is observed in the Trop-

ical Atlantic Rainforest, highlighting the significance of APX in modulating H_2O_2 levels, once this enzyme relies on AsA to regulate H_2O_2 levels. Despite seasonal shifts, the moss maintained comparable levels of H_2O_2 and MDA, indicating the effectiveness of the antioxidant system across both seasons and domains. During the dry season, *B. subpinnata*'s antioxidant system exhibited heightened enzyme activities, particularly in the Tropical Atlantic Rainforest, when meteorological variations between rainy and dry seasons are more pronounced.

P.0031 To study the diversity of mosses in Tirap, Arunachal Pradesh, India

Chimyang N[1,2], Evelin H[1]and Uniyal P.L[2]

1 Mycorrhizal Technology and Bryophytes Laboratory, Rajiv Gandhi University, Arunachal Pradesh, India. 2 Department of Botany, University of Delhi, Delhi, India.

An explorative study of mosses was conducted from 2021-23 in Tirap district of Arunachal Pradesh, a part of the Eastern Himalayas. Tirap is located in the eastern part of the state spanning an area of 2,362 square km with elevation ranging from 200–4,000 m above the sea level. The study documented 155 moss species, belonging to 82 genera and 28 families. The widely distributed taxa belonged to the families - Brachytheciaceae (16), Hypnaceae (13), Mniaceae (12), Meteoriaceae (11), Lecobryaceae (10), Polytrichaceae (9), Fissidens (9), etc. The majority of the taxa were documented from higher elevation (1,500-2,000 m). The terricolous mosses were the most dominant and is followed by epiphytic, epixylic and epilithic mosses. The study is a first report from this part of the state revealing a rich diversity of mosses. Besides increasing our knowledge on the mosses of this region, the study opens a plethora of opportunities to study their importance in the ecosystem.

P.0032 Macrolepiota procera as a source for Ag-mycogenic nanoparticles synthesis and their characterization

Muhammad Hanif[1,*], Fatima Arif[1]

*1 Department of Botany, Government College University, Lahore Pakistan. *dr.mhanif@gcu.edu.pk*

Fungi have the remarkable ability to secrete/produce proteins, polysaccharides, vitamins, and amino acids which can be incorporated as stabilizing, reductant, and capping mediators in the production of biogenic metallic nanomaterials. The prime objective of the research work was the mycosynthesis of biogenic metallic nanomaterials. The prime objective of the current study was *Macrolepiota procera* (Scop.) Singer extract-based production of silver-mycogenic nanoparticles (AgmyNPs) by solution combustion method. The AgmyNPs were characterized by various analytical techniques. They produce peculiar spectral peaks of UV–Vis spectroscopy at 380 nm, X-ray diffraction (XRD) at 2θ values of 38.1°, 44.1°, 67.4° and 77.7°. The XRD study also corroborates the presence of alkali metal that is Ag and face-centered cubic (FCC) structure of AgmyNPs, and Fourier-transform infrared (FTIR) spectroscopy form 800 to 3726cm^{-1} which confirmed the formation of the AgmyNPs. AgmyNPs were further investigated for their antibacterial potential against gram-positive bacteria (*Bacillus licheniformis*, *B. meuralis*) and gram-negative bacteria (*Azotobacter pasteurensis*, *A. rhizospherensis*). The antibacterial testing was executed at four different concentrations of the dilutions of the prepared by AgmyNPs employing well diffusion method. As compared to Penicillin, a standard antibiotic, AgmyNPs showed maximum zones of inhibitions of 8 mm, 2.25 mm against *A. parteurensis*, *A. rhizospherensis* while no inhibitory zone was observed against *B. licheniformis*. The excellent zone of inhibition was noticed against *B. meurilis*.

P.0033 Quantitative analyses of morphological variation in a calcified red alga Corallina berteroi

Miho S. Kitazawa[1], Safiye E. Sarper[2], Kazuya Horibe[3]

1 Osaka University, Toyonaka, Japan. 2 RIKEN BDR, Kobe, Japan. 3 RIKEN CBS, Wako, Japan.

Corallinales is an order of red algae (Rhodophyta), characterized by a calcified hard body. Coralline algae have recently attracted the attention of many researchers because of their importance in marine ecosystems and vulnerability to climate change. Recent studies on species identification by DNA barcode methods have revealed that marine macroalgae including coralline algae, show wide intraspecific variations in their morphology in response to the environmental changes. However, despite its ecological importance, the degree of this morphological plasticity is not fully documented. Therefore, we quantified the morphological diversity of segmented coralline algae sampled in March and November 2022 from western and northern Japan. Most of our specimens were identified as a universally distributed species, *Corallina berteroi*, by mitochondrial cytochrome c oxidase subunit I (COI) sequence. Segmented coralline algae have branched thallus, composed of repetitions of calcified hard regions (intergenicula) and flexible non-calcified nodes (genicula). Quantitative analyses of intergeniculum shape using the Elliptical Fourier Transformation method followed by Principal Component Analysis showed that one axis (PC1), corresponding to a shape change between wide fan shape and narrow rectangular shape, explained approximately 60 % of the shape variation in autumn specimens. PC1 showed a correlation with branching numbers at the distal node of the intergeniculum, suggesting that PC1 can describe the complexity of branching patterns. Sampling from several sites with different environmental conditions suggested several candidates for environmental factors that cause shape differences along the PC1 axis, such as temperature, pH, and agitation by waves. For instance, specimens with wider intergeniculum shapes tended to inhabit tide pools characterised by lower temperature and pH. Spring specimens showed larger variations and tended to show wider shapes, suggesting temperature as a primary candidate, though further examination, especially laboratory cultivation, is required to conclude.

P.0034 Diversity and phylogeny of endolichenic fungi associated with Parmotrema and Heterodermia lichens of Shivamogga, India

Y. L. Krishnamurthy[1], D. Pusphavathi1

1 Dept. of Applied Botany, Kuvempu University, Shankaraghatta, Karnataka, India.

Lichen is a symbiotic association of algae and fungi, recognized as self-sustaining ecosystem constitute indeterminant number of bacteria, actinomycetes, fungi, and protozoa. We evaluated the endolichenic fungal assemblage in view of the dearth of knowledge on endolichenic fungi (ELFs), particularly from part of central western Ghats, Karnataka, and analyzed phylogenetic position using ITS and ITS+Tub2 gene set. Out of 17 lichen thalli collected from 5 ecoregions, recovered 42 morphospecies, belongs to the class Sordariomycetes, Eurotiomycetes, Dothideomycetes, Leotiomycetes, Saccharomycetes. About 19 and 13 ELFs genera have been reported from *Parmotrema* and *Heterodermia* thallus. Among the ecoregions EC2 showing highest species diversity (*Parmotrema* (1-D) = 0.9382, (H)=2.865, Fisher-α =8.429, *Heterodermia* (1-D) = 0.8038, H = 1.894, F-α =4.57) followed the EC3 and EC1. Xylariales are predominant colonizer reported from at least in one thallus from four ecoregions. Species delimitation and phylogenetic position reveals the closest resemblance of Xylariaceous ELFs with plant endophytes. In addition, the non-sporulating isolate ELFX04, ELFX05, ELFX08 and ELFX13 form monophyletic clade with *Xylaria psidii, X. feezeensis, X. berteri* and *Hypoxylon fragiforme* respectively. The observation highlights that the deciduous forest harness high number of endolichenic fungi and dominant portion of these fungi are non-sporulating, still exist as cryptic. Beside the phylogenetic analysis, two endolichenic isolated namely ELFX03 and ELFX06 will not have BLAST similarity and not form clades with any of the described species. Highlighting the importance of successful amplification of most phylogenetic markers like RPB2, building of comprehensive taxonomic databases and application of multi-omics data are further needed to understand the complex nature of endolichenic fungi.

P.0035 Seasonal shifts in moss secondary metabolome and phenology in response to altitude

Brenda Riquelme[1,2], Roy Mackenzie[1,2], Leonardo Pérez de Souza[3], Matías Troncoso[1], Javier Martínez-Abaigar[4], Encarnación Núñez-Olivera[4], Jonathan Maldonado[5], Bernard Goffinet[6], Liu Yang[7]

1 Universidad de Magallanes, Cape Horn International Center, Puerto Williams, Chile. 2 Millennium Institute Biodiversity of Antarctic and Subantarctic Ecosystems, Santiago, Chile. 3 Department of Molecular Physiology, Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany. 4 Universidad de La Rioja, Facultad de Ciencia y Tecnología, Logroño, Spain. 5 Dept. of Biology, Faculty of Chem-

istry and Biology, Universidad de Santiago de Chile, Santiago, Chile, 6 Key Laboratory of Southern Subtropical Plant Diversity, Fairy Lake Botanical Garden, Shenzhen & Chinese Academy of Sciences, Shenzhen, China. 7 Dept. of Ecology and Evolutionary Biology, University of Connecticut, Storrs, USA.

The acclimation responses of bryophytes to environmental variability involve genetic regulation and the synthesis of various secondary metabolites that play roles in DNA repair, antioxidative defense, structural biopolymer for dehydration tolerance, and many other processes. We compared the secondary metabolomes and the reproductive phenology of *Polytrichum strictum*, a significant pioneer moss species in polar tundra environments. The sampling was done during austral spring, summer and autumn in two distinct tundra ecosystems on Navarino Island, Chile: in a high mountain site at 620 m.a.s.l. and a Sphagnum peatland site at 60 m.a.s.l. Using an LC-HRMS platform and an untargeted approach, we analyzed the polar/medium polarity metabolome of *P. strictum*. Results were processed using the GNPS platform, and molecular networking facilitated the annotation of metabolites. Besides, we also monitored the development of the sporophytes every month for two years. Our results show that biflavonoids, flavonoids, and coumarins are the most diverse groups of secondary metabolites in *P. strictum*, suggesting their potential involvement in various stress response mechanisms. Differences in the moss metabolome were observed between the compared sites during the same season. On the other hand, we found a remarkable shift in the reproductive phenology of P. strictum in both populations studied. We hypothesize that phenological stages and some key metabolites are mainly influenced by a mixed effect of altitude and seasonality. This study highlights the plasticity of subantarctic bryophytes, shedding light on how these organisms respond to environmental changes in polar tundra ecosystems.

P.0036 A revision of the genus Groutiella (Orthotrichaceae, Bryophyta) in the Greater Antilles.

Amelia L. Mateo Jiménez1[2,3], Francisco Lara[2,4], Ricardo Garilleti[5], Isabel Draper[2,4]

1 Universidad Autónoma de Santo Domingo, Santo Domingo, Dominican Republic. 2 Departamento de Botánica, Universidad Autónoma de Madrid, Madrid, Spain. 3 Doctoral School (EDUAM), Universidad Autónoma de Madrid, Madrid, Spain 4 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain. 5 Universidad de Valencia, Spain.

Groutiella Steere is a small genus of about ten species in the subfamily Macromitrioideae. Although it has undergone a recent global revision, its diversity in the Caribbean has not previously been addressed. The different islands of this region, including Cuba, Jamaica, Puerto Rico, and Hispaniola, offer a wide range of habitats derived from climatic variations along elevational gradients and environmental alterations caused by natural disasters and human land use. This ecological heterogeneity seems optimal for the establishment of different species of *Groutiella*, which are relatively phytophilous and xerophilous mosses that primarily grow as epiphytes, but can also be found on rocks, in humid tropical environments. To understand the complexity of the group and its distribution across the major Caribbean islands, our review has been based on the examination of herbarium material (JBSD, NYBG, and MAUAM), complemented by own collections gathered through elevational transects in several mountain areas of the Dominican Republic. Our results indicate that up to ten species of *Groutiella* can be recognized in the Greater Antilles. One of these is a new record for the region, and two are proposed as new species for science. Only four species are widespread, with one found on all four islands, and three on three of them. Two species are shared by two islands, while the remaining four are exclusively found on one island. Hispaniola harbors the highest diversity, with seven species (six from Dominican Republic and five from Haiti), followed by Cuba with six species. Overall, *Groutiella* has been recorded across nearly the entire elevation range of the region, from 100 to 2200 m asl, inhabiting various vegetation types, including low-altitude coffee cultivation areas, tropical rain forests, and mountain pine forests.

P.0037 Diversity of mosses in Papum Pare District, Arunachal Pradesh, India

Pherkop Mossang[1,2], NonyaChimyang[1,2], Vinay Shankar[3], P.L. Uniyal[2], Heikham Evelin*[1]

1 Mycorrhizal Technology and Bryophytes Laboratory, Department of Botany, Rajiv Gandhi University, Arunachal Pradesh, India. 2 Department of Botany, *University of Delhi, Delhi, India. 3 Department of Botany, Gaya College, Gaya, India. *heikham.evelin@rgu.ac.in*

Arunachal Pradesh is one of the Northeastern states of India and falls under the Indo-Burmanand the Eastern Himalayan Biodiversity hotspots. The state is known for housing diverse, rare and endemic flora, however the information on moss diversity is very scarce. Therefore, we investigated the diversity of mosses in Papum Pare District of Arunachal Pradesh, India. The study revealed a total of 130 species belonging to 51 genera and 37families of mosses. The family Hypnaceae has the highest members of species with 14, followed by Neckeraceae (10 species) and then followed by Bartramiaceae, Bryaceae, Pottiaceae and Polytricaceae, each family with eight species in it. The members of families like Meteoriaceae, Neckeraceae, Stereophyllaceae and Thuidiaceae were observed growing epiphytically. While the members of Bartramiaceae, Brachytheciaceae, Bruchiaceae, Fissidentaceae and Hypnaceae were mostly found flourishing on terrestrial habitat. Other families such as, Bryaceae, Ditrichaceae, Pottiaceae preferred growing on rocks and cemented walls. In addition, members of Bryaceae, Hypnaceae and Neckeraceae were observed to be most frequent occurring of all the families. This study provides the first ever report on the Bryophytes of Papum Pare District of Arunachal Pradesh. Evidently, different seasons and humid climatic condition favours the growth of many unique and remarkable moss species, possibly including those species facing threats and are at the brink of extinction. Consequently, more research is necessary to increase our comprehension and awareness of the diversity of mosses in the study area.

P.0038 Climate change impacts on tropical lowland understory bryophytes

Nada Nikolić[1], Gerhard Zotz[2], Maaike Y. Bader[1]

1 Faculty of Geography, University of Marburg, Marburg, Germany. 2 Institute for Biology and Environmental Sciences, University of Oldenburg, Oldenburg, Germany.

Bryophytes and lichens are increasingly recognized for their important functional roles in many ecosystems. Although taxonomically unrelated, these cryptogams have a common ecophysiologically relevant feature, they are both poikolohydric. As poikilohydric organisms, they equilibrate their water content with the environment moisture conditions. Since their hydration status fluctuates strongly, their physiological activity varies accordingly, ceasing when they dry out and resuming as they are rewetted, resulting in carbon balances that are strongly coupled with the microclimate. In some habitats these microclimate-restricted carbon balances might be the reason for low bryophyte and lichen abundance and biomass, like for example in the understory of tropical lowland forests. To test this and to gain insights in future tropical-bryophyte carbon balances, we conducted a climate-change simulation experiment in the rainforest of La Selva, Costa Rica. During the 18 months of experiment, we followed and measured survival, growth, drying rates and responses of CO_2 exchange to environmental conditions for several bryophyte species exposed to warming and/or CO_2 fertilisation. Parallel to the experiment, we used a model we developed to estimate carbon balances based on microclimatic input data (collected in situ, during the experiment), with water absorption and loss, net photosynthesis and dark respiration as rate variables, and carbon gain through time as the main output. Here we present part of the results from the experiment and a comparison between carbon balances modelled based on our understory microclimatic data and climate data from the field station to stress out the importance of temporally and spatially fine-resolution microclimate data for ecophysiological, ecological and biogeographical studies of these tiny poikolohydric organisms.

P.0039 An approach to the bryological flora of Cuba, with emphasis on hornworts (Anthocerotophyta)

Yoira Rivera-Queralta[1]

1 Centro Oriental de Ecosistemas y Biodiversidad (Bioeco), Cuba.

The Caribbean comprises a set of islands of different ranges, sizes, altitudes, soil types, and environmental niches; it is extremely complex including its geology and biogeography. In the region, the island of Cuba has one of the richest insular floras in the world and is considered one of the hotspots for biodiversity. Despite the advances in Cuban bryology, it is still considered insufficiently explored mainly referring to its taxonomy, ecology, and population status. The present study, based on a literature review and consultation with specialists, updates the status of the diversity of Cuban hornworts. Ecological niche models are developed based on environmental and biotic variables to determine the potential distribution of the group. In the National System of Protected Areas, the representation of the group is also analyzed, and conservation actions are proposed. Fifteen infrageneric taxa are recognized, three of which are considered doubtful records. The greatest diversity of hornworts is recorded in the humid forests of the eastern region of the island.

P.0040 Approach to the checklist of marine macroalgae of the Balearic Islands

Lluís Salom-Vicens[1], Pere M. Mir-Rosselló[1], Marcello Dante Cerrato[1], Llorenç Gil[1], Carles Cardona[1,2], Samuel Pinya[1]

1 Universitat de les Illes Balears, Palma, Spain. 2 Centre Forestal de les Illes Balears, Escorca, Spain.

Marine macroalgae play a crucial role in coastal ecosystems, contributing to biodiversity and serving as environmental health indicators. Therefore, updated and unified checklists are required as a baseline for further studies. This study compiles a preliminary checklist of the macroalgae recorded in the western Mediterranean archipelago of the Balearic Islands. A checklist was compiled consulting published manuscripts, online datasets (GBIF), citizen science projects (Biodibal), and fieldwork on the 4 main islands. Our data reveal a total of 314 different species of macroalgae inhabit the Balearic Sea. The largest number of species was found in Cabrera (258), a National Park that has been object of high sampling effort, while the average number of species for the other islands is 63,75. This highlights the lack of work on marine macroalgae in the four main islands. The most represented taxonomic group in the archipelago are Rhodophyta (198 species), Ochrophyta (67 species) and Chlorophyta (49 species). Up to 10 species (3%) are considered as invasive. Cabrera has a similar algae proportion to the entire archipelago, with Rhodophyta at 63%, Chlorophyta at 16%, and Ochrophyta at 21%. For the remaining islands, excluding Mallorca, Ochrophyta are the most abundant, followed by Rhodophyta and Chlorophyta. Comparing the Balearic Islands with Cyprus, located on the opposite side of the Mediterranean, reveals that despite sharing the same total number of species and nearly identical counts of alien species, they exhibit distinct proportions in taxonomic groups. Variations in proportions become evident across the diverse islands situated in the central Mediterranean. This checklist allows to make a first approximation on the marine phycological composition of the Balearic Islands and highlights the necessity to implement bases that facilitate future phycological studies in the Balearic Islands. It also serves as a knowledge repository for future research in marine ecology and habitat conservation.

P.0041 Ecological dynamics of Subarctic lichen communities under snow cover: insights and implications

Lilith Weber[1], Pekka Niittynen[2], Julia Kemppinen[3], Leena Myllys[1], Miska Luoto[4], Nick Pepin[5], Annina Kantelinen[1]

1 Finnish Museum of Natural History, University of Helsinki, Finland. 2 Department of Biological and Environmental Science, University of Jyväskylä, Finland. 3 Geography Research Unit, University of Oulu, Finland. 4 Department of Geosciences and Geography, University of Helsinki, Finland. 5 Department of Geography, University of Portsmouth, UK.

Arctic ecosystems are changing rapidly, with widespread reports of increasing air temperature and decreasing snow cover area and duration. Previous studies investigating the composition and spatial patterns of cryptogam communities in the Arctic and Subarctic have mainly considered large warming thermal gradients and were limited in their representation of small-scale and near-ground spatial variability of snow and vegetation. The general importance of snow conditions for lichens has been widely acknowledged, but snow information and microclimatic data are rarely available or utilized. In our study, we inventoried the complete lichen community present at 74 sites in two areas of Finnish Lapland. We are utilizing microclimatic data from a network of loggers, which directly provide information on temperature and humidity from the sampling plots. This was supplemented by manual snow depth measurements on-site, as well as fine-scale satellite imagery. Focusing on the epiphytic lichen community in the typical mountain birch (*Betula pubescens* ssp. *chzerepanovii*) forests we found a previously unknown diversity of species as well as a significant impact of snow on the species composition and distribution of taxa along the birch stems. This is not only noticeable for such well-known examples as *Parmeliopsis ambigua* and *Melanohalea olivacea* but also for several crustose species. Identifying specialists that are adapted to specific snow conditions is crucial for assessing the effect of climate change on subarctic lichen communities.

P.0042 Which better explains the distribution of the lichen species, the mesoclimate or the microclimate? Menegazzia in Chile, study case

David Alors[1], Johana Villagra[1], Quiñones Natalia[2], Cecilia Rubio[2], Jarle W. Bjerke[3]

1 Department of Biology and Chemistry, Universidad Católica de Temuco, Temuco, Chile. 2 Farmacy Faculty, Universidad de Valparaiso, Valparaiso, Chile. 3 The Arctic–Alpine Botanic Garden Tromsø, Tromsø, Norway.

The *Menegazzia* genus comprises up to 18 species in Chile inhabiting the cold temperate climate from the relic forest of Fray Jorge to the Antarctic and Magallanes Region. Out of the 18 species 16 were recorded in the Conguillío National Park (Rubio et al. 2013) The other two species, *M. megalospora* and *M. magellanica* are endemic of the southernmost regions of Chile. We installed 20 temperature and humidity sensors (ibuttons) in the forests of the Conguillío National Park on the trunk of different trees. In addition to recently collected samples we used information form the herbarium (UV). By comparing the occurrence of the *Menegazzia* species in the Conguillío National Park associated to microclimatic sensor and the occurrence of *Menegazzia* species at regional scale (centre-south and South Chile) we want to characterize the niche preference of *Menegazzia* species and identify which one is a better predictor of occurrence microclimate or mesoclimate. Finally, we discuss the vulnerability of the species in the context of global warming. Acknowledgments: This study is part of the project Fondecyt de Iniciación en Investigación 11230474. References: Rubio, C., Saavedra, M., Cuéllar, M., Díaz, R., & Quilhot, W. (2013). Epiphytic lichens of Conguillío National Park, southern Chile.Gayana Botanica,70(1), 66-81

P.0043 Specific whole-chromosome identification through oligonucleotide-based chromosome painting in Brassica species

Mariana Baez[1], Ludwig Mann[2], Tony Heitkam[2], Annaliese Mason[1]

1 Plant Breeding Department, University of Bonn, Bonn, Germany. 2 Institute of Botany, Technische Universität Dresden, Dresden, Germany.

Brassica is a good model for studying polyploidization and for utilisation of interspecific hybridization for crop improvement, as the *Brassica* genus includes diploid species (2n = 2x = 16, 18, 20) and their allotetraploid hybrids (2n = 4x = 34, 36, 38). Interspecific hybrids between all these species show varying frequencies of non-homologous recombination between genomes which can be important for introgression breeding and production of new varieties. Hence, identification of individual homologous and homoeologous chromosome pairs from different subgenomes in these species is important for studies of plant breeding and evolution. Here, the aim is to develop and demonstrate the advantage of oligo-based painting probes in identifying subgenome-specific chromosome pairs. This method will allow high-precision analysis of chromosome rearrangements and introgression events between the *Brassica* subgenomes in established and synthetic allopolyploids and interspecific hybrids. Diploid A, B, and C genomes from *B. rapa*, *B. nigra*, *B. oleracea* and allopolyploid subgenomes AB, AC, and BC from *B. juncea*, *B. napus*, and *B. carinata* were used for the probe design. Oligos specific to chromosomes *B. napus* A01 ($A^{n}01$) and *B. rapa* A01 ($A^{r}01$) and to *B. napus* C1 ($B^{n}C1$) and *B. oleracea* C1 ($B^{o}01$) were selected. Oligo painting probes for chromosome A01 (*B. rapa*) and chromosome C1 (*B. oleracea*) were designed, with a total of 20,000 and 27,000 oligo sequences, respectively, with high specificity along the chromosome length. Probes showed high *in silico* specificity to these chromosomes within allopolyploids containing A/C subgenomes. Fluorescence *in situ* hybridization analysis using the A01 oligo probe on *B. rapa* and *B. napus* mitotic chromosomes identified one single chromosome pair. Current fluorescence *in situ* hybridization analysis using these oligo-based probes is underway in other *Brassica* species to confirm this specificity.

S.007. ADVANCES IN PHYLOGENOMICS AND SYSTEMATICS OF THE BRASSICACEAE

P.0044 Taxonomic notes of the Aethionema armenum (Brassicaceae) complex in Turkey

Kuddisi Ertuğrul[1], Tuna Uysal[1], Meryem Bozkurt[1], Hakkı Demirelma[1], Emrah Şirin[1], Burcu Y. Çitak[1]

1 Department of Biology, Faculty of Science, Selçuk University, Konya, Turkey.

The genus *Aethionema* W.T.Aiton is represented by 60-70 species in the world, and most of them are distributed in the Iran-Turan phytogeographic region. The genus is represented by 57 taxa in Türkiye. Türkiye is not only the main gene center for the genus, but also the main center of diversification along with Iran. *Aethionema* is one of the taxonomically problematic genera within the Brassicaceae family. One of the species that shows the most variation within the genus is *Aethionema armenum* Boiss.. Even, four of the 12 new species recently published are closely related to this species. For this purpose, the morphological variation and phenetic relationships of the populations of *A. armenum* complex collected from different localities in Türkiye were investigated. Additionally, the internal transcribed spacer (ITS) sequences of nuclear ribosomal DNA (nrDNA) of the populations of species were analyzed. Morphometric data were analyzed with the PRIMER program. Parsimony and Bayesian analyzes were performed using PAUP and MrBayes programs, respectively. As a result, many taxa related to *A. armenum* need to be synonymized (*A. ertughrulii* Yıld., *A. alidaghenicum* Yıld. and *A. dumelicum* Yıld.), and many taxa previously considered synonymous (*A. pseudoarmenum* Stapf & Sprague and *A. recurvum* Hausskn. & Bornm.) within the *A. armenum* complex need to be resurrected. Acknowledgements: We are also grateful to the foundation TUBITAK (Project Number: 118Z995) and S.U.BAP (Project Number: 20401025) for financial support.

P.0045 Resolving the Brassicaceae Tree of Life backbone using the mitogenome

Lisa J.M.A. Dominicus[1], Kasper P. Hendriks[1,2], Ihsan A. Al-Shehbaz[3], Dmitry A. German[4], Klaus Mummenhoff[2], Frederic Lens[1]

1 Functional Traits, Naturalis Biodiversity Center, Leiden, The Netherlands. 2 Department of Biology, Botany, University of Osnabrück, Osnabrück, Germany. 3 Missouri Botanical Garden, St. Louis, USA. 4 South-Siberian Botanical Garden, Altai State University, Barnaul, Russia.

The mustard family (Brassicaceae; ~4,000 species) is a medium-sized family with great economical and scientific importance, including many crops and the ultimate plant model species *Arabidopsis thaliana* and *Brassica napus*. However, despite its importance, species relationships within the family remain partly unresolved, especially the deeper relationships ('backbone'). Recent studies based on nuclear and chloroplast DNA sequences showed cytonuclear discordance and difficulties in resolving backbone relationships and consistently placing rogue taxa in the phylogeny. However, little research has been done on the use of the mitogenome in resolving species relationships. This is possibly explained by the fact that mitochondrial DNA evolves slowly and is maternal inherited, which in fact could contribute to resolving the backbone and confidently positioning the rogue taxa within the family. Here we present the most complete and robust mitogenomic phylogeny of the Brassicaceae, including ~400 species, all 349 genera, and all 58 tribes, based on sequence data of introns and exons of 40 mitochondrial genes. While work in progress, we expect our results will increase our confidence in backbone relationships within the family, providing further insight into the origins of the subfamilies and supertribes, which will aid scientists comparing species from different clades within the family.

P.0046 Progress in reconstructing the evolutionary history of arctic and alpine Draba (Brassicaceae)

Ingrid E. Jordon-Thaden[1,2]

1 University of Wisconsin Madison, Madison, USA. 2 Florida Museum of Natural History, University of Florida, Gainesville, USA.

Draba is a species rich and morphologically and ecologically diverse lineage, and genomic changes within their ~6-9 million year history have been rapid, resulting in extraordinary trait variation and is the largest in the Brassicaceae. *Draba* have a range of reproductive modes, sexual systems, hybridization types, polyploid levels, ecological niches, and distribution types throughout the arctic and alpine habitats they inhabit. The phylogenetics and phylogeography of *Draba* have been studied extensively and have advanced our understanding of evolutionary relationships and historical processes. Nevertheless, additional work is needed to gain a more inclusive view of *Draba* and resolve relationships among its 400+ species. A lack of a well resolved phylogenetic tree for *Draba* limits use of many comparative approaches that require “comprehensive” sampling, hampering our ability to test hypotheses and elucidate evolutionary patterns and events. This presentation summarizes existing work, particularly with North American *Draba*, that has been completed over the last decade and highlights creative ways to tackle many remaining questions concerning this large genus. I will explain how I am using genome sequences and population-level genomics approaches focusing on widespread and endemic taxa to obtain a clearer picture of evolutionary history, apomixis, and hybridization dynamics within this complex genus. The history of *Draba* features exciting stories involving long-distance dispersal, glacial refugia, and cryptic speciation, all of which occurred during the most recent ice ages, making this an excellent system in which to understand plant evolutionary dynamics in response to climate change.

P.0047 Adaptive potential and long-term evolutionary success of a clonally reproducing plant species

Marcus A. Koch[1], Nora Walden[1]

1 Center for Organismal Studies (COS) Heidelberg, Department of Biodiversity and Plant Systematics, Heidelberg University, Heidelberg, Germany.

Sexual reproduction is known to drive plant diversification and adaptation. However, it is intriguing to study vegetatively reproducing systems adapting to broader environmental conditions. Here we investigate the evolutionary and spatiotemporal history of a dodecaploid Eurasian deciduous woodland species, *Cardamine bulbifera*, which reproduces and spreads via vegetative structures only. The species has been among the most successful range-expanding understorey woodland plants in Europe, raising the question of the genetic architecture of its gene pool, since its hexaploid but putatively outcrossing closest relative, *C. quinquefolia*, displays a smaller distribution range in Eastern Europe towards the Caucasus region. *Cardamine bulbifera* is of early Pleistocene origin, with a history of past gene flow with its hexaploid sister species *C. quinquefolia*, likely during the last glacial maximum in shared refuge areas in Eastern Europe, Western Turkey and the Crimean Peninsula region. Caucasian endemic diploid *C. abchasica* is considered an ancestral species providing additional evidence for the origin of the species complex in the Caucasus region. *Cardamine bulbifera* successfully expanded its distribution range postglacially towards Central and Western Europe accompanied by a transition to exclusively vegetative propagation being the major innovation to rapidly expand the distribution range following postglacially progressing woodland vegetation throughout Europe. In northeastern Austria we discovered a refuge population system along the very biodiversity-rich Thaya valley harboring genotypes from the ancestral but also the recently colonized areas. Plastome data and nuclear genomic ddRAD analyses of the population system indicate prevalence of five clonotype groups in particular ecological woodland niches referring to six genetic clusters in total as revealed by admixture and SplitsTree analyses including the ancestral species. All eastern plastome types co-segregate with the respective proportion of the nuclear genome indicating limited geneflow and long-term persistence of clonal variants contributing to population-level fitness and adaptive potential.

P.0048 Evolutionary new centromeres in Arabideae genomes

Petra Hloušková[1], Stanislav Kostiuk[1,2], Milan Pouch[1,2], Terezie Mandáková[1,3], Martin A. Lysak[1,2]

1 Central European Institute of Technology, Masaryk University, Brno, Czech Republic. 2 National Centre for Biomolecular Research, Faculty of Science, Masaryk University, Brno, Czech Republic. 3 Department of Experimental Biology, Faculty of Science, Masaryk University, Brno, Czech Republic.

In the Arabideae (Brassicaceae), centromere repositioning has been proposed as a key mechanism differentiating otherwise collinear chromosomes between species. In ten species, more than 30 evolutionary new centromeres (ENCs) were identified by cytogenomic analyzes. Here, we performed whole-genome sequencing and *de novo* assembly in six Arabideae species. By combining PacBio HiFi and ONT nanopore sequencing, we obtained a telomere-to-telomere genome assembly for the early-diverging *Pseudoturritis turrita* and two species of more recent origin (*Draba nemorosa* and *D. podolica*). In *P. turrita*, the 0.58- to 1.25-Mb "paleocentromeres" consist of four tandem repeats (monomer size 149, 176, 186 and 63 bp) and LTR retroelements (Ale, CRM, Retand). Compared to centromere positions in *P. turrita*, centromeres were repositioned by 4 Mb (median) in *D. nemorosa* and by 17 Mb in *D. podolica*, with both *Draba* species sharing the structure of all eight chromosomes including relative centromere positions. In *D. nemorosa*, centromeres (0.47 to 2.14 Mb long) consist mainly of 145-bp satellite arrays invaded by Ale retrotransposons. In *D. podolica*, seven centromeres (0.99 to 2.41 Mb long) are dominated by Ale elements, while only one centromere contains both the 145-bp satellite and Ale retrotransposons. As centromeres in both *Draba* species have the same positions, we propose that the ENCs predate the speciation and that the species-specific centromere differentiation occurred later. Satellite-based vs. retrotransposon-rich centromeres and short vs. long centromere shifts in the two *Draba* species reflect their different genome size and repeat content (155 Mb and 30% in *D. nemorosa*, 493 Mb and 69.1% in *D. podolica*). In *Draba* genomes, 50% of ancestral centromeric regions show no apparent structural signatures, whereas the other half of paleocentromere sites were reshuffled by multiple small-scale inversions. Acknowledgments: This work was supported by the Czech Science Foundation (grant no. 23-06840S).

P.0049 Dispersion, speciation and diversification patterns of the Erysimum genus across the Macaronesia

Melissa Viveiros Moniz[1], Modesto Berbel[1], Ana García-Muñoz[1], José María Fernandez Palacios[2], Miguel Menezes de Sequeira[3], Silvia Castro[4], João Loureiro[4], Mohamed Abdelaziz[1], A. Jesús Muñoz Pajares[1]

1 Departamento de Genética, Universidad de Granada, Granada, Spain. 2 Island Ecology and Biogeography Group, Instituto Universitario de Enfermedades Tropicales y Salud Pública de Canarias, Universidad de La Laguna, Spain. 3 Madeira Botanical Group, Faculty of Life Sciences, University of Madeira, Funchal, Portugal. 4 Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal.

Dispersal and local colonizations have a significant role in the dispersion of species from continents to oceanic islands and among these islands. A high degree of endemic biodiversity is a typical characteristic of oceanic archipelagos, such as the ones that form the Macaronesia biogeographic unit. Combining genomic and climatic data, the evolutionary trends and speciation patterns of the *Erysimum* species inhabitant to the Macaronesia were established based on phylogenetic analyses, population structure analyses, and niche modeling. Phylogenetic analyses were performed for single nucleotide polymorphisms (SNP) from whole nuclear genomes and whole plastidial DNA sequences using two methods: maximum likelihood (ML) and Bayesian inference (BI), with the RAxML and MrBayes software, respectively. SCalable pOPulation structure inferencE (SCOPE) was used to perform a model-based clustering analysis on both SNP and cpDNA data. The ecological contribution of several environmental variables was assessed using the MaxEnt software and niche overlapping indices were calculated in R. *Erysimum* colonizations in the Macaronesia appear to have started with a common continental ancestor and later occurred dispersal to Madeira. After speciation and polyploidization, *Erysimum* dispersed to the Canary Islands, spreading across the archipelago, and at last to Cabo Verde. We believe that the polyploidy of *Erysimum* might have been a contributing factor to the overall success of its colonization. Our results also suggest that local adaptation took place in the Canary Islands, where two different species haveadapted to different habitats (high mountain vs. shadowed lower altitude areas) and constrained gene-flow is occurring between individuals of the same species across different islands. Climate modeling results confirmed that the species present in the same islands have their own distinct ecological boundaries.

P.0050 Effects of ploidy and genetic diversity on the heterosis patterns exhibited by a selfing clade

Carlos Olmedo-Castellanos[1], Ana García-Muñoz[1], Camilo Ferrón[2], A. Jesús Muñoz Pajares[1], Mohamed Abdelaziz[1]

1 Department of Genetics, Faculty of Sciences, University of Granada, Granada, Spain. 2 Biodiversity & Conservation Area, Rey Juan Carlos University, Madrid, Spain.

Outbreeding Response is the difference between phenotypic traits in cross-pollinated (outcrossing) offspring versus their self-pollinated (selfing) parentals (heterozygote vs. homozygote, as genetic diversity is lower in selfing individuals compared to outcrossing individuals). Heterosis is the phenomenon in which offspring shows a higher fitness than the average of both parents. Although heterosis is widely known for its role in agriculture, it has a key role in evolutionary processes. In highly inbred selfing plant populations, it is likely to accumulate recessive alleles that are masked in heterozygote loci. Thus, once they are found again in heterozygosis, there could be a positive effect in phenotype and fitness. One example is *Erysimum incanum*, a selfing species located in the Iberian Peninsula and Morocco which has three ploidy levels. To study heterosis, we measured a series of traits related to floral and plant size as well as fitness components of selfing and outcrossing offspring from controlled crosses in greenhouse for every ploidy level. With these data, we calculated individual contribution to heterosis for and we estimate its relationship with individual fitness (as the product of seeds and fruits). Also, we analysed how evolvability could be affected by heterosis levels in each trait, heterozygosity and ploidy levels to see if evolutionary potential changes with these variables. According to the results, there are significant heterotic patterns which would be relevant to understand the evolutionary history of these populations that could stand for a promotion of cross-pollination in these selfing populations.

P.0051 Deciphering the evolutionary puzzle of Erysimum (Brassicaceae): insights from phylogenomic, chromosome number and genome size data

Marek Šlenker[1*], Richard Bačák[2], Barbora Šingliarová[1], Terezie Mandáková[3,4], Katarína Skokanová[1], Ingrid Turisová[2], Peter Turis[2], Janka Smatanová[1], Adam Kantor[1], Judita Zozomová-Lihová[1**]

*1 Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovakia. *marek.slenker@savba.sk; **judita.zozomova@savba.sk 2 Department of Biology, Ecology and Environment, Faculty of Natural Sciences, Matej Bel University, Banská Bystrica, Slovakia. 3 Central European Institute of Technology, Masaryk University, Brno, Czechia. 4 Department of Experimental Biology, Faculty of Science, Masaryk University, Brno, Czechia.*

Erysimum is a genus characterized by extensive species diversity and evolutionary complexities, displaying recent and rapid diversification, notable karyological diversity, instances of cryptic species and hybridization within specific groups. This intricacy is exemplified in two taxonomically unsettled species complexes, *E. odoratum* and *E. virgatum*, distributed across central and southeastern Europe and each harboring several endemics, which prompted us to investigate their evolution, phylogenetic relationships, genome structure and polyploidy. The *E. odoratum* complex is revealed to be non-monophyletic, as it splits into unrelated Carpathian and Balkan lineages. The widely distributed tetraploid *E. odoratum* s.str. (2n=32) shows substantial, geographically structured genetic diversity, encompassing populations with reduced chromosome number (2n=22), indicative of ongoing post-polyploid descending dysploidy, as well as a phylogenetically nested clade of Carpathian diploids. Genome-wide analyses of Carpathian diploids demonstrate geographic rather than taxonomic structure, with Western, Eastern (both 2n=14), and two Southern Carpathian (2n=14 and 2n=16) lineages identified. While morphological distinctions between the tetraploid *E. odoratum* and the Carpathian diploids are evident, differentiation among the diploids is subtle, regardless of whether one considers traditional taxonomic treatment or genetic structuring. Phylogenetic patterns within the Balkan lineage support the existence of three related diploid species (2n=12), displaying exceptionally high (up to 2-3-fold) and geographically structured genome size variation. Transitioning to the *E. virgatum* complex, it comprises two sister lineages differing in genome size, despite sharing the same hexaploid level. The Carpathian lineage includes three related endemics, while the Alpine lineage exhibits east-west differentiation and includes lower-altitude relatives. Our results underscore the significance of isolation by distance as a major factor contributing to differentiation in both species complexes. Furthermore, the observed patterns suggest that their evolution may be influenced by genomic processes such as large-scale chromosomal rearrangements and proliferation of repetitive DNA.

S.008. ADVANCES IN SEED CONSERVATION OF WILD SPECIES

P.0052 Compatibility of entomopathogenic nematodes with plant extracts and post-exposure virulence test under laboratory condition

Adeola Abiola Oso[1], Tshimangadzo Ramakuwela[2], Anofi Omotayo Tom Ashafa[1]

1 Department of Plant Sciences, Faculty of Natural and Agricultural Sciences, University of the Free State, Phuthaditjhaba, Republic of South Africa. 2 Insect Pathology Unit, Agricultural Research Council- Small Grain, Bethlehem, South Africa.

The efficacy of both botanical pesticides and entomopathogenic nematodes (EPN) is largely dose-dependent and driven by environmental conditions. Combination of the EPNs and botanicals may enhance their efficacy; thus, we investigated the compatibility of the medicinal plants *Alepidea amatymbica* and *Elephantorrhiza elephantina* with five locally isolated EPN strains, three Steinernema (*S. khoisanae*, *S. biddulphi* and *S. innovationi*) and two Heterorhabditis (*H. bacteriophora* and *Heterorhabditis sp.* SGI 244). The experiments were designed to evaluate EPNs survival in plant extracts extracted using water and ethanol at 1%, 0.75%, 0.50%, 0.25% and 0.125% concentrations and nematode viability post-exposure. A concentration of 1000 IJs/mL in distilled water was used. Incubating extracts of *A. amatymbica* and *E. elephantina* with EPNs influenced the survival and virulence of the EPN species examined. The percentage survival of the EPNs post-exposure to the plant extracts was dependent on the plant extraction method and concentration in *A. amatymbica* but not in *E. elephantina*. The ethanol extraction method supported high percentage survival both at smaller and larger concentrations. The surviving infective juveniles (IJs) were virulent to Tenebrio molitor in both the aqueous and ethanol extracts of *A. amatymbica* and *E. elephantina*. However, virulence was observed to be strain-specific and not IJ concentration-dependent. Percentage mortality (against *T. molitor*) of strains with low percentage survival in aqueous extract of *A. amatymbica* compared effectively with those of higher percentage survival. The compatible relationship between extracts of the two plants and the EPN strains may lead to improved pest control in agricultural farming systems relative to either one of them applied individually.

P.0053 Connecting living collections to germplasm banks: the quasi-in situ approach in alpine conservation

Marco Canella[1-2], Núria Beltran-Sanz[2], Nicoletta La Rocca[1], Francesco Dal Grande[1-2]

1 University of Padova, Padova, Italy. 2 Botanic Garden of Padova, Padova, Italy.

Seed collection of Plant Genetic Resources (PGR) is a key step to maintain affordable *ex-situ* cryopreserved germplasm ready for *in-situ* conservation actions. However, cryopreservation of alpine wild plants is hindered by aspects related to seed and germination biology such as their low longevity. Alpine plant propagation is in addition high resource demanding and challenging, mainly because of knowledge gaps in germination protocols. To more accurately assess these gaps, we gathered and compared data from Alpine Botanical Gardens (ABG) distributed along the whole European Alpine Arc. Specifically, we interviewed curators of 14 ABG and merged the species lists into a taxonomically harmonised database. Following the gap-analysis approach - developed to assess crop biodiversity stored in germplasm banks - we checked for the presence of seed accessions of species preserved in ABG querying the global database Genesys PGR. In addition, we checked for the presence of high conservation interest species in the collections, such as endemics, endangered or critically endangered, EU policy species. In order to understand which taxa require additional basic research on germination niche modelling, we searched the seedlings requirements of all the records via the Seed Information Database. According to our preliminary results, ABG living collections represent a rich reservoir of locally acclimated propagation material useful to enhance accessions of germplasm banks. ABG are also important sources of technical knowledge on PGR propagation and in several cases also on plant population monitoring and *in-situ* reintroduction. Our study sets the basis for focused conservation-oriented partnership among gardens on the Alpine region that has the potential to enhance seed conservation in term of quantity, quality, and ecological knowledge.

P.0054 Morphology, chlorotype, phytochemical content, and antioxidant activity of Philippine Camia (Hedychium philippinense K.Schum.)

Daryl B. Ceribo[1], Emmanuel Bonifacio S. Timog[2], Renerio P. Gentallan Jr.[1], Leah E. Endonela[1], Roselle E. Madayag[3], Michael Cedric B. Bartolome[1], Kristine Joyce O. Quiñones[1], Nadine B. Coronado[4], Bartimeus Buiene S. Alvaran[5], Teresita H. Borromeo[1]

1 Institute of Crop Science, College of Agriculture and Food Science, University of the Philippines Los Baños, Philippines. 2 Department of Forest Biological Sciences, College of Forestry and Natural Resources, University of the Philippines Los Baños, Philippines. 3 Agriculture Systems Institute, College of Agriculture and Food Science, University of the Philippines Los Baños, Philippines. 4 Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños, Philippines. 5 International Rice Research Institute, Los Baños, Philippines.

Hedychium philippinense K.Schum., an endangered Philippine-endemic epiphytic herb, garnered an increasing research interest despite limited literature. In Mindanao, Philippines, it was reportedly used by the Talaandig tribe as tonic, post-partum, and birth control, yet further studies in various disciplines are still lacking. **Taxonomy:** The said species name was mentioned in 26 references from its first publication in 1904 up to 2023. Herbarium specimens were accessed online, in PNH, and in CAHUP. An unpublished herbarium specimen revealed that the species distribution is extended to the island of Palawan. Based on literature and taxonomists, the species identity used for the following experiments was determined. **Morphology:** Morphological observation of the specimens and live plants highlighted delineating characters such as narrow flowers and glabrous leaf surfaces, with an observed variation in stigma position relative to the anther. Based on observed herbarium specimens and online images such as from CDFP, the species flowered from November to May and set fruits year-round, highest in April. **Chlorotype:** For the first time, the chloroplast genome was assembled *de novo* then uploaded in NCBI GenBank. The Maximum Likelihood tree generated with five other *Hedychium* species and outgroup demonstrated close relationship to *Hedychium coronarium* J.Koenig; however, the chlorotype analysis, especially in IR junction sites, revealed distinctive features of *H. philippinense* in contrast to *H. coronarium*. **Phytochemistry:** Qualitative phytochemical screening of rhizome ethanolic extracts showed the presence of flavonoids and saponins, while antioxidant assays exhibited a mean DPPH scavenging activity of 76.79%, and a mean total phenolic content of 3.44 $mg_{GAE}/g_{extract}$. The rhizome extract's lethal concentration (LC_{50}) against brine shrimp was determined to be 1,230.27 µg/ml. These elucidated properties provided immense baseline information which could be used for continued utilization in health and organic agriculture research of this understudied and underutilized species.

P.0055 Addressing the challenges of dormancy and low seed quality to improve germination and propagation for woodland tree planting

Ademola Adetunji[1], Sabrine Bousselmi[2], Rae Cook[3], Elena Fouce Hernandez[1], Davide Gerna[1], Juergen Kolb[2], Thalita Nishime[2], Michael Schmidt[2], Charlotte Seal[1], Antje Wolff[4], Johannes Wolff[4], Louise Colville[1]

1 Royal Botanic Gardens, Kew, Richmond, UK. 2 Leibniz Institute for Plasma Science and Technology, Greifswald, Germany. 3 Elsoms Seeds Ltd, Spalding, UK 4 phenoLytics GmbH, Germany.

The drive to increase woodland cover, improve biodiversity and reduce carbon emissions through tree planting in the UK has increased demand for native seed, but dormancy and low seed quality are barriers to upscaling tree production.

Most temperate, broadleaved tree seeds are shed in the autumn and have deep dormancy, which restricts germination until the following spring. Breaking seed dormancy for nursery propagation requires periods (sometimes several months) of warm and cold stratification, which are often only partially effective. Moreover, there is variability in the quantity and quality of seeds produced by trees and a large proportion of seeds may be empty or infested. Therefore, tree seed germination may be slow and unpredictable, limiting the production of seedlings for tree planting. In this project we are testing the potential of two high throughput technological innovations for improving seed quality of 6 UK native tree species. Plasma-based treatments for breaking dormancy and improving seed germination and seedling growth. Plasma treatments have been effective in dormancy alleviation and improving germination of a few model and crop species but have not been tested on seeds of broadleaved trees. 3D X-ray phenotyping to quantitatively assess seed quality and the effects of plasma treatments on germination and seedling development. This technology can be leveraged to optimise seed screening and sorting to remove damaged and defective low-quality/unviable seeds to improve the supply of high-quality tree seeds. The project will enhance knowledge of dormancy mechanisms and germination requirements of tree seeds and enable improved propagation of trees from seeds. The development and optimisation of plasma treatments and phenotyping algorithms for diverse tree seeds will enable the wider application of these technologies to improve seed quality and enhance tree production for reforestation.

P.0056 Native Vicia spp. species as Nature Based Solution in poplar plantation: a study case in the Po-Valley, N-Italy

Anna Corli[1,2], Simone Orsenigo[1,2], Alma Balestrazzi[1,2], Alessio Giovannelli[2,3], Pier Mario Chiarabaglio[4], Andrea Mondoni[1,2]

1 University of Pavia, Pavia, Italy. 2 National Biodiversity Future Center, Palermo, Italy. 3 National Research Council of Italy, Sesto Fiorentino, Italy. 4 CREA – Research Centre for Forestry and Wood, Casale Monferrato, Italy.

Nature-Based Solutions (NBS) are promoted as a tool for solving environmental (e.g., flooding, soil degradation) and social (e.g., food and water insecurity) issues through the implementation of natural systems for balancing benefits on nature ecosystems and society. Plants play a key role as NBS, being involved in ecosystem services such as floods reduction, slope stabilization, enhancement of soil fertility and biodiversity conservation. Among the NBS in agroecosystems, cover crops can balance production with biodiversity since they increase the functional diversity with positive effects on ecosystem functions; within this context, native species are the best candidate for restoration practices. The poplar cultivation represents one of the most relevant wood chain in Europe for plywood veneer and other wood-based panels, with the highest shares in France, Turkey and Italy. In this system, cover crops are suggested to halt soil erosion and enrich organic matter, although their implementation is insufficiently investigated compared to other crop systems such as vineyards and olive groves. We explored the use of native *Vicia* species as cover crops in poplar plantations. The species are annuals, occurring also in this agroecosystem; as legumes, they fix nitrogen, thus decreasing reliance on inorganic nitrogen for the plantation. Moreover, *Vicia* can provide a valuable source of forage for wild pollinators. We characterized the germination requirements of six *Vicia* species and we tested their potential as NBS in a mesocosm experiment cultivated with *Populus nigra*. We evaluated *Vicia* performance (survival, establishment, flowering, fruiting, regeneration) and its effect on soil nutrients content, weeds reduction and pollinators attraction performing soil analysis pre- and post-planting, evaluating *Vicia* coverage in selected area and determining and counting insect visitors, respectively. The results will help in the selection of a subset of species to be used for their role in improving ecosystem services as intercropping in poplar plantations.

P.0057 Germination of threatened arable species Agrostemma githago L. and Centaurea cyanus L. to develop efficient in situ and ex situ conservation

Martina D'Agostino[1], Silvia Assolari[2], Francesco Boscutti[3,4], Giacomo Trotta[3,5], Marco Vuerich[3], Thomas Abeli[1]

1 Roma Tre University, Rome, Italy. 2 SemeNostrum, Udine, Italy 3 University of Udine, Udine, Italy. 4 National Biodiversity Future Center, Palermo, Italy. 5 University of Trieste, Trieste, Italy.

In recent decades, global plant biodiversity has declined dramatically showing a worrying increase in the number of endangered species, with an estimated two out of every five plants threatened with extinction. This led to the need to implement effective conservation strategies, including conservation translocations. These actions are closely linked to *ex situ* conservation, such the institution of seed banks. Seed banks allow the conservation and the study of seeds to better understand the biology, ecology and genetics of endangered species, crucial knowledge for the implementation of *in situ* conservation actions. In this perspective, we collected seeds of two wild arable species, *Agrostemma githago* L. and *Centaurea cyanus* L., which, due to the rapid intensification of agriculture, have undergone a dramatic decline. Their germinability was studied in relation to the ripening stage (collecting seeds once a week during all the ripening period), germination temperature (5 temperatures ranging from 5°C to 30°C) and donor population site. *C. cyanus* exhibits its optimum germination at a temperature of about 10°C. Germination progressively decreases with the advancement of the ripening stage. *A. githago* showed a broad range of optimal temperatures for germination from with 100% of germination between 5°C and 25°C but an abrupt drop in germination between 25°C and to 30 °C (from 100% to 0%). The donor population site of seed collection did not affect germination in the two species. This study provided the opportunity to expand the knowledge of the reproductive biology of these two species in order to define appropriate conservation actions, reflected in adequate seed collection and subsequent outplanting, in order to implement the effectiveness of the *in situ* and *ex situ* conservation.

P.0058 Morphological characterization of fruits and seeds of Syagrus vagans (Bondar) A.D.Hawkes (Arecaceae), a species endemic to Brazil.

Jamille C. Silva[1], Raquel A. Gomes[1], Maria A.R. Ferreira[1], Marcos V.C. Freitas[2], Jailton J. Silva[3], Lucia H.P. Kiill[3], Bárbara F. Dantas[3]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Universidade Federal do Vale do São Francisco, Petrolina, Brazil. 3 Embrapa Semiárido, Petrolina, Brazil.

Syagrus vagans, locally known as Ariri, has great economic potential as an ornamental palm tree, as its reproductive and vegetative structures provide a wide variety of uses. The species has a low percentage and slow germination, which may be directly linked to the morphological traits of the fruits and seeds. The morphological characterization of fruits and seeds enables to assemble ecophysiological information on the species, as well as assisting its conservation and large-scale propagation for cultivation as an ornamental plant. The objective of this study was to evaluate the biometric characteristics of S. vagans fruits and seeds, thus generating relevant information that helps to characterize the germinative and ecological aspects of the species. The work was developed with fruits collected in an area under controlled irrigation at Petrolina, Penambuco, Brazil. The evaluations consisted of measuring the length and diameter of fruits and seeds with a digital calliper, as well as the individual weight of the fruits, weighed on an analytical scale. Data for each characteristic were subjected to descriptive analysis using the statistical program R. Fruit length varied between 20.13 and 58.24 mm, with an average of 33.96 ± 0.27 mm. The diameter of the fruits varied between 6.88 and 46.70 mm, with an average of 22.32 ± 0.25 mm and the weight was around 8.06 g. The length of the seeds varied between 17.00 and 29.92 mm, with an average of 25.44 ± 0.17 mm and their diameter varied between 7.32 and 18.69 mm, with an average of 11.54 ± 0.17 mm. The evaluations showed that there is variation in the accessed biometric dimensions of fruits and seeds of this native wild species, which may be related to variability within the population and irrigation of the mother-plants.

P.0059 Conserving genetic diversity of wild flora in the Netherlands through seed banking: an example of collaboration at national level

Seppe De Mits[1], Joukje Buiteveld[1], Nils van Rooijen[2], Rik Lievers[1]

1 Centre for Genetic Resources, Wageningen University & Research, Wageningen, the Netherlands.
2 Wageningen Environmental Research, Wageningen University & Research, Wageningen, the Netherlands.

The Netherlands, as many countries, is committed to conserving its native biodiversity in alignment with international treaties such as the Convention on Biological Diversity. Government-funded national programs have been installed to conserve sources of genetic diversity. While this was traditionally focused on crop varieties, in recent years the scope has broadened to include building a seed bank of wild woody flora and crop wild relatives as safety back-up. The foundation “Het Levend Archief” (The Living Archive) has emerged parallel to these developments. This NGO aims to coordinate collaboration between scientists and expert-volunteers to build a ‘back-up’ seed collection of our botanical heritage, all native plant species in The Netherlands, with an initial focus on nationally red listed species. Within each initiative, species and populations with priority for conservation are selected. By combining data on current and past species distribution with expert knowledge about the species’ ecology, population history and genetic diversity, a selection of target populations is made. Professionals join forces with expert-volunteers for seed collecting. After a training, these volunteers are able to monitor populations in their area and collect seeds at the optimal moment. Besides building a seed bank, these projects and their associated networks of expert-volunteers provide an opportunity to gather knowledge about species ecology, the state of populations, and variation between populations, especially associated to phenology and seed characteristics of lesser-known species. In addition, by involving citizens in such a project, more awareness for the need of genetic conservation is raised. Here we showcase the Dutch seed banking initiatives on wild flora. What are their different approaches and conservation priorities? How do they collaborate at national level and what are the opportunities and challenges of involving volunteers?

P.0060 Multi-objective approach for plant conservation through ex-situ activities at the Botanical Garden of the University of Valencia. Conservation, research, and education

Elena Estrelles[1], Eva García-Martínez[1], Luís Martínez-Oliver[1], Olga Mayoral[1], Pilar Soriano[1]

1 Jardí Botànic - ICBiBE, Universitat de València, València, Spain.

The Valencian Wild Flora Germplasm Bank, located in the Botanical Garden of the University of Valencia, covers *ex-situ* conservation activities of the Valencian flora, co-financed by the University and the “Generalitat Valenciana”. Long-term preservation of seeds and spores of wild plants is our main aim. Today we are aware that achieving effective biodiversity conservation requires a multi-objective approach. Three aspects must be addressed, conservation, research and education. At this respect, specific data, results and activities, are presented. Conservation procedures of seeds and spores are currently well established. Therefore, plant germplasm conservation activities constitute the routine of the *ex-situ* conservation unit. An analysis of the species of the Valencian flora preserved in our germplasm bank is provided, to determine the current conservation status of threatened species and narrow endemics from the Valencian Community. Research on germination of seeds and spores is one of the challenges of a germplasm bank. Research support is required, especially when dealing with narrow endemic, rare or threatened species. Dormancy, photoblastism, longevity or stress tolerance are significant factors when we address wild plant propagation. The germination study of *Reseda hookerii*, one of the most threatened species in our territory, is presented. Education and science communication have today a key role facing Sustainable Development Goals. The germplasm bank makes available work protocols with seeds and spores, through our web site (https://www.jardibotanic.org/?apid=protocols-228). The objective is encouraging citizens to participate in propagation activities, with diverse motivation, from gardening to simply plant knowledge and use. Likewise, we hope that these protocols become practical tools for teaching proposals, to introduce concepts like flora conservation, plant propagation and their role in climate change mitigation. As part of this work, the results of a survey carried out with high school students after hands-on activities, based on some of our protocols, are analyzed.

P.0062 Evaluation of sexual and asexual propagation of Hechtia tehuacana (Bromeliaceae) at the Valley of Zapotilán, Puebla-Mexico

María Dolores García Suárez[1], Alejandor Hernández García[1], Yareli Odemaris Buendía López[1], José Ángel Lechuga Corchado[2], Héctor Serrano[3]

1 Departamento de Biología, Universidad Autónoma Metropolitana Iztapalapa, Mexico. 2 Departamento de Biotecnología. Universidad Autónoma Metropolitana Iztapalapa, Mexico. 3 Departamento de Ciencias de la Salud. Universidad Autónoma Metropolitana Iztapalapa, Mexico.

Hechtia tehuacana B.L. Rob. (Bromeliaceae) is an endemic and patchy distributed terrestrial bromeliad growing at the arid zone and in the Tehuacán-Cuicatlán Valley Biosphere Reserve, a megadiversity and endemism center particularly at the Valley of Zapotitlán Puebla, Mexico. Is a dioicous plant that forms seeds in capsules. Plant sexual and asexual reproduction were evaluated. Seed germination tests were used to obtain effective seed germination capacity under different light conditions (red, far red, blue, green, complete light and darkness), different temperatures (4, 12, 20, 25, 32 and 48°C), soil depth (surface, 0.5, 1.0 cm) and two different pH. Asexual reproduction was evaluated *in situ* at open sky and under shade protected environment, where mother plants and their plantlets production were measured, and orientation registered. *Hechtia tehuacana* has orthodox seeds, indistinct photoblastic, germinate 46% under red light; optimum temperature seed germination at 32 °C (77%) decreasing at 48°C (32%) but not at 4°C; they do prefer to germinate at soil surface, in slightly basic pH soils (7.5-7.9). Population largely is maintained by 64% of young plants formed by mother plants 0.5 -1 m high, producing phalange plantlets. Most of the family groups (36.8%) were found under tree shade mainly oriented to the NE-NO below *Vachellia farnesiana*, *Netulma laevigata*, *Castela tortuosa*, *Beaucarnea gracilis*, *Agave* sp., *Opuntia* sp. and *Stenocereus stellatus*. Plantlets grow preferentially (47%) to the NE of the mother plant. Under open sky plantlets prefer N-NO growth, they show no normal distribution with significant difference. Double shade protection is an interesting factor in the growth of this specie and seed germination prove to have a profound adaptation to arid conditions. Both sexual and asexual reproduction characteristics could explain the highly adapted growth, conservation, ecology, and maintenance success of Hechtia *tehuacana* to this harsh and fragile semiarid environment.

P.0063 Morphological and agronomic trait diversity of Brassica rapa genetic resources conserved at the National Agrobiodiversity Center

Bum-Soo Hahn[1], Parthiban Subramanian[1], Seong-Hoon Kim[1], Yoon-Jung Lee[1], Ae-Jin Hwang[1], Hyeonseok Oh[1], Young-Wang Na[1]

1 National Agrobiodiversity Center, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju-si, Jeollabuk-do, Republic of Korea.

The Brassica genus boasts a remarkable array of crops with a global distribution, ranking as the world's second major oilseed crop, surpassed only by soybean. Notable members of the *Brassica* genus encompass a morphologically diverse spectrum, including bok choy, broccoli, Brussels sprouts, cabbage, cauliflower, canola, Chinese cabbage, kale, kohlrabi, mustard, and turnips. This study focused on investigating the morphological diversity within *Brassica rapa*, wherein 52 germplasms spanning 15 subspecies were cultivated under field conditions during the fall seasons of 2022 and 2023. The predominant cotyledon colors observed in *B. rapa* seedlings were green and dark green, with 65% of seedlings displaying a purple hypocotyl. Anthocyanin pigment presence in the leaf petiole was infrequent (23.1%), as was its occurrence in the midrib (5.8%) and leaf surfaces (34.6%). Plant height ranged from 16.4 to 73 cm, while width spanned from 21.4 to 93.4 cm. Plant habit exhibited a distribution among spreading-type (53.8%), erect (28.8%), and semi-erect (17.3%), with the predominant plant shapes being dome-shaped (46.2%) and inverted-pyramid shaped (28.9%). B. rapa members did not produce white or pale yellow flowers; instead, the flowers were predominantly yellow-colored. Pods were primarily green or yellow-green, lacking any pigments. Turnip-like root-modifications were exclusive to plants of the subspecies B. rapa subsp. rapa and B. rapa subsp. rapifera. Principal component analysis of the observed traits revealed the grouping of B. rapa subspecies into eight diverse clusters. Further studies focusing on genetic components can enhance our understanding of the molecular phylogeny among these Brassica subspecies.

P.0064 Understanding the diversity of conserved Brassica crop wild relatives (CWRs) through their morphological and agronomic traits

Parthiban Subramanian[1], Seong-Hoon Kim[1], Yoon-Jung Lee[1], Ae-Jin Hwang[1], Hyeonseok Oh[1], Young-Wang Na[1], Bum-Soo Hahn[1]

1 National Agrobiodiversity Center, National Institute of Agricultural Sciences, Rural Development Administration, Jeonju-si, Jeollabuk-do, Republic of Korea.

Given the narrowing gene pool in crops resulting due to continuous breeding for a few selective traits and the loss of biodiversity due to changing climate conditions, gene banks offer an excellent choice for the conservation of plant genetic resources. Brassica is one of the most diverse and largest genera of plants, cultivated and consumed all over the world in various forms. In the present study we cultivated Brassica species outside the six species of the triangle of U, commonly referred as Brassica crop wild relatives (CWRs). A total of 54 Brassica CWR resources spanning 42 species were grown under field conditions during fall seasons of 2022 and 2023. We recorded and compared forty-five morphological and agronomic traits at various stages of plant growth. During the seedling stage, *Brassica pupuraria*, *B. rupestris*, and *B. incana* exhibited the the longest cotyledons (1.4-1.8 cm), while *B. deflexa, B. aucheri* and *B. maurorum* possessed the shortest cotyledons (0.2 -0.4 cm). In the vegetative stage, *B. drepanensis, B. incana, B. barrelieri,* and *B. montana* were characterized with larger leaves, thick and long petioles whereas, *B. gravinae, B. desnottesii, B. souliei, B. aucheri* and *B. repanda* had smaller leaves with thin and shorter to absent petioles. Some species such as *B. barrelieri, B. oxyrrhina* and *B. maurorum* exhibited highly-lobed leaves, while other species such as *B. elongata* were unlobed. The habit and plant height/width varied widely, ranging from flat, short rosette type to tall herb types. Principal component analysis of the observed traits indicated the grouping of these Brassica CWRs into six different types as described by the triangle of U. Further analysis based on the genetic composition can provide a comprehensive understanding of the phylogeny of the Brassica CWRs.

P.0065 Germination characteristics and physiological changes of Pinus densiflora seed stored for 20 years under two storage temperatures

Da-Eun Gu[1], Sim-Hee Han[1], Ja-Jung Ku[1]

1 National Institute of Forest Science, Suwon, Republic of Korea.

This study aimed to evaluate the germination characteristics and physiological changes of *Pinus densiflora* seeds stored for 20 years under two different temperatures. Seeds collected from a clonal seed orchard were stored for two decades at temperatures of 4°C and -18°C, with the moisture content adjusted to

5-7%. Analysis of the stored seeds included assessing germination characteristics, electrolyte leakage, and carbohydrate content. Results indicated significant differences in seed viability and physiological activity based on the storage temperature. Seed germination rates were 55% and 83% at 4°C and -18°C, respectively, with corresponding T50 (the days required to achieve 50% of the final germination percentage) of 6.29 days and 8.14 days, meaning that the seeds stored at 4°C experienced a significant decrease in viability over the 20-year period, whereas those stored at -18°C retained their viability. Analysis of electrolyte leakage, indicative of cell membrane integrity and seed aging, revealed higher electrical conductivity and more leakage of inorganic salts in the seeds stored at 4°C (44.8 μS/cm), suggesting lower viability compared to those stored at -18°C (26.8 μS/cm). Notably, the amount of inorganic salts leaked from the stored seeds followed the order of K, Ca, Na, Mg, and Fe. Although the content of carbohydrates in dry seeds did not differ significantly between temperatures, variations were observed during the moisture absorption process for germination, with respective values of 4.86 mg/g and 3.88 mg/g at 4°C and -18°C, indicating differences in carbohydrate metabolic activity. In conclusion, *P. densiflora* seeds can be stored for more than 20 years at -18°C without losing viability and physiological activity if proper moisture control is maintained

P.0066 Seed storage behaviour of endemic vascular plants

Udayangani Liu[1], Tiziana A. Cossu[1]

1 Royal Botanic Gardens, Kew, Wellcome Trust Millennium Building, Wakehurst, Ardingly, UK.

Seed's response to dehydration in terms of desiccation tolerance is called seed storage behaviour. It is an important seed trait to assess their potential for conservation through seed banking which requires drying and cooling of seeds. However, not all the seeds are amenable to this routine as seeds from different taxa may respond differently. Using the prediction tool developed by authors of Wyse et al. (2018, https://doi.org/10.1093/aob/mcx128) and occurrence, bioclimate and other trait data from available sources, we explored seed storage behaviour among endemic plants (22,360 taxa, 21,876 species, 3391 genera and 199 families) which have had global level conservation assessments for their extinction risk. Predictions are generated as a probability gradient from desiccation tolerant (0, orthodox) to sensitive (1, recalcitrant). We examined how predicted trait varied across taxonomic families, lifeforms, bioclimate of habitats where plants occur and their red list categories.Overall, 82% of endemic taxa bear orthodox seeds and suitable for conservation through seed banking. This includes 80% of threatened and 85% of non-threatened endemics. Remaining 18% (3946 taxa, 48 families and 436 genera) potentially bear recalcitrant seeds and require alternative measures for conservation. The incidence of recalcitrant was more frequent among gymnosperms than angiosperms (dicotyledons > monocotyledons), families with few naturally occurring genera, lifeforms such as trees and shrubs, and habitats experiencing tropical rainforest and monsoon and temperate humid subtropical climates. Recalcitrant seeds were absent among annuals, cycads, and parasitic plants, and habitats experiencing temperate cold-summer Mediterranean, continental Mediterranean-influenced hot-summer humid, and polar ice cap climates. There were 21 families which had ≥50% recalcitrant taxa: predominantly recalcitrant(100%, Lauraceae, Elaeocarpaceae, Rhizophoraceae, and Cymodoceaceae); notably more recalcitrant than orthodox (≥70%, Myristicaceae, Podocarpaceae, Dipterocarpaceae, Fagaceae, Chrysobalanaceae, Magnoliaceae, Sapotaceae, Pittosporaceae, Arecaceae, Lecythidaceae, Araucariaceae, Malpighiaceae,Clusiaceae, and Ebenaceae); and marginally recalcitrant (54%, Calophyllaceae) or more recalcitrant (61-67%, Sapindaceae, and Meliaceae).

P.0067 Incidence of seed dormancy among endemic vascular plants

Udayangani Liu[1], Tiziana A. Cossu[1]

1 Royal Botanic Gardens, Kew, Wellcome Trust Millennium Building, Wakehurst, Ardingly, UK.

Seed dormancy is an innate constraint where seeds are prevented from germination under environmental conditions that would otherwise promote germination in nondormant (ND) seeds. It also one of main determinants of population and species-level processes (e.g., colonization, establishment, distribution, adaptation, speciation, and extinction), ensuring germination to occur under appropriate seasonal conditions, thereby reducing extinction risk and providing the opportunity for subsequent adaptive divergence. Inability to break seed dormancy is an obstacle preventing dormant but healthy seeds from germinating during curatorial activities in seed banks. We compiled a total of 27,067 seed dormancy records from literature and summarised for 17,332 endemic taxa (16,903 species, 1771 genera, and 256 families) and explored variation in incidence of different dormancies: physiological (PD); morphological (MD); morphophysiological (MPD); physical (PY); and physiophysical (PYPD). We found 91% of endemic taxa were known to bear dormant seeds. Only 9% of taxa had exclusively ND seeds without any identified dormancy and could germinate in a wide range of environmental conditions. Some taxa were documented for having both dormant (PD or PY) and ND seeds, but such occurrences were very infrequent (each ≤0.3% of taxa). Whilst all five main dormancy types were found among endemics, 77% of taxa had only one type of dormancy, but their incidence of occurrence varied. We found PD to be the most frequent seed dormancy state of endemics as 57% of taxa possessed PD seeds as their only dormancy type. Incidence of other single type dormancies among taxa were: MPD (11%); PY (8%); MD (1%); and PYPD (~0.1%). PY and PYPD occurred only in dicotyledons. Eight different combinations of multiple dormancies were found among 14% of taxa. However, only the MPD/MD combination (~8% of taxa) was found notably frequent compared to others (P.8 to <2% of taxa).Many taxa had MPD/MD than only MD seeds.

P.0068 Long-term seed conservation of Armenian orchids (Orchidaceae)

Anush A. Nersesyan[1,2], Astghik Papikyan[1,2], Sona Galstyan[1,2], Aisyah Faruk [3]

1 Institue of Botany after A. Takhtajyan of the Academy of Sciences of the Republic of Armenia, Yerevan, Republic of Armenia. 2 Nature Heritage NGO, Armenia. 3 Millennium Seed Bank, Royal Botanic Gardens, Kew, UK.

The *Orchidaceae* family in Armenia is represented by 14 genera and 44 terrestrial species. Nine species are included in the Red List of Armenia (2010). Fourteen species occur outside the Protected Areas of Armenia. Under the project "*Enhancing the capacity and capability of orchid conservation in Armenia*" funded by Darwin Initiative Capacity and Capability Fund, we are studying seed behaviour of these charismatic species for long-term conservation. Our study will identify optimal conditions of terrestrial orchid seeds of Armenian species, focusing on low-cost methods. During three field seasons, seeds of more than 20 orchid species from the genera *Anacamptis, Cephalanthera, Dactylorhiza, Epipactis, Gymnadenia, Limodorum, Ophrys, Orchis*, and *Platanthera*, were collected across Armenia and placed under different relative humidity (RH) conditions: 15%, 30%, and 50% RH. Each were then placed in different storage temperatures: +5°C, -20 °C, and -80 °C. The experiments were conducted at the Millennium Seed Bank, in the South of England and the Seed Bank of Armenian Flora of the Institute of Botany after A. Takhtajyan of the National Academy of Sciences of the Republic of Armenia. Initial results show that optimal conditions are often dependent on orchid species. Long-term duplicates are sent and stored at the Millennium Seed Bank. To further the conservation of orchids in Armenia, A. Takhtajyan Institute of Botany submitted a proposal to the Higher Education and Science Committee of the Ministry of Education, Science, Culture and Sport of the Republic of Armenia to continue investigation on seed conservation issues and macroecological studies on the populations of orchids found across Armenia.

P.0069 Native species for greening agroecosystems: a selection process based on plant traits

Micol Orengo[1], Anna Corli[1,2], Thomas Abeli[2,3], Andrea Mondoni[1,2], Graziano Rossi[1]

1 Department of Earth and Environmental Sciences, University of Pavia, Pavia, Italy. 2 National Biodiversity Future Center, Palermo, Italy. 3 Department of Science, Roma Tre University, Rome, Italy.

The trend observed in the last decades of converting natural ecosystems in intensive farmland has led to a significant loss of biodiversity and habitat degradation. In this context, Nature Based Solutions (NBS) provide ways to reduce the pressure of human activities on the environment. Aiming to protect crops from soil erosion, improve water retention and increase soil nutrient content, greening with herbaceous ground covers have been implemented as NBS alongside both herbaceous and woody crops. Most greening efforts today apply seed mixes from agronomic species, but they are often demanding in terms of resources, thus being able to outcompete the crops. In contrast, native species represent a less demanding alternative and simultaneously increase functional diversity, supporting ecosystem services and improving overall biodiversity; however, studies on native species are still in their infancy and site-specific. We aim to design a selection process to identify suitable native species for greening, based on the study of plant functional traits. To do this, we examined most frequently occurring traits in three functionally selected agronomic mixes (nutrients addition, biomass production, erosion control) using online databases such as TRY, then narrowed down fundamental traits shared by the species within each mix type (e.g. germination traits, nitrogen fixation). Data on the same traits were then collected for the species from the native species pool and each was ranked according to its suitability in different greening uses. The study is focused on the Oltrepò region (North-Apennines, Italy), enabling us to apply this selection method in an area where the practice of greening has been largely employed in woody crops (vineyards and olive groves). Results from the species selection process will be helpful in defining mixes of spontaneous species to be used for greening the N-Apennine region and, more broadly, in defining a protocol for future selection endeavours.

P.0070 Characterization and valorization of autochthonous legume ecotypes from the Molise region

Alessandra Renella[1], Martina Falcione[1], Massimiliano Corso[2], Gabriella S. Scippa[1], Dalila Trupiano[1]

1. University of Molise, Pesche, Italy 2. Institut Jean-Pierre Bourgin, Universite Paris-Saclay, INRAE, AgroParisTech, Versailles, France.

High genetic variability, specialized metabolites (terpenoids, flavonoids, and alkaloids), and health-promoting compounds are characteristics of autochthonous ecotypes. However, autochthonous ecotypes are seriously threatened by extinction, mainly because of their replacement by commercial varieties. Therefore, it is crucial to recognize the distinctive properties of autochthonous ecotypes to preserve them, drawing the interest of local farmers and consumers involved in their conservation. The present study aimed to characterize using a multi-level approach (morphological, genetic, and metabolomic analysis) three autochthonous lentil ecotypes from different villages in the Molise region (Capracotta, CA; Rionero Sannitico, RS; and Agnone, A) in comparison to other autochthonous ecotypes, one from Umbria (Castelluccio di Norcia, CS), one from Lazio (RA), and one commercial variety (TR). In the first phase, 14 IBPGR morphological descriptors and 8 ISSR molecular markers were used to evaluate diversity, genetic variability, and phylogenetic relationships among different ecotypes. Except for A and CS, the morphological descriptors, clustering, and principal component analysis (PCA) revealed a high similarity between the ecotypes. Instead, the PCA and clustering analysis of the genetic profiles divided all ecotypes into two main groups: one group consisted of the ecotypes from the Molise region, and one was formed by the other three. Untargeted metabolomics, performed by liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS), revealed that 809 MS peaks (metabolic characteristics) of those 544 were differentially expressed among lentil ecotypes (P ≤ P.5). According to the PCA and PLS-DA score plots, the metabolite compositions of autochthonous ecotypes differed significantly from each other. To identify ecotype-specific metabolic features, an enrichment analysis will be carried out. Furthermore, physiological tests (i.e., aging tests and antioxidant assays) and an in vitro assay of bioactive compounds will be carried out to explore the beneficial properties of the identified metabolic features, supporting valorization and conservation activities of autochthonous ecotypes.

P.0071 Effect of temperature and light on seeds germination of Adenophora liliifolia (L.) A.DC

Dubravka Sandev1, Sanja Kovačić[1]

1 Botanical Garden, Department of Biology, Faculty of Science, University of Zagreb, Croatia.

Adenophora liliifolia (L.) A.DC grows scattered from Central and Eastern Europe to North-Western and Central Asia, inhabiting various types of shady forests and wet grasslands. In spite of its wide distribution, the populations have been small and declining through most of its range. In Croatia, this Natura 2000 species is very rare, appearing dispersed within the territory of IPA Gorski kotar & Kupa river valley. In the Botanical Garden of the Faculty of Science, University of Zagreb, germination study was conducted with the aim of shedding light on the topic of *A. liliifolia* seed ecology and consequently advancing conservation efforts. Freshly matured seeds were exposed to warm and cold stratification in duration of four to sixteen weeks. Germination was investigated through different regimes of incubation parameters, i.e. illumination (light/dark) and temperature (5, 15/6, 23 °C). *Adenophora liliifolia* seeds had higher germination rate after 8 and 12 weeks of cold stratification. Light conditions and incubation temperature of 23 °C were proved to be the most appropriate for successful seed germination (85.3% after eight weeks and 84% after twelve weeks of cold stratification). The observed patterns in seed behaviour are consistent with the conditions of the natural habitat in Croatia. The knowledge gathered from these patterns is vital for successful *ex situ* and *in situ* conservation strategies necessary for this small population to survive.

P.0072 Seed ultrastructure as a useful tool in taxonomy: analysis of selected species of the genus Polystachya Hook. (Orchidaceae)

Katarzyna Sanek[1], Sławomir Nowak[2], Marta Kolanowska[1], Konrad Kaczmarek[1], Agnieszka Rewicz[1]

1 Faculty of Biology and Environmental Protection, University of Łódź, Łódź, Poland. 2 Faculty of Biology, University of Gdańsk, Gdańsk, Poland.

Polystachya Hook. is a large genus comprising about 230 species, mostly epiphytic orchids. The genus is characterized by a pantropical distribution, although the vast majority of its representatives grow in the tropical part of Africa. To date, analyses of species in the genus *Polystachya* have only dealt with general shape variation, e.g., leaf shape or inflorescence structure. In contrast, literature data on the seed morphology of species in the genus *Polystachya* Hook. (Orchidaceae) is extremely scarce. The aim of this study was to investigate the seed morphology of *Polystachya* and related taxa involving their biometric analysis (length, width, perimeter, surface area) and their ultrastructure observed with a scanning electron microscope. *Polystachya* species are mainly characterized by small seeds with test cells with very thick cell walls. In most of the taxa studied, a spiral cell wall arrangement and a smooth periclinal wall were observed. This structure is unique to the genus, so it diagnoses it within the orchids. In conclusion, the ultrastructure of the seeds of the analyzed taxa shows a high degree of similarity, which prevents it from being used as a taxonomically relevant feature. Even if combined with additional data such as seed size, shape and distribution of cells in the seed coat. This may be due to the fact that many of the representatives studied belong to only a few sections, most of which are closely related. However, individuals from morphologically strongly distinct groups, sometimes even treated as separate genera (*Unguiculabia* Mytnik & Szlach. or *Epiphorella* Mytnik & Szlach.), showed less similarity. The results obtained significantly expand the poor knowledge of the carpology of the group analyzed. To determine the complete variability of seeds within the *Polystachya*, further studies should focus on fewer sections and groups of endemic taxa, such as those from Madagascar.

P.0073 Germination of Aristolochia hypoglauca and Aristolochia zebrina (Aristolochiaceae) under different light intensities

André V. Suzuki[1], Lucas A. Silva[2], Nelson T. L. Pena[3], Jadson B. Zampirollo[2], Valquíria F. Dutra[2], Anderson Alves-Araújo[4], Elton J. de Lírio[1,5], Joelcio Freitas[6]

1 Universidade Federal do ABC, Santo André, Brazil. 2 Universidade Federal do Espírito Santo, Vitória, Brazil. 3 Universidade Federal de Viçosa, Viçosa, Brazil. 4 Universidade Federal da Bahia, Salvador, Brazil. 5 Universidade de São Paulo, São Paulo, Brazil. 6 Instituto Nacional da Mata Atlântica, Santa Teresa, Brazil.

This work aimed to analyze the effect of luminosity on the germination of Aristolochia hypoglauca Kuhlm. and Aristolochia zebrina J.Freitas & F.González to test whether the occurrence of species in open areas is related to the germination taxa in higher light intensities, as well as to verify the best conditions for germination of both species, aiming conservation actions. The species are categorized as Endangered (EN) in the Espírito Santo state Threatened Species List and the Official National List of Threatened Species, respectively. Aristolochia hypoglauca occur in bush borders in dense montane and submontane ombrophile forests, while A. zebrina occurs in open areas in ombrophile forests of Tabuleiro and Restinga. We used three treatments: 100%, 50% and 0% of luminosity (LUM) in each species. After 38 days, the seeds with radicle or visible endosperm were considered as germinated. For A. hypoglauca the germination rate submitted at 100% LUM was 68%, for 50% LUM = 66%, and for 0% LUM = 26%. Seeds of A. zebrina in 100% LUM resulted in a 22% germination rate; 50% LUM = 34% and 0% LUM = 26%. In a comparison of germination taxa between species, there is no significant difference for the 0% LUM treatment. For A. hypoglauca a higher percentage of germination occurred in the treatments of 50% and 100%, indicating a positive photoblastic behaviour. In contrast, for A. zebrina, there was no significant difference between the three treatments, which were considered neutral photoblastic. The germination behaviour was expected for A. hypoglauca, which responds to the high luminosity conditions where the species occurs. However, for A. zebrina its germination may be related to other factors present in the environment.

P.0074 Tree species' germination in a warming planet: a meta-analysis spanning biomes, species, and populations

Eduardo Vicente[1], Marta Benito Garzón[1]

1 BIOGECO INRAE, University of Bordeaux, Pessac, France.

Most knowledge on trees' adaptation to environmental changes relies on adult individuals, leaving early-life stages understudied. One of the most sensitive to climate processes at early stages is germination, i.e. the transition from seed to seedling. To fill this knowledge gap, we present a comprehensive quantitative analysis of the variation in tree populations' germination responses to temperature changes across biomes. We investigated how germination responses are influenced by temperature variations at the population level, assessed population adaptation to local temperature conditions, and estimated germination niches for selected species under current and future climate scenarios (SP5-8.5; 2080). To this aim, we performed a meta-analysis of published literature spanning from 1996 to 2023, focusing on germination proportions and time across populations in different biomes. A total of 50 articles covering 63 species and 250 populations worldwide were reviewed, encompassing boreal, temperate, Mediterranean, and tropical-subtropical regions. Our findings reveal that temperature-induced warming generally accelerates germination time across biomes, with more consistent shifts observed than in germination proportions. Intra-specific variation plays a significant role in germination responses, particularly for boreal and temperate species, mediated by temperature-related variables at seed origin. In contrast, precipitation-related factors are more influential for Mediterranean and tropical-subtropical species. Tropical species displayed higher local adaptation to warming whereas adaptation lags were observed in non-tropical biomes. Germination niches' prediction suggested germination reductions for tropical-subtropical and Mediterranean species under future climate scenarios, while temperate and boreal species predictions generally displayed overall increases, especially in cold margins. In conclusion, our study underscores the importance of population-level adjustments in modulating germination responses to climate change and emphasizes the sensitivity of germination phenology. Therefore, we advocate for the consideration of these processes and their ecological implications in future research on forest vulnerability to climate change.

S.009. AEROBIOLOGY. ADVANCES IN THE ATMOSPHERIC POLLEN RESEARCH AND CHALLENGES IN THE CONTEXT OF GLOBAL CHANGE.

P.0075 Pollen as an environmental factor in inflammatory diseases

José de la Torre[1], Inés Rodríguez I[1], Rafael Pérez[1]

1 Departamento de Análisis Clínicos. Hospital Comarcal Axarquía, Málaga, Spain.

Anemophilous pollen is introduced into the bronchi by respirations and through mucuciliary sweeping and insensible swallowing they pass into the digestive tract, where they can act as antigenic molecules. Between 6 and 36% of stool samples were sent to the laboratory for microscopic examination are found to contain pollens. 90% of these patients presented abdominal pain and/or diarrhoea. In Southeast Asian countries, pollen levels in the air are very low and inflammatory bowel diseases are also very low, in contrast to Europe and North America where pollen levels are usually high and inflammatory bowel diseases are high. A retrospective observational study was carried out during the years 2017-2022 of 300 stool samples from 100 patients with digestive symptomatology, and 300 stool samples from 100 patients without symptomatology. Stool pollen shows a seasonal response with three peaks coinciding with the pollen calendar of Vélez-Málaga. The retrospective observational study of stool samples from patients in our area showed the same distribution and the stool pollen counts varied from 125 to 1000 grains/g. Forty-five percent of patients with pollen in stool had abdominal symptoms for more than 5 months. Samples from patients without pollen in faeces, their symptoms did not last more than 2 months on average and calprotectins were all less than 100µg/g.

Note: This abstract was translated with AI.

P.0076 Pollen morphology of some species of Acanthaceae from the Western Ghats of India

Maria Emilia Mascarenhas[1]

1 Department of Botany, St. Xavier's College, Mapusa, Goa, India.

The family Acanthaceae is an eurypalynous one, and the pollen diversity within the family is significant. The family is one of the most species-rich in the Western Ghats, with a good proportion of endemic components. However, earlier pollen studies from outside the country did not adequately cover the family from this region. Pollen samples of 29 endemic Acanthaceae (19 species and 10 varieties) were collected from the Western Ghats of Maharashtra, Goa and Karnataka of India. Pollen was acetolysed and studied using a light microscope (LM). Among these taxa, the pollen morphology of eight species and five varieties has been analysed for the first time in this paper. The pollen shape, number of pores/colpi, exine ornamentation and light microscope photographs have been provided. Pollen morphology ranges from spherical to prolate to sub-prolate. Similarity is seen between the pollen of Barleria L. and Eranthemum L.; Dicliptera Juss., Justicia L. and Rungia Nees; Gymnostachyum Nees and Haplanthodes Nees; Calacanthus T.Anderson ex Benth. and Hygrophila R.Br. All the species of Strobilanthes Blume studied here had prolate pollen except S. ixiocephalus which had spherical pollen. Neuracanthus Nees had no similarity with any of the other genera studied. Pollen morphology is an excellent diagnostic character for the family Acanthaceae and is conserved within the genera. Hence, pollen studies can be indispensable for delimiting the tribes, sub-tribes and genera.

P.0077 How does aerobiology behave in a neotropical city?

Álex Espinosa-Correa[1], Fernando Alzate-Guarín[1]

1 Grupo de Estudios Botánicos GEOBOTA, Instituto de Biología, Facultad de Ciencias Exactas y Naturales, Universidad de Antioquia, Medellín, Colombia.

Aerobiology in the tropics is still a science in development, where sampling and analysis are needed to understand the dynamics that occur there. Airborne pollen concentrations in the city of Medellín were measured using a Hirst-type sampler and correlated with meteorological parameters (relative humidity, rainfall, temperature, and wind speed) and air pollutants ($PM_{2.5}$, PM_{10}, NO_x). Sampling was conducted over three years from (2019-2022), and pollen grains were detected on all days of sampling. The annual pollen integral (APIn) was 46,826, 51,536, and 43,608 pollen * day/m3 for each of the three sampling years. A total of 26 pollen types were identified, with *Cecropia*, Urticaceae, *Fraxinus*, Moraceae, Cupressaceae, Myrtaceae, *Pinus*, and Arecaceae being the most abundant. The highest pollen concentrations were observed from December to January and in July-August, corresponding to the months with the lowest rainfall. The Main Pollen Season (MPS) ranged from 247 to 301 days in duration. During all sampling days, aerovagant pollen was found present in the atmosphere of the city of Medellín. The highest hourly pollen concentrations occurred around noon, whilst something very different and rarely reported occurs with *Cecropia*, which is much more abundant at night, from 20:00 to 1:00 h. Relative humidity and rainfall showed negative correlations, while temperature and wind speed exhibited positive correlations, which has also been observed in different samples around the world. $PM_{2.5}$ and NO_x display significant negative correlations, whereas PM_{10} exhibits significant positive correlations. These results underscore the influence of atmospheric variables on airborne pollen in a tropical city. Furthermore, they suggest the potential use of pollen as an indicator of air quality in the urban environment.

P.0078 Study of reproductive phenology in grasses related to airborne pollen concentration in Madrid (Spain). Preliminary results

Ángel Cascón[1], Jorge Romero-Morte[1], Montserrat Gutiérrez-Bustillo[1], Jesús Rojo[1].

1 Department of Pharmacology, Pharmacognosy and Botany, Complutense University of Madrid, Madrid, Spain.

Grasses are the dominant species in many natural and human-managed habitats. In addition to their ecological importance, we must consider their importance from the public health point of view, since grasses are one of the main cause of pollen allergy worldwide and particularly in Mediterranean areas and in the centre of the Iberian Peninsula. For this reason, grasses are a taxonomic group widely studied from the aerobiological point of view and the interpretation by phenological in situ observation is very interesting. In this work we studied the reproductive phenology of 27 abundant grass species in the city of Madrid (Spain). Sampling was carried out at two sampling points. Phenological observations were based on the percentage of flowering individuals, and were carried out weekly from March to May 2022. In addition, airborne Poaceae pollen concentrations were recorded daily with a volumetric Hirst-type sampler located in the Faculty of Pharmacy of the Complutense University of Madrid. This is a biological air quality station belonging to the Madrid Region Palynological Network. The peak flowering periods of the species were compared with the airborne pollen concentration to determine the most important species in pollen emission and dispersal in Madrid. The results showed that species of the genera *Bromus*, *Hordeum* or *Avena* are early flowering annual species and coincide with pollen concentrations in the air (pollen curve) that do not exceed 50 grains/m^3. On the other hand, in the group of species that flower from May to the beginning of June (late flowering species), there are annual species such as *Lolium rigidum* Gaud. and *Trisetum paniceum* Lam., and mainly perennial species such as *Piptatherum mileaceum* L., *Elymus repens* L. and *Dactylis glomerata* L. whose flowering coincides with the maximum pollen concentrations of grasses in the city of Madrid.

P.0079 First insights on Pollen Sense Automated Particulate Sensor (APS-300) for airborne Olea pollen monitoring in the Mediterranean area

Qasim Farooq[1,2], Jose Oteros[1,2], Moisés Martínez Bracero[1,2], Carmen Galán[1,2]

1 Department of Botany, Ecology and Plant Physiology, Agrifood Campus of International Excellence, University of Cordoba, Córdoba, Spain. 2 Andalusian Inter-University Institute for Earth System IISTA, University of Cordoba, Córdoba, Spain.

Accurate and repeatable pollen analysis and detection are essential for airborne pollen monitoring. In Europe, it is carried out by hand counting, a labor-intensive and comparatively slow procedure. For this reason, new automatic approaches are required to address these issues. Despite the fact that a great deal of work has been done with varying degrees of success, there are still a lot of problems with automatic pollen monitoring. In this work, we provide the results of field testing a unique automated real-time pollen imaging sensor in Cordoba, Spain. First, we conducted a comparison of the pollen concentrations obtained using a manual Hirst-type spore-trap and an automated real-time pollen sensor (APS-300, Pollen Sense LLC) between March 13, 2023, and June 15, 2023, using parallel measurements. At the Rabanales Campus of the University of Cordoba in Spain, both samplers are located in the same station. Second, we evaluated the quality of the retrieved pollen concentrations detected with both samplers. The Hirst-type trap recorded an average daily pollen concentration of 1,535(pollen grains/m^3) during the study period, while APS-300 recorded 2,129 (pollen grains/m^3). While the Hirst-type trap reported a peak concentration of over 8,000 (pollen grains/m^3), the APS-300 recorded the highest concentration of over 9,000 (pollen grains/m^3) on April 27. The daily *Olea* pollen concentration measured by both systems demonstrated an extremely significant correlation, with R equal to 0.91. The APS-300's real-time and mobile features make it highly effective in tracking *Olea* pollen. In terms of human effort and time resolution, it is a major advance over manual counting approaches. Nevertheless, more research is needed to enhance automated pollen detection methods.

P.0080 Aerobiology of Texas Panhandle with special reference to pollen data analyzed for two decades

Nabarun Ghosh*[1] Aubrey Howard[1], Lyanna DeLeon[1], Maritrinh Nguyen[1], Prabir Banerjee**[2]

*1 Professor of Biology, Aerobiology Laboratory, Department of Life, Earth and Environment Sciences, West Texas A&M University, Canyon, Texas, USA 2 Head, Gastroenterology, Charnock Hospital, Kolkata, India. *nghosh@wtamu.edu, **drprabir2003@gmail.com.*

Aeroallergens are often the cause of serious allergic and asthmatic reactions, affecting millions of people each year. In each geographical area, there are different species that compound a characteristic airborne pollen calendar controlled by the meteorological conditions changeable in areas and years. We used a Burkard Spore Trap for aeroallergen sampling that provided us with the information regarding the onset, duration, and severity of the pollen season that clinicians use to guide allergen selection for skin testing and treatment. We also used pollen grains from different plant species of our locality for identifying and characterizing the pollen through Scanning Electron Microscopy. We examined the samples with an SEM (TM-1000) after gold coating and Critical Point Drying. We measured the pollen grains using the TM-1000-imaging software that revealed the micro-morphology with the size of colpi, sulci and the detailed microstructures. This information can aid data for classification and circumscription in Angiosperm taxonomy. For viewing the fluorescence in pollen, we used2-3 drops of Fluorescein-based dyes with deionized water on the slides. The slides were mounted and observed under the microscope. During the last two decades, the use of SEM has greatly increased our knowledge of the microstructure of pollen. Mature pollen grains are stable in a vacuum: this allows quick preparation for SEM examination. The low level of technical expenditure required, in combination with the high structural diversity exhibited and the intuitive ability to understand the "three dimensional", often aesthetically appealing micro-structures visualized, has turned pollen studies into a favorite tool of many taxonomists. The daily weather was recorded including temperature, wind speed, precipitation, humidity, average soil temperatures. This allowed the estimation of the clinical significance of the various pollen types by combining data concerning in vivo allergenicity and terminal velocity as a means to judge the clinical significance.

P.0081 Monitoring invasive plant with aerobiology data and aerial photography

Guillermo Guada[1], María Fernández-González[1], Pedro A. Araujo Nespereira[2], J. José Uzal Dapena[2], F. Javier Rodríguez-Rajo[1]

1 Department of Vegetal Biology and Soil Sciences, Faculty of Sciences, University of Vigo, Ourense, Spain. 2 Department of Marine Geo-science and Territory Rationalization, Faculty of Sciences, University of Vigo, Ourense, Spain.

We studied the relationship between airborne pollen of the invasive plant *Acacia dealbata* Link and its increase in surface area using aerobiological data and aerial photography. Our objective is to test if the aerobiological data reflect the increase in surface area of *Acacia*. For this purpose, pollen monitoring was conducted using the Lanzoni VPPS 2000 volumetric trap, and the evolution of the *Acacia* surface mapped using the Spanish Geographic Information System of Agricultural Plots (SIGPAC) viewer and aerial photographs provided by the national plan of Aerial orthophotography (PNOA). The use of drones was also used in the field to delimit and verify the occurrence on inaccessible areas. The study period ranged from 2003 to 2017, during which time aerial photos were used to measure surface area. The measured area increased from 261.3 ha in 2009 to 364.9 ha in 2017, resulting in a 39.7% increase over the entire study period. Regarding pollen, the main pollen season occurs from January to April, with the greatest percentage of grains in March. The pollen integral shows a tendency to increase, reaching up to 5 times more pollen throughout the study period. The surface area expansion observed in the mapping is also reflected in the trends of *Acacia* pollen growth in air, with an annual increase of 5.3 pollen grains per year. This increase in pollen is much greater than the increase in areas invaded, which indicates the high degree of *Acacia* adaptation in the studied area. This study shows how airborne pollen count monitoring and mapping are useful tools for invasive plant management decision making.

P.0082 Developmental stages of female strobili and the effects of spray pollination for Cryptomeria japonica

Naoko Miyamoto[1], Kazuya Iizuka[2], Yukinori Konno[3], Soichiro Nagano[4], Jin'ya Nasu[1], Yuichiro Oribe[4], Nobuaki Takeda[4]

1 Tohoku Regional Breeding Office, Forest Tree Breeding Center, Forestry and Forest Products Research Institute, Iwate, Japan. 2 School of agriculture, Utsunomiya University, Tochigi, Japan. 3 Miyagi Prefectural Forestry Technology Institute, Miyagi, Japan. 4 Forest Tree Breeding Center, Forestry and Forest Products Research Institute, Okayama, Japan.

The applicability of spray pollination for *Cryptomeria japonica* in the field, as an artificial pollination promotion technique, was examined to effectively utilize a small amount of pollen while improving workability. First, the effect of storage time of the pollen grain–water suspension on pollen activity was evaluated. Pollen grains stored for 12 h in the suspension had a similar germination activity to those evaluated immediately after the suspension was prepared. Then, spray pollination with three levels of pollen concentrations (0.2%, 0.5%, and 1.0%) on multiple mother tree clones with female strobili at different developmental stages (start, half-open, and full-open) was tested. In addition, to evaluate whether mating following spray pollination was successful, the seedlings grown from the collected seeds were subjected to paternity analysis using DNA markers. There was no effect by spray pollination on the levels of cone yield and the 100-seed weight (p > P.5). Conversely, spray pollination at 1.0% pollen concentration had a significant positive effect on the seed germination rate (p < P.5). Spray pollination at the two pollen concentrations of 0.5% and 1.0% had a significant positive effect on the ratio of seedlings (mating success rate) for the spray pollen used (p < P.5 and p < P.1, respectively). The mating success rate with the 1.0% pollen concentration was higher than that with the 0.5% concentration. Among the three female strobili developmental stages, the mating success rate tended to be higher when spray pollination was performed at the half-open stage. A mating success rate of 0.362 was predicted using a spray pollination with 1.0% at the half-open stage of strobili. In summary, spray pollination was shown to have beneficial effects on mating even in the field.

P.0083 Pollen spectrum analysis between two cities in the province of Córdoba, Spain.

Thalia Morales[1], Carmen Torres[1], María José Tenor Ortiz[1], María Castro[1], Quasim Farroq[1], Purificación Alcázar[1], Carmen Galán[1]

1 Andalusian Institute for Earth System Research, University of Córdoba, Spain.

A comparative study was carried out between two localities in southern Spain (Province of Córdoba, Andalusia), one rural (Hinojosa del Duque) at 542 m a.s.l., one urban (Córdoba capital), 123 m a.s.l. Sampling was performed for two years (2021 - 2022). Aerobiological sampling was performed using a Hirst-type 7-day pollen trap, in accordance with the procedure developed by the European Aerobiology Society (EAS). As a result, 54 pollen types were identified in both locations. In total, 33 pollen types were classified as herbaceous and 21 as arboreal. The mean Annual Pollen Integral (APIn) determined for Córdoba was 239,973 pollen grains/m³, while in Hinojosa was lower, with 180.612 pollen grains/m³. The most abundant pollen types varied in both locations. In Córdoba, 13 pollen types were identified with at least 1%: *Olea* (38%), *Quercus* (21%), Poaceae (7%), *Cupressus* (7%), Moraceae (4%), Urticaceae (4%), *Platanus* (3%), *Corylus* (3%), *Pinus* (2%), *Fraxinus* (2%), and *Plantago,* Asteraceae and *Populus* with 1%. In Hinojosa, 8 pollen types were identified: *Quercus* (38%), *Olea* (24%), Poaceae (13%), *Cupressus* (6%), Urticaceae (6%), *Plantago* (3%), *Pinus* and Amaranthaceae with 1%. The main pollen season (MPS) in Córdoba starts one month earlier than in Hinojosa, and it is also longer. Several deviations between the urban and rural sites were also noted. Córdoba exhibited higher annual pollen concentrations, largely driven by *Olea* concentrations. The urban site exhibited a greater range of pollen concentrations and pollen types due to the increased presence of ornamental plants, such as *Platanus.* For Hinojosa, *Quercus* is the most representative arboreal pollen type in both years and an increase in altitude delays the onset of floral phenology and the duration of flowering is shorter, because of the thermal gradient experienced as altitude increases, for that reason Hinojosa we recorded lower APIn.

P.0084 Detection and control of grapevine pathogenic fungi: Plasmopara viticola, Erysiphe necator and Botrytis cinerea. A systematic review

Guillermo Muñoz-Gómez[1], Federico Fernández-González[1], Rosa Pérez-Badia[1]

1 University of Castilla-La Mancha, Institute of Environmental Sciences, Toledo, Spain.

Fungal diseases are a problem in viticulture due to the economic losses they cause. The intensive use of fungicides for their control and prevention has negative impacts on the environment and human health. To minimize these impacts, integrated crop management has been promoted and efficient and sustainable prevention and control strategies for these diseases have been developed. The aim of this work has been to carry out a systematic review of the studies that deal with control systems and early detection of grapevine pathogenic fungi: *Plasmopara viticola* (downy mildew), *Erysiphe necator* (powdery mildew) and *Botrytis cinerea* (grey mould). This review has been performed following the standard PRISMA 2020 protocol and includes 129 studies that show the current knowledge on this topic. Aerobiological sampling is useful to determine the presence and abundance of these pathogenic fungi in vineyards. Volumetric traps are the most used spore samplers. In the samples obtained, spores are identified and quantified by optical microscopy or molecular techniques. Molecular and remote sensing techniques allow fungal infection to be detected before the onset of symptoms. Grapevine pathogenic fungi synchronize the beginning and end of their life cycles with budbreak (spring) and grapevine senescence (autumn), and the course of the different stages of the life cycle depends on climatic variables of each year. Therefore, forecasting models that inform about the time of onset and evolution of the grapevine diseases mainly take into account meteorological variables, as well as airborne spore concentrations from previous days in some cases. Up to now, warning systems established to alert farmers to the development of fungal diseases are effective but have not yet been successfully implemented in vineyards.

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P.0085 Agricultural activities as key factor in the disproportionate increase of airborne spore concentration in non-rural areas

Alberto Rodríguez-Fernández[1], Ana María Vega-Maray[1], Rosa M. Valencia Barrera[1], Carlos Blanco-Alegre[2], Tibor Molnar[3], Delia Fernández-González[1,4]

1 Department of Biodiversity and Environmental Management (Botany), University of León, León, Spain. 2 Department of Physics, University of León, León, Spain. 3 Institute of Agricultural Sciences and Rural Development, Szent István University, Szarvas, Hungary. 4 Institute of Atmospheric Sciences and Climate-CNR, Bologna, Italy.

Alternaria is a cosmopolitan and saprophytic fungus genus that compromises more than 300 species. Many species of this genus are catalogued as important phytopathogens, causing significant yield and economic losses in the agricultural sector. Moreover, *Alternaria* airborne conidia are linked to respiratory disorders, mainly asthma, in sensitized population to fungus. Traditionally, it has been observed that in rural areas, the concentration of *Alternaria* spores in the air was higher than in cities. However, land use and the long-medium distance transport of spores can lead to significant increases in the concentration of these spores in cities as well. This study aims to identify the impact of agricultural activities, carried out in locations not in close proximity to the monitoring station, have on the *Alternaria* airborne spore load in urban areas. The study was conducted in Valladolid (Central-Northwest of Spain) over a 5-year period using a volumetric Hirst spore-trap Lanzoni VPPS 2000, following the methodology proposed by CEN legislation EN 16868:2019. Daily spore concentration was measured following the methodology proposed by Galán et al. (2021), and land use maps within a 30 km radius of monitoring station were produced. In addition, wind parameters were analyzed in combination with spore concentration using a conditional probability function. The results of this study show that cereal crops act as the major sources of *Alternaria* conidia, and days with the highest concentration values matching with the period during which harvesting activities are taking place in the region. These findings highlight the relevance of emission source analysis in aerobiological studies of fungal spores, as well as the need to establish as risk days of environmental exposure to *Alternaria* during the period when agricultural activities are taking place, even in non-rural areas.

P.0086 Intradaily variations in three different areas in the atmosphere of Malaga city (Southern Spain)

Rocío Ruiz Mata[1], M. Mar Trigo[1], Enrique de Gálvez Montañez[1], Marina Muñoz García[1], Marta Recio[1], Antonio Picornell[1]

1 Department of Botany and Plant Physiology, University of Malaga, Malaga, Spain.

Airborne pollen is one of the main causative agents of allergic diseases in cities all over the world. Pollen concentrations vary throughout the day, but they may be not equal at different points all over the city, due to such concentrations are influenced by the presence of nearby pollen emission sources, wind direction and structure of the city. The knowledge of the influence of these parameters is interest for allergic people, especially in cities with a touristic interest such as Malaga. The objective of this study is to analyse and compare the intradaily behaviour of main pollen concentration in three different points of the city of Malaga in order to search for differences and compare the influence of the pollen emission sources in the nearby areas. Aerobiological data were obtained using three Hirst-type volumetric pollen trap. One of them was installed in the NW of the city, the second in the city centre, and the third one in the East coast. The study was carried out between 2019 and 2023. The samples were mounted and counted following the recommendations of the Spanish Aerobiology Network. The countings have been done hourly, considering only days without precipitations with daily mean concentration values equal or greater than that of the main pollen season for each point and year. After that the results of two-hour intervals were expressed as percentages over the daily total and the intradiurnal pattern obtained were studied. Some differences between sampling points were observed in the intradiaily patterns of the pollen types studied, due to the location of the nearby pollen emission sources, especially regarding the hour of the maximum peaks. This reflects the need to carry out aerobiological samplings in several points of a city in order to obtain a more precise and useful information to the allergic population.

P.0087 Pollen morphology sheds light on Palicoureeae and Psychotrieae (Rubiaceae) systematics

Filipe Torres-Leite[1], Hian Carlos Ferreira de Sousa[2], Tatiana Tavares Carrijo[3], Claudia Barbieri Ferreira Mendonça[2], Mário Luís Garbin[3], Renato Gondenberg[1,4], Carla Poleselli Bruniera[5], Vania Gonçalves Lourenço-Esteves[2]

1 Universidade Estadual de Campinas, Brasil. 2 Universidade Federal do Rio de Janeiro, Museu Nacional, Brasil. 3 Universidade Federal do Espírito Santo, Alegre, Brasil. 4 Universidade Federal do Paraná, Curitiba, Brasil 5 Universidade Federal de São Paulo, Diadema, Brasil.

The Palicoureeae and Psychotrieae tribes have undergone taxonomic rearrangements involving the inclusion and exclusion of taxa, especially within the genus *Psychotria* L., to achieve the monophyly of the groups. In this context, several species of *Psychotria* are being transferred to *Palicourea*. Pollen morphology can offer a useful information for taxa delimitation, also providing a morphological basis for phylogenetically supported groups. Here we present the palynological study of 37 species of Palicoureeae and Psychotrieae tribes circumscribed under the genera *Eumachia* DC. (3 spp.), *Palicourea* (17 spp.), *Psychotria* (13 spp.), *Rudgea* Salisb. (3 spp.), besides *Geophila repens* (L.) I.M. Johnst. Acetolyzed pollen grains were analyzed under light microscopy, measured, and photomicrographed. Additionally, scanning electron microscopy was employed to analyze the pollen surface of non-acetolyzed grains. Two groups of species were recognized based on pollen polarity. The major group comprises the species with apolar (33 spp.) and inaperturate (32 spp.) pollen grains. These species differed among each other by the pollen size varying from medium, large, or very large, and by the surface ornamentation, which shows foveolate, rugulate, granulate, perforate, scabrate, microreticulate-equinolate, microreticulate, or reticulate sexine. Considering the species with apolar pollen grains, *Geophila repens* was the only one with a pantoporate aperture. Isopolar pollen grains were observed in a minor group comprising the species of *Eumachia*, one species of *Rudgea,* and two species of *Psychotria*. The studied species exhibited diverse pollen morphology, particularly in the sexine ornamentation. Notably, there was a consistent morphological similarity between *Psychotria* and *Palicourea* species that present apolar pollen grains. This finding supports the current nomenclatural transfer of species from *Psychotria* to *Palicourea*.

P.0088 Pollen diversity in Lepidaploa R.M.King & H.Rob. (Asteraceae)

Vania Gonçalves-Esteves[1], Simone Cartaxo-Pinto[1], Tatiana Tavares Carrijo[2], Roberto Lourenço Esteves[1], Claudia Barbieri Ferreira Mendonça[1]

1 Universidade Federal do Rio de Janeiro, Museu Nacional, Rio de Janeiro, Brasil. 2 Universidade Federal do Espírito Santo, Alegre, Brasil.

Pollen morphology has been playing an important role in the taxonomy of *Lepidaploa*. The great diversity in the echinolophate pattern was used to distinguish this genus from the closely related *Lessingianthus*. However, since the pollen morphology of the approximately 150 species currently recognized in *Lepidaploa* has not been comprehensively examined, the subject remains open for further investigation. In this study, pollen material from 26 species of *Lepidaploa* was analyzed using light microscopy and scanning electron microscopy. For the former, the pollen material was acetolysed, and for the latter, non-acetolyzed pollen grains were analyzed. The species had medium or large pollen grains, suboblate, oblate-spheroidal or prolate-spheroidal, small, or large polar area, 3-colporate, endoaperture in apertural gaps, presenting in three forms: a- two muri transversal individualizing three gaps, b- two muri not completely fused, c- without transversal muri. Equinolophate sexine, with gaps that form four patterns of organization: 1) three apertural gaps, six abapertural, six parapertural pairs, six interapertural and two polar, 2) three apertural gaps, six abapertural, six parapertural pairs, six interapertural, two polar and three equatorial, 3) three apertural gaps, six abapertural, six pairs of paraapertural and six interapertural, with "Y" formed by the union of the walls of the interapertural gaps, 4) three apertural gaps, six abapertural, six pairs paraapertural, six interapertural and three equatorial. Pollen characters, such as the number of lacunae and aperture area morphology, were useful to distinguish the species of *Lepidaploa*. However, some of these patterns were also described for pollen grains in *Lessingianthus*.

P.0089 Recent changes on grasses phenological stages in Cordoba, Spain (2022-2023)

María José Tenor Ortiz[1], Purificación Alcázar[1], Moisés Martínez-Bracero[1], Carmen García-Llamas[1], Rocío López-Orozco[1], Thalía Morales[1], Carmen Galán[1]

1 Andalusian Institute for Earth System Research, University of Córdoba, Córdoba, Spain.

Phenology is defined as the study of recurring biological events in the life cycle of plants, animals, and all biological organisms, and their synchronization with changes in weather and climate. Grasses are the group of plants that cause the most respiratory allergies in humans, described as the most important cause of pollinosis in Europe due to the allergenicity of their pollen. This study focuses on observing how the grass phenological stages have varied during 2022 and 2023, in the surroundings of the city of Córdoba (Spain), in comparison to 2000-2021. The study area is located on the thermo-Mediterranean bioclimatic belt of the Mediterranean region within the Holarctic kingdom. The phenological stages studied include pre-flowering (BBCH 60), start of flowering (BBCH 61), full flowering (BBCH 65), end of flowering (BBCH 67), and fruiting (BBCH 69). Fifteen species of grasses have been selected, which are presented in the three types of cover studied: pasture, riverbank, and shrub. A comparison between time periods has been made to observe changes in phenological trends caused by variations in temperature and precipitation. The full flowering phase has advanced in the last two years, resulting in a shorter duration for the first two phases. In the three types of studied land cover, full flowering is brought forward, which is related to an increase in temperature in April in both years, but especially in 2023. In different cover types, when compared with the historical data, Hordeum leporinum starts fruiting earlier due to its sensitivity to temperature increase; Bromus diandrus has a shorter phenology period due to water availability, accentuated by rising temperatures.; Dactylis glomerata begins flowering earlier; however, being a perennial grass, its phenological response to environmental changes is slower.

S.010. AFRICAN TAXONOMY: A COLLABORATIVE EFFORT TOWARDS BIODIVERSITY CONSERVATION

P.0090 A preliminary examination of diversity and evolution in an enigmatic genus of woody plants - Gymnanthemum Cass. (Compositae)

Mihajamalala A. Andriamanohera[1,2], Benoit Loeuille[3], Higor Antonio-Domingues[3], Ana R. G. Simões[3], Isabel Larridon[3], Morgan R. Gostel[1]

1 Botanical Research Institute of Texas, Fort Worth, USA. 2 University of Texas at Arlington, Arlington, USA. 3 Royal Botanic Gardens, Kew, Richmond, UK.

With 1,500 species and 130 genera, Vernonieae is one of the most species-rich tribes in the mega-diverse Compositae family. Vernonieae is often referred to as the "evil tribe" due to its large size and cosmopolitan distribution. In addition, a combination of overly general diagnostic characters has complicated efforts to resolve relationships among subtribes and delimit genera. In the Gymnantheminae subtribe, this complexity is illustrated by a particular genus *Gymnanthemum*. The genus spans much of the (sub-) tropics in the Eastern Hemisphere particularly in Madagascar, a biodiversity hotspot, where approximately half of its species thrive. *Gymnanthemum* is recognized based on only a few generalized characters such as being a shrub or tree habit and having phyllaries with broad and smooth shields. However, this description has led to confusion regarding the circumscription of species within this genus. Our present research combines molecular phylogenet-

ic inference, comparative morphology, and careful study of herbarium vouchers to clarify the distinction between *Gymnanthemum* and other genera in Vernonieae. Our preliminary results indicate that *Gymnanthemum*, as currently circumscribed, is not monophyletic, which emphasize the need for an integrative taxonomic approach to distinguish this taxon and identify more useful diagnostic characters. Beyond the impact of our work on advancing the systematic knowledge of *Gymnanthemum*, this research will also address broader questions regarding the biogeography and evolution of plant diversity in tropical Africa and Madagascar. Our findings will also contribute to the effective dissemination of taxonomic knowledge through the Global Compositae Database, an innovative public repository managed by the International Compositae Alliance (TICA), which is recognized by the World Flora Online as a Taxonomic Expert Network.

P.0091 Assessing the distribution of naturalized alien plant species on different habitats in southern Spain

Diana Zugasti-Hervás[1], Yoel Aroca-Martínez[1], Marcos Moreno-Rabadán[1], María D. Jiménez[1], Juan A. Delgado[1]

1 Universidad Complutense de Madrid, Madrid, Spain.

Plants' dispersal ability is mainly determined by the morphology of their generative dispersal units (also known as diaspores or propagules) and is crucial for both: the spread of plant species to new habitats and regions, and 2) the regulation of plant coexistence through processes of colonization. Another key plant trait is the growth form (sensu Raukianen), since it reflects plant adaptation to deal with climatic conditions, especially extreme conditions such as frost and drought. In this study, we use both dispersal ability and growth forms to assess the presence of 66 naturalized alien plant species in terrestrial habitats in Andalucía (Spain). We hypothesize that alien species in different habitat types will present predominant life forms, responding to microclimatic differences, and exhibit different dispersal syndromes due to varying colonization opportunities. Contrary to our initial predictions, we found that dispersal modes did not exhibit a significant correlation with the presence of alien species in the terrestrial habitats under study. This finding stands in contrast to previously reported results concerning the abundance of alien species in Mediterranean islands. However, our investigation did reveal the influence of growth forms, with phanerophytes notably absent from agricultural environments, and chamaephytes and hydrophytes overrepresented in seminatural and agricultural habitats, respectively. In contrast, therophytes, geophytes, and hemicryptophytes were present consistently across all habitats. These results suggest that environmental constraints are more relevant than dispersal constraints in explaining the presence of naturalized alien plant species in particular habitats.

P.0092 Distribution of the alien flora of Sardinia (Italy) across habitat types

Giuseppe Brundu[1,2], Flavio Marzialetti[1,2], Vanessa Lozano[1,2]

1 Department of Agricultural Sciences, University of Sassari, Sassari, Italy. 2 National Biodiversity Future Center, Palermo, Italy.

To date, the alien flora of the island of Sardinia (Italy – 24,090 km²) lists 640 alien species (348 casual, 215 naturalized, and 77 invasive) over a total flora of ca. 2700 taxa (Portal to the Flora of Italy. Available at http:/dryades.units.it/floritaly). Based on expert knowledge and on the available scientific literature, we assessed the distribution of the alien plant species across 15 main habitat types, according to the categorization proposed by Pyšek et al. 2022 (in Preslia 94: 447–577) (i.e., Natural forest, Plantation forest, Open forest, Scrub, Natural grassland, Human-mantained grassland, Sandy, Rocky, Dryland, Saline, Riparian, Wetland, Aquatic, Ruderal, and Agricultural). We added the class Plantation forest (with alien trees) due to the importance of this type of land-use in Sardinia both for its extension and for being a place where naturalization commonly takes place. Additionally, we used the University of Sassari Department of Agricultural Sciences database on invasive alien plants in Sardinia (Brundu et al. 2003 – In: Plant Invasions, Backhuys Publ.) which holds occurrences collected by GPS in the field (since 2000, and periodically verified for their persistence) and it is made up by ca. 20,000 occurrences, to assess through GIS analysis the distribution across the habitat types of the Sardinia Nature Map (Camarda et al., 2011 - ISPRA, 222/2015). This Nature Map uses the CORINE Biotopes and HD legends (with a total number of 93 habitat types). As a result, we present here the first preliminary assessment of habitat preferences for the alien flora of Sardinia. While casual and naturalized species are mostly found in ruderal habitats and, to a lesser extent, in agricultural habitats, invasive alien species are found in larger array of habitats, spanning over all the 15 main categories considered in the present study. Research funded by the European Union, NextGenerationEU.

P.0093 Status of the distribution, ecology and diversity of alien flora in the island of Menorca – Reserve of Biosphere

Miquel Capó[1], Joshua Borràs[2], Pere Fraga[3], Juan Rita[2], Joana Cursach[2]

1 Plant & Animal Ecology Lab. Centro para la Conservación de la Biodiversidad y el Desarrollo Sostenible. Departamento de Sistemas y Recursos Naturales. Universidad Politécnica de Madrid, Madrid, Spain. 2 Research Group of Plant Biology under Mediterranean Conditions. Departament de Biologia. Universitat de les Illes Balears. Palma, Spain. 3 Jardí Botànic de Marimurta. Fundació Carl Faust. Blanes, Spain.

Mediterranean ecosystems are among the most vulnerable to biological invasions, with the alien flora and fauna experiencing exponential growth in recent decades. This impact is particularly detrimental on islands, where the introduction of alien species can severely affect native plant species and the overall functioning of the ecosystem. As it is well-known, the establishment of these species is not homogeneous and depends on the habitat suitability of each species. In this study, we evaluated the current status of plant alien species on Menorca (Balearic Islands, western Mediterranean Basin), considering that the entire island is managed under Biosphere Reserve criteria. Specifically, we focused on the link between alien species and: (1) habitat specificity, (2) land uses, and (3) geographic distribution. We divided the island into 11 grids of 10×10 km2 each and explored eight habitats in each of them: dunes, rocky coastline, wetlands, shrublands, cliffs, crops, roadside, and torrents. For each grid, we visited three different sites per habitat and compiled the floristic inventory of alien species, adding a semiquantitative measure of abundance using the DAFOR method (Dominant, Abundant, Frequent, Occasional, and Rare levels). In general, we found 120 alien species throughout the entire study system, distributed across different habitats and geographic locations. Number of introduced species was higher in coastal areas, crops, and torrents. From a geographic perspective, sites close to urban areas exhibited more species or higher abundances than sites surrounded by natural areas. Interestingly, we identified 12 new alien species for the island, some of them with potentially invasive behavior. This study emphasizes the importance of monitoring and studying the patterns of introduction and their relationship with ecological and geographical ranges. Consequently, this study will provide information to guide management actions, especially valuable in areas like Biosphere Reserves where the conservation of biodiversity is of utmost priority.

P.0094 On the presence of Cactaceae species naturalized in the Mediterranean: challenges on recording effort and plant identification

Marcello Dante Cerrato[1,3], Iván Cortés-Fernández[1], Pere M. Mir-Rosselló[1,3], Carles Cardona[1,2], Lorenzo Gil[1]

1 Interdisciplinary Ecology Group, Department of Biology, University of the Balearic Islands, Palma, Spain. 2 Centre Forestal de les Illes Balears, Institut Balear de la Natura, Palma, Spain. 3 Research Group On Plant Biology Under Mediterranean Conditions, Departament de Biologia, Universitat de les Illes Balears-Agro-Environmental and Water Economics Institute, Palma, Spain.

Plant introductions are a pressing environmental concern, with some families showing traits for rapid adaptability. Among these families, *Cactaceae* stands out in the Mediterranean area for its substantial establishment and flourishing. Over recent decades, there has been a significant surge in the presence of *Cactaceae*, both in the number of recorded species and their distribution across the area. This study systematically gathers information on *Cactaceae* species through diverse sources, including online databases, manuscripts, and citizen science data (such as iNaturalist). A list of species and their distribution across Mediterranean regions is compiled. The findings reveal 78 recorded taxa, although this number remains contentious due to the high taxonomical complexity, particularly within genera like *Opuntia*, *Cylindropuntia* and *Echinopsis* s.l. The prevalence of recorded species is notably higher in western Mediterranean areas, particularly Catalonia and Valencia, followed by neighboring regions like the BalearicIslands, Sicily, and mainland Italy. Moderate occurrences are observed in western North African and central Mediterranean regions around the Adriatic Sea, while eastern Mediterranean regions, including the Middle East and Egypt, exhibit less records. *Opuntia*, *Cylindropuntia*, and the *Echinopsis* complex can be considered the genera with higher species richness. However, distribution among regions is higher for *Opuntia* (*O. ficus-indica* and *O. stricta*), *Cylindropuntia* (*C. imbricata*) and *Austrocylindropuntia* (*A. subulata*), leaving cactoideae taxa confined to few or only one region. Literature comprehensively describes *Cactaceae* in the Western-Mediterranean, while platforms like iNaturalist prove relevant to assess their presence in central and eastern Mediterranean regions. Furthermore, iNaturalist challenges existing taxonomical knowledge by hinting at the potential existence of cryptic species that require thorough taxonomic evaluation. *Cactaceae* in the Mediterranean represents a complex instance of plant introduction, necessitating further investigation, enhanced identification tools, and field data to better comprehend its invasion dynamics.

P.0095 The importance of cities as source of alien species to filling the gaps of knowledge

Fiona Corominas[1], Lluís Vilar[1,2], Jordi Bou[1,2]

1 LAGP, Institute of the Environment, University of Girona, Girona, Spain. 2 BioLand – Biodiversity and landscape research group, University of Girona, Girona, Spain.

Alien flora is one of the most important elements of the biodiversity crisis and the threat that represents could increase considerably due to the global change. Consequently, knowing it's distribution and abundance plays a key role on environmental managing for preserving native flora. Urban landscapes are an important origin source of alien flora, as gardens are considered one of the most commune cause on introduction. Therefore, cataloguing alien floras in natural areas of urban landscapes provides interesting information about this problematic. The aim of this study is to identify the abundance and distribution of a city's alien flora to analyse the distribution patterns and to model dispersion dynamics. Girona, a city surrounded by natural areas dominated by Mediterranean vegetation and crossed by rivers, is taken as the study case. A high-resolution cartography of alien flora has been produced, sampling and georeferencing it over all the urban landscape and the natural areas of its surroundings. The results show that 160 species have been identified in natural conditions and some of them are first presence at regional scale, also a considerable percentage are considered invasive. The distribution of alien flora shows a pattern related to the proximity of urban areas and a hotspot at river ecosystems, identifying these types of areas as more susceptible to plant invasions. Instead, Mediterranean vegetation is less affected by alien plants as there are no available niches and perturbations do not create the optimal conditions for colonization, although urbanizations and isolated houses with gardens are a clear source of them. The results prove the importance of filling the gaps on urban landscapes because are the main source of alien plants spread. To conclude, since the first stages of invasion are important for successful alien species management, urban landscapes need to be studied and catalogued.

P.0096 Occurrence of Aristolochia baetica (Aristolochiaceae) on the southern Croatian island, NE Mediterranean

Katija Dolina[1], Kristina Ćurčija[2]

1 Institute for Marine and Coastal Research, University of Dubrovnik, Dubrovnik, Croatia. 2 Public institution Lokrum reserve, Dubrovnik, Croatia.

Aristolochia L. (Aristolochiaceae) is a species rich genus with 540 accepted species distributed throughout the world, mainly in tropical-subtropical regions. In the Euro-Mediterranean region, 46 *Aristolochia* species and five subspecies have been listed. In Croatia, the genus *Aristolochia* is represented by four species: *Aristolochia clematitis* L., *A. lutea* Desf., *A. pallida* Willd. and *A. rotunda* L. The occurrence of *A. baetica* L., a species native to Algeria, Morocco, Portugal and Spain, is reported and documented here for the first time for Croatia. In spring 2022, *A. baetica* was recorded for the first time in the southern part of the country on the small island of Lokrum (72 ha), which is a nature reserve and part of the Natura 2000 ecological network. This evergreen perennial vine is represented by a small population consisting of three individuals twining their branches around the *Pistacia lentiscus* L tree. The species was found on calcareous soil at an altitude of 5 metres a.s.l., alongside a path in a clearing with *Quercus ilex* L. and evergreen maquis, which is occasionally maintained by mowing. The following species were found at this site: *Quercus ilex* L., *Phillyrea latifolia* L., *Viburnum tinus* L., *Vinca major* L. etc. Prior to this study, *A. baetica* had not been found in Croatia or in neighbouring countries. The pathways of introduction of the species to the island are still unclear. It is likely that the appearance of *A. baetica* is due to human influence. We believe that the discovery of *A. baetica* in Croatia contributes to the knowledge about the chorology and ecology of the species in European countries. Further observations are needed to find out whether the climatic and other ecological conditions are suitable for the spread of the plant and what impact the species might have on local biodiversity.

P.0097 Casual, naturalized, and invasive alien flora in eastern and north-eastern Iberian Peninsula and the Balearic Islands

Carlos Gómez-Bellver[1], Neus Ibáñez[1], Neus Nualart[1], Jordi López-Pujol[1]

1 Botanic Institute of Barcelona, Barcelona, Spain.

Biological invasions are considered one of the main causes of planetary biodiversity loss. In the case of plants, they are primarily a consequence of anthropogenic activities, with main causes being the transportation of people and goods, the importation of plants or seeds, the disposal of garden waste, and the contamination of seeds of agricultural interest. Given the significance of this phenomenon, a PhD dissertation focused on all alien plants (casual, naturalized, or invasive) distributed in the north and north-east of the Iberian Peninsula (Catalonia and Valencia) and the Balearic Islands was recently (2023) completed. As a result, a catalog with updated and detailed information—up to the year 2020—on these species and their main characteristics was compiled, along with distribution maps. Taking advantage of this forum we have updated the catalogue of the alien flora of this region (including any update of the distributional range on the already catalogued species). Over 1400 alien species have been observed in the studied area, confirming this region as one of the main invasion hotspots in Europe. The highest richness of alien plants is found in coastal and nearby areas, especially in places with a high concentration of human population. Neophytes (species introduced between 1500 and 1970) and recent neophytes (post-1970) predominate (with close percentages), while archaeophytes (pre-1500) are in the minority. Our study confirms that plants intended for cultivation in gardens are the primary cause of introductions of alien species in Europe in recent decades.

P.0099 A taxonomic revision of Hydnora (Hydnoraceae): a poorly known genus of holoparasitic plants

Sebastian A. Hatt[1,6], Chris Thorogood[2,3], Jay F. Bolin[4], Lytton J. Musselman[5], Duncan D. Cameron[6], Olwen M. Grace[7]

1 Royal Botanic Gardens, Kew, Richmond, UK. 2 Department of Plant Sciences, University of Oxford, Oxford, UK. 3 University of Oxford Botanic Garden and Arboretum, Oxford, UK. 4 Department of Biology, Catawba College, Salisbury, USA. 5 Department of Biological Sciences, Old Dominion University, Norfolk, USA. 6 Department of Earth and Environmental Sciences, University of Manchester, Manchester, UK. 7 Royal Botanic Garden Edinburgh, Edinburgh, UK.

Hydnora (Hydnoraceae) is a poorly known genus of holoparasitic plants distributed across Africa, Madagascar and southern Arabia. Species of *Hydnora* are characterised by their underground habit, unusual fleshy flowers and complete absence of leaves or photosynthetic tissue. Here, we present a poster summarising our taxonomic monograph of *Hydnora*: the first detailed monograph of the genus since 1935. Our monograph provides detailed descriptions, full synonymy, distribution maps and discussion concerning confusable taxa for each species, along with notes on ethnobotany, ecology and conservation. We place particular emphasis on the taxonomic value of osmophore geometry and positioning in living and dried material, which are consistent within species. We also provide the first detailed assessment of host range across the genus. *Hydnora hanningtonii* Rendle and *H. solmsiana* Dinter are reinstated from synonymy, and *H. bolinii*

Hattis newly described here. The infrageneric classification is reviewed and a key is provided for both living and dried material. Species are accompanied by both illustrations and photographs of living and dried material where possible.

P.0100 Checklist of the non-native vascular flora of continental Ecuador

Ileana Herrera[1,2], Anahí Vargas[1], Kimberly Rizzo[1], Zhofre Aguirre[3], Felipe Espinoza De Janon[4], Brunny Espinoza-Amén[5], Andrés Espinoza-Maticurena[1,6], Efraín Freire[2], Kevin Panchana[1], Verónica Sandoya[7], Katya Romoleroux[8], Carmen Ulloa Ulloa[9], Nora H. Oleas[10], Isabella Dillon[1], Alejandra Moscoso-Estrella[11], Carlos Gómez-Bellver[12], Vanessa Lozano[13,14], Sebastián Pardo[3], Isabela Vieira[1], Jordi López-Pujol[1,12]

1 Centro de Investigaciones, Universidad Espíritu Santo, Samborondón, Ecuador. 2 Instituto Nacional de Biodiversidad, Quito, Ecuador. 3 Herbario Reinaldo Espinosa, Universidad Nacional de Loja, Loja, Ecuador. 4 School of Biological Sciences, University of Edinburgh, Edinburgh, UK. 5 Vrije Universiteit Brussel, Department of Biology, Brussels, Belgium. 6 Fundación para la Conservación e Investigación JaPu, Guayaquil, Ecuador. 7 School of Biological Sciences and Engineering, Yachay Tech University, Urcuquí, Ecuador. 8 Herbario QCA, Escuela de Ciencias Biológicas, Pontificia Universidad Católica del Ecuador, Quito, Ecuador. 9 Missouri Botanical Garden, St. Louis, USA. 10 Facultad de Ciencias de Medio Ambiente, Universidad Tecnológica Indoamérica, Quito, Ecuador. 11 Departamento de Biología, Escuela Politécnica Nacional, Quito, Ecuador. 12 Institut Botànic de Barcelona (IBB, CSIC-CMCNB), Barcelona, Spain. 13 Department of Agricultural Sciences, University of Sassari, Sassari, Italy. 14 National Biodiversity Future Center, Palermo, Italy.

Inventorying non-native species in continental Ecuador is still in its infancy. The only attempt to date to produce a list of non-native species for continental Ecuador is the one published on the Global Register of Introduced and Invasive Species (GRIIS) database, reporting 577 species of vascular plants. Therefore, the aim of this study is to provide an up-to-date inventory of the non-native vascular flora of continental Ecuador. Our list reported 1,176 non-native plant species in continental Ecuador which nearly doubles the number of taxa of non-native plants previously reported. This list was complemented with data on taxonomy, life-form, lifespan, biogeography, first year record, and spatial-temporal distribution. Among the total taxa, 50% (582) were cultivated (i.e., not having any record of them as escaping from cultivation), 43% (502) were growing spontaneously, and 8% (*n* = 92) had an unknown status. The families with the highest number of non-native taxa growing spontaneously were Poaceae (17%, *n* = 83), Asteraceae (10%, *n* = 49), and Fabaceae (8%, *n* = 41). Most of non-native plant taxa in the wild (69%; *n* = 346) originated from Asia or/and Africa. Although the first record of a non-native wild plant in Ecuador was in 1799, the number of taxa introductions increased exponentially since 1915. The biogeographical region with the majority of taxa (87%, *n* = 435) was the Andes. We found reported uses in continental Ecuador for 73% (*n* = 367) of non-native taxa that occur in the wild; among these, the most frequent were ornamental (39%, *n* = 196), medical (34%, *n* = 170), and food crop (21%, *n* = 107) uses, which should be regarded as the main pathways of (intentional) introduction. Our results provide valuable insights for early detection, prioritization, and management of non-natives vascular plants present in continental Ecuador.

P.0101 Ecological and morphometric study of the genus Carpobrotus in the Western Mediterranean Basin

Eduard López-Guillen[1], Joan Pere Pascual-Díaz[1,2], Laura Valenzuela[1], Daniel Vitales[1], Sònia Garcia[1], Neus Nualart[1], Jordi López-Pujol[1]

1 Botanic Institute of Barcelona (CSIC-CMCNB), Barcelona, Spain. 2 Departament de Biologia Animal, Biologia Vegetal i Ecologia, Facultat de Biociències, Universitat Autònoma de Barcelona, Bellaterra, Spain.

The genus *Carpobrotus N.E.Br.* has more than a dozen species that are native to the Southern Hemisphere, mainly, Southern Africa. However, some of these species have naturalized outside their native range as a result of being used as ornamental plants, as well as for stabilization of coastal dunes. The genus has become invasive all across the Mediterranean Basin, posing a great threat to biodiversity. As of today, as there are three species within this genus that are considered invasive (*C. chilensis*, *C. edulis* and *C. acinaciformis*), which are known to produce hybrid forms and result in a taxonomic complex that is hard to tell apart from the parental forms. Therefore, the taxonomy and biogeography of the genus *Carpobrotus* remains unclear and under discussion. The populations of the Western Mediterranean Basin were initially assigned to *Carpobrotus edulis* for most of the cases, however most recent studies suggest that they could belong to different species and, probably, to the hybrid forms between them. In this study we analyzed various morphological characteristics of the reproductive and vegetative organs from over 30 populations stretching from southern Spain to southern Italy. We also extracted the bioclimatic variables from a much wider set of populations (nearly 400) from the same geographic area. These data were used in order to: (i) test whether different entities can be identified based on morphometric characters, (ii) describe entities based on these characteristics and (iii) see if there are differences in their ecological niche of different morphotypes.

P.0102 Prioritizing invasive non-native plants through expert-based decisions across continental Ecuador

Vanessa Lozano[1,2], Jordi López Pujol[3], Ileana Herrera[4,5]

1 Department of Agricultural Sciences, University of Sassari, Sassari, Italy. 2 National Biodiversity Future Center, Palermo, Italy. 3 Institut Botànic de Barcelona (IBB, CSIC-CMCNB), Barcelona, Spain. 4 Escuela de Ciencias Ambientales, Universidad Espíritu Santo, Samborondón, Ecuador. 5 Instituto Nacional de Biodiversidad, Quito, Ecuador.

An up-to-date list of invasive non-native species is a fundamental tool supporting prevention and control. It forms the basis for informed decision-making, resource optimization, and collaborative efforts across various sectors and geographic boundaries. In Ecuador different projects have involved the leading of scientific societies drawing up a list of the invasive non-native species found in the continental part of the country (i.e., excluding the Galapagos Islands) and mostly in protected areas that need to be stringently controlled, developing important approaches for biodiversity conservation. However, engaging with local communities and stakeholders to gather information on non-native plants and their impacts is necessary for managing invasive species. The main aim is to present the first list of candidate invasive non-native plant species that should be prioritized for their management based on their highest potential threat to biodiversity in continental Ecuador and develop a simple and replicable methodology to select these species. It is expected that one of the most important results will be to present the first list of priority emergent invasive non-native plants that can be the cornerstone of the National List of Invasive Plants of Continental Ecuador for which early management actions such as eradication are still feasible. By establishing a well-defined prioritization process, Ecuador can efficiently allocate resources and implement targeted management strategies to address the most urgent threats posed by non-native plants. This proactive approach is essential for minimizing the ecological, economic, and social impacts associated with invasive species.

P.0103 Woody plant diversity in a 15-ha forest dynamics monitoring plot in Ankarafantsika National Park, NW Madagascar

Wataru Noyori[1], Yutaro Fujimoto[1], Sato Hiroki[2], Shuichiro Tagane[3], Rabarison Harison[4], Kaoru Kitajima[1]

1 Graduate School of Agriculture, Kyoto University, Kyoto, Japan. 2 Graduate School of Asian and African Area Studies, Kyoto University, Kyoto, Japan. 3 The Kagoshima University Museum, Kagoshima University, Kagoshima, Japan. 4 Faculty of Sciences, University of Antananarivo, Antananarivo Madagascar.

Madagascar, famous for rich flora with extremely high levels of endemism, is facing a rapid and widespread loss of natural forests and other floristically rich habitats. We have a conducted quantitative floristic survey of Ankarafantsika National Park, which currently holds the largest area of natural forests within the seasonally dry forest biome in NW Madagascar. We set up a 15 ha (300 m x 500 m) plot on gentle hills (150-190 m ASL) covered with a thick layer of coarse white sand (Jardin Botanic A). We mapped, measured for diameter, and identified to species or genus all trees exceeding 5 cm in diameter at breast height (DBH) within the 15 ha plot, as well as those above 1 cm DBH in the central 200 m by 300 m area. These data were supplemented by a transect survey of 5 m x 100 m in nearby areas within which all vascular plants were recorded. A photographic guide of JBA flora is prepared, with a set of voucher specimens deposited to the herbarium of the University of Antananarivo. We enumerated ca. 130,000 woody stems within the 15 ha, which encompassed 60 families with ca. 130 genera. The 15-ha plot on extremely infertile sandy soil trees consisted of a dense stand of relatively small trees, mostly less than 15 m and diameter of 20 cm. Evergreen trees and lianas were dominant, despite the prolonged dry season (April – November), perhaps because evergreen leaf habits are linked to nutrient conservation strategies. The most diverse families were Rubiaceae, Fabaceae, and Apocynaceae, while Oleaceae, Putranjivaceae, and Rubiaceae emerged as dominant families. These botanical and ecological data contribute to a better understanding of how this forest has maintained a biologically diverse community on the extremely infertile soil, as well as to designing strategies for its effective conservation.

P.0104 Taxonomy and Phylogenomics: modern classification and biogeography of the Putranjivaceae (Malpighiales)

Alejandro Quintanar[1], Irene Villa-Machío[2], Patricia Barberá[2], David J. Harris[3]

1 Real Jardín Botánico de Madrid CSIC, Madrid, Spain. 2 Missouri Botanical Garden, Saint Louis, USA 3 Royal Botanic Garden Edinburgh, Edinburgh, UK.

We present an overview of the current status and results of our studies in the family Putranjivaceae (Malpighiales). It includes dioecious evergreen trees from tropical and subtropical territories of the World that frequently inhabit evergreen moist forests with high rainfall regimes, where they are especially diverse and considered indicators of their conservation status, but also extend into monsoon or semi-evergreen seasonally dry forests. The Putranjivaceae are distributed between two genera, *Putranjiva* Wall. (4 spp.), from south and southeast Asia, and the pantropical ironplums' genus *Drypetes* (219 spp.). *Drypetes* is especially well-known because of the difficulties found by naturalists to properly identify its species, mostly due to the lack of a global taxonomic revision for a century, and to factors linked to the particular features of these plants. The family is much more diverse in Africa (86 spp.) than in America (20 spp.), as well as just moderately less than in Asia and Pacific (117 spp.), which could contravene the consideration of Africa as the "odd man out" for species diversity in the tropics. Hardly sampled in molecular phylogenies published to date, we currently perform the first phylogenomic study focused on these plants, which is aimed to clarify their systematics, as well as to reconstruct their enigmatic biogeographical history. Since 2020 we have already published 7 new African species, and we now complete the family treatment for *Flore d'Afrique Centrale* and an updated world checklist that is to be used as a taxonomic backbone for the *WFO Plant List*. Likewise, we have already published IUCN Assessments for 11 species and plan to assess in the near future the whole African species set with our eye on the conservation of this fascinating group of plants.

P.0105 Expansion of the network of migration routes for invasive alien plant species on the Balkan Peninsula and the Pannonian Plain

Milica Rat[1], Bojana Bokić[1], Boris Radak[1], Dubravka Milić[1], Goran Anačkov[1]

1 University of Novi Sad, Faculty of Sciences, Department of Biology and Ecology, Novi Sad, Serbia.

Invasive species changed the perspective of nature conservation in the 20th century. Man-made habitats were the first to be colonised and human health was seriously affected by invasive alien species. Towards the end of the last century, it was clear that many species were already naturalised and that it was not possible to take measures to control them. However, as the introduction of new species was not yet complete, sustainable measures needed to be taken to prevent future introductions. One of the proposed measures was the definition of introduction pathways for invasive species. For this reason, an ongoing study was developed in Serbia to identify and continuously monitor terrestrial introduction pathways for invasive plant species. At the beginning of the study, the most important habitat types affected by invasive plants were identified. The next step was to identify the locations where invasive plants had already been discovered. Based on this data, the field research study was then launched. The field research focused on two points: 1) transport routes and 2) areas with preserved natural habitats. The results showed that these two groups are colonised by different invasive plants and that the migration routes, even those in the initial stages, are found in protected areas. For this reason, the known migration routes were used as a precursor for predictive modelling that identifies 1) new routes not covered by our study and 2) expected changes in the future. This information will be a valuable resource for the development of a sustainable management programme for invasive plants in Serbia and the wider region of the Pannonian Plain and the Balkan Peninsula. It is expected that the results will complement the measures implemented in neighbouring EU countries and that the proportion of new introductions can be minimised through a developed early warning system.

P.0106 Improvement of knowledge about invasive alien flora in Spain: a comprehensive and innovative approach

Sara Santamarina[1], Adrián García Rodríguez[1], Jorge Miguel Isabel Rufo[1], Carmela Capistrós Bitrián[1], Marta Viu Cuerda[2], Noelia Vallejo Pedregal[2]

1 Department of Natural Environment, TRAGSATEC, Madrid, Spain. 2 Directorate-General of Biodiversity, Forests, and Desertification, Ministry for Ecological Transition and the Demographic Challenge, Madrid, Spain.

Invasive alien species presents a threat to biodiversity conservation. To confront this challenge, the Ministry for Ecological Transition and the Demographic Challenge of Spain (MITECO) initiated in 2022 an innovative project to learn about the current status, distribution and trends of invasive exotic flora species in the national territory. Target species include flora taxa from the Spanish Catalog of Invasive Exotic Species (Royal Decree 630/2013) and those from the List of Invasive Alien Species of Union Concern (Commission Implementing Regulation (EU) 2016/1141) detected in Spain. The innovative methodology involves conducting samplings using a mobile application for data collection, the development of a pilot project for remote sensing monitoring, the citizen science initiative InvaPlant to promote social awareness and detection through the iNaturalist app, as well as coordination among public administrations. The obtained data will be compiled in the Integrated Information System of the Directorate-General of Biodiversity, Forests, and Desertification of MITECO, centralizing the generated knowledge. Preliminary results highlight the potential of adopting various innovative techniques to address the issue. The app used for samplings allowed a comfortable, traceable, and efficient real-time data collection process. Species suitable for remote sensing monitoring were identified and the foundation for their long-term monitoring was stablished. InvaPlant initiative gathered large-scale data thanks to citizen involvement. The combination of innovative monitoring techniques, information sources, and collaboration among public administrations is an effective approach to improve understanding of invasive alien flora. The collected information will contribute to meet legal commitments and will be use to design new strategies for biodiversity conservation in Spain.

P.0107 Updated list of Bryophytes from Cape Verde Archipelago

Manuela Sim-Sim[1,2], Anabela Martins1, César Augusto Garcia[1]

1 Centre for Ecology, Evolution and Environmental Changes & CHANGE - Global Change and Sustainability Institute, Departamento de Biologia Vegetal, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal. 2 Centre for Ecology, Evolution and Environmental Changes & CHANGE - Global Change and Sustainability Institute /MUHNAC - Museu Nacional de História Natural e da Ciência, Lisboa, Portugal.

In Europe, the Macaronesian archipelagos stand out as a hotspot of biodiversity with high numbers of endemic plant species. The early land plant lineages comprised as bryophytes (liverworts, mosses, and hornworts) diversified less than vascular plants in Macaronesia, but especially the northern Macaronesian archipelagos (Azores, Canaries, Madeira) still harbour a high bryophyte diversity that plays a vital role in ecosystem functioning. The southern Macaronesian Cape Verde archipelago harbours a high botanical diversity as well. Although Laurisilva vegetation is absent, the Cape Verde islands provide an important refuge for vascular plants and bryophytes, particularly communities at higher elevations. Furthermore, Cape Verde stands out due to its mixture of representatives of Afrotropical, Neotropical, Mediterranean and Asian elements. The most recent studies on the vegetation of Cape Verde highlight the coexistence between Macaronesian and Mediterranean floristic elements, and African tropical continental flora. The aim of the present study was to update the list of the bryophytes from Cabo Verde (Patiño & González-Mancebo 2005) based on thoroughly investigating species records, and the regional distribution by island using previous publications, herbarium collections, and field observations by our group between 2016 and 2019. Presently, there are 187 known taxa of bryophytes in Cape Verde, including five subspecies and seven varieties, totaling 49 liverworts (including two hornworts) and 138 mosses. This corresponds to 94 genera (25 liverworts and 69 mosses) and 45 families (18 liverworts and 27 mosses). The moss families with the highest number of taxa are Pottiaceae, Bryaceae, Brachytheciaceae, Fissidentaceae, and Bartramiaceae. Regarding liverworts, notable families include Ricciaceae, Lejeuneaceae, and Frullaniaceae. Additionally, the islands with the highest number of taxa in Cape Verde are Santo Antão, Fogo, and São Nicolau.

References: Patiño Llorente, J., & González-Mancebo, J. M. (2005). División Bryophyta. Lista preliminar de especies silvestres de Cabo Verde (hongos, plantas y animales terrestres), 34-37.

P.0108 The genus Lomaridium (Blechnaceae, Polypodiopsida) in the African continent

Rubén Vázquez[1], Lucie Bauret[2], Germinal Rouhan[2], Manuel Pimentel Pereira[3]

1 Universidad Complutense de Madrid, Madrid, Spain. 2 Sorbonne Université, Université des Antilles, Paris, France. 3 Universidade da Coruña, A Coruña, Spain.

Lomaridium C. Presl, a genus in the leptosporangiate fern family Blechnaceae Newman, includes around 15-20 species widely distributed in tropical and subtropical regions from two main diversity centres, the Neotropics and Africa-Madagascar. They are characterised by their long-creeping rhizomes covered by denticulate scales and by their dimorphic fronds and hemi-epiphytic habit. Although the genus is well defined morphologically and phylogenetically, species delimitation remains controversial, and a taxonomic revision is warranted. African species of *Lomaridium* are poorly known and barely represented in the phylogenies implemented to date. *Lomaridium* is especially morphologically diverse in Madagascar, where several endemic taxa have been defined, including terrestrial/epilithic forms with short-creeping rhizomes. Another interesting taxon is *L. attenuatum*, a species widely distributed throughout the southeastern continental regions that is morphologically very variable and probably hides cryptic diversity. We carried out a taxonomic revision based on morphological characters observed mostly on herbarium materials, as well as a molecular phylogenetic study using three plastid markers (*rps*4, *trn*L-*trn*F and *rbc*L). Thanks to this evolutionary framework, we addressed the biogeographic history of the genus, as well as the anatomical transition from the hemi-epiphytic to the terrestrial habit that has taken place in this fern genus. We found synapomorphies that support the subordination of the terrestrial taxa with short rhizomes in *Lomaridium*: *L. attenuatum* var. *giganteum*, *L. bonapartei* and *L. xiphophyllum*. These species have transitioned towards a terrestrial habit, and some characters changed along with this transition, such as the presence/absence of projections on the rhizome scales margins, or the papillose vs. smooth frond axes. The phylogenetic study explains certain morphological divergences within *L. attenuatum*, which would correspond to different taxonomic entities. Finally, we propose four new combinations and describe a new species in *Lomaridium*.

P.0109 Moss genera Pelekium and Thuidium in sub-Saharan Africa

Adéla Zámečníková[1], Vítězslav Plášek[,2]

1 Department of Biology and Ecology, University of Ostrava, Ostrava, Czech Republic. 2 Institute of Biology, University of Opole, Opole, Poland.

Between 1962 and 1978, Stanisław Lisowski collected a significant amount of material in sub-Saharan Africa. These herbarium specimens are housed in KRAM (Poland). Currently, the identification and taxonomic revision of these specimens within the genera Pelekium and Thuidium is in progress. Initial results from evaluating the ecological requirements of these species are presented. The studied species grow in central Africa, in forests with humid to semi-arid climates, at altitudes of up to 3,700 m above sea level. They primarily occur on soil in limestone rocky areas. Given the morphological similarities between the taxa of both genera, we present the main identifying characteristics that are stable and applicable for the practical determination of individual species.

S.011. ALPINE PLANT ECOLOGY AND DIVERSITY: FROM SPECIES TO ECOSYSTEMS.

P.0110 Effects of shrub encroachment on soil properties and microbial communities in alpine mountains

Alba Anadon-Rosell[1,2], Núria Roca[3], Laura Escarmena[3], Marc Sánchez-Vega[3], Enrique Navarro[4], Rebecca Boden[5], Frederik Märker[2], Estela Illa[3,6]

1 CREAF, Cerdanyola del Vallès, Spain. 2 Institute of Botany and Landscape Ecology, University of Greifswald, Greifswald, Germany. 3 Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals. Facultat de Biologia. Universitat de Barcelona, Barcelona, Spain. 4. IPE-CSIC, Zaragoza, Spain. 5 Fakultät für Umwelt & Natürliche Ressourcen, Universität Freiburg, Freiburg, Germany. 6. Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Barcelona, Spain.

Woody plant encroachment is a process occurring at high elevation and high latitude ecosystems across the globe as a consequence of global change. While prior studies have addressed the impacts of encroachment at community and ecosystem scale, little is known about the effects of individual shrubs, and how soil properties and communities change under shrub canopies. Our aim was to determine the effect that individuals of two widespread circumpolar dwarf shrub species, Dryas octopetala (DO) and Empetrum nigrum subsp. hermaphroditum (EH), have on the properties and the microbial communities of the soil they colonise. In the alpine mountains of Finse, Norway, we selected four individuals of each species and extracted soil cores at the interior, periphery and exterior of the shrub canopy. We analysed soil physico-chemical characteristics, and the affinity of the soil microbial community for C substrates. We also collected shrub leaves, branches and rhizomes to measure functional traits and xylem growth rings. We found a decrease in C:N ratios from the interior to the exterior, but no clear patterns for soil pH, moisture or nutrient availability. Although dissolved organic carbon and dissolved nitrogen did not differ between positions, we found a significant effect of shrub leaf traits on these parameters. We also found clear differences in leaf functional traits along the canopy for both species, with more conservative leaves at the periphery than the interior. The soil microbial community had a lower affinity for C substrates in the interior than in the exterior of DO canopies, and a larger amount of active microbial biomass in the interior than the periphery of EH. The effects found at individual scale mirror those found in studies at community and ecosystem scale, indicating that shrub individuals have the ability to modify the soil and its microbial communities from early stages of encroachment.

P.0111 Flavonoid glycosylation in Rhodiola rosea (Crassulaceae) shows evidence for hybridization of chemically distinct lineages

Hyuga Hirano[1], Koh Nakamura[2], Masaaki Ozeki[3], Yoshinori Murai[1,4]

1 United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology, Tokyo, Japan. 2 Botanic Garden, Field Science Center for Northern Biosphere, Hokkaido University, Hokkaido, Japan. 3 Natural Environment Division, Nagano Environmental Conservation Research Institute, Nagano, Japan. 4 Department of Botany, National Museum of Nature and Science, Ibaraki, Japan.

Plants synthesize a variety of secondary metabolites to adapt to their environments. Flavonoids are involved in adaptive mechanisms such as UV-protection in alpine environments, and they are mainly accumulated as glycosides in vacuoles. Flavonoids are glycosylated by UDP-glycosyltransferases (UGTs), and their sugar donor selectivity is specific to each enzyme. Differences in the genetic sequences encoding these UGTs have been used in molecular phylogenetics to reveal the modification of flavonoid glycosides and explain their phylogenetic relationships. *Rhodiola rosea* is a succulent plant distributed in alpine and boreal areas of the northern hemisphere. In Japan, this plant is found in harsh environments in geographically distant areas, including coastal to alpine rocky areas in Hokkaido and northern Honshu, and in alpine rocky areas in the central Honshu. Differences in growth environments may indicate that they are different lineages or have different mechanisms of environmental adaptation. To verify this hypothesis, we investigated their flavonoid glycosides and glycosylation patterns. Leaf samples of *R. rosea* were collected from 12 sites in Japan, and their chemical compositions were analyzed using various chromatographic methods. In this result, herbacetin and gossypetin were the basic skeletons of each flavonoids, but the flavonoid glycosylation patterns varied in different regions. The major flavonoid glycosides were attached to glucose in all regions. However, in samples from northern Japan and the Northern Alps of central Honshu, these glycosides were modified with glucuronic acid, while samples from Mt. Yatugatake and a part of the Southern Alps, both in central Honshu, were modified with xylose. Both glycosylation patterns were observed in samples from Mt. Arakawadake in the Southern Alps. These results suggest a phylogeographic scenario that two different lineages occur in Japan and have hybridized in places where their distributions overlap, as well as providing an important clue to reveal the complex mutational mechanism of glycosyltransferases.

P.0112 Vegetation changes at high-elevation high-latitude mountain

Inka Kuusisto[1], Carlos Gonzales Inca[2], Sanna Huttunen[3], Risto Virtanen[4]

1 Herbarium (TUR) and Kevo Subarctic Research Station, Biodiversity Unit, University of Turku, Finland. 2 Department of Geography and Geology, University of Turku, Finland. 3 Herbarium (TUR), Biodiversity Unit, University of Turku, Finland. 4 Department of Biology, University of Oulu, Finland.

High-latitude arctic environments have been warming at unprecedented rates- and these may have strong impacts on high-elevation cryptogam assemblages with sparse vascular plant cover. Here we investigate the changes in high latitude-high elevation cryptogam-vascular assemblages under 32 years by resurveying a transect study in 2022, earlier surveyed in 1990 on Mt Ritničohkka, NW Finnish Lapland. We used ordination methods with adonis to detect the possible temporal differences in community structures. To study the responses of individual species we conducted Indicator species analysis. We also calculated weighted Ellenberg's indicator values for studied plots and studied changes in community qualities. Furthermore, we divided our data into vascular plants, mosses, liverworts and lichens to see how different plant groups respond to temporal and altitudinal changes. In total, 196 taxa were observed of which 38 were vascular plants and 158 cryptogams. We observed temporal vegetational changes in the composition of plant assemblages. These changes were partly elevation-dependent. For example, the total number of vascular plants increased during the study period and the cover of liverworts increased. The changes were species-specific and more than 10 percent of the species showed a significant temporal change. High latitude-high elevation plant communities are about to reassemble into novel compositions of bryophytes, lichens and vascular plants.

P.0113 Are mosses from sub-Antarctic areas affected by the "ozone hole" more tolerant to ultraviolet-B radiation?

Roy Mackenzie[1,2], Gonzalo Soriano-Sancha[3], Brenda Riquelme[1,2], Laura Monforte[3], María Ángeles Del-Castillo-Alonso[3], Rafael Tomás-Las-Heras[3], Javier Martínez-Abaigar[3], Encarnación Núñez-Olivera[3], Leonardo Pérez de Souza[4], Bernard Goffinet[5], Liu Yang[6]

1Universidad de Magallanes, Cape Horn International Center, Puerto Williams, Chile. 2 Millennium Institute Biodiversity of Antarctic and Subantarctic Ecosystems, Santiago, Chile. 3 Universidad de La Rioja, Facultad de Ciencia y Tecnología, Logroño, Spain. 4 Department of Molecular Physiology, Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany. 5 Dept. of Ecology and Evolutionary Biology, University of Connecticut, Storr, USA. 6 Key Laboratory of Southern Subtropical Plant Diversity, Fairy Lake Botanical Garden, Shenzhen & Chinese Academy of Sciences, Shenzhen, China.

The anthropogenic degradation of stratospheric ozone, the "ozone hole," and the subsequent increase in ground-level ultraviolet-B (UV-B, 280-315 nm) radiation, are particularly significant in Antarctica. Extensive research has been conducted in mosses in this continent, however, sub-Antarctic land areas can also be affected by the ozone hole, yet they remain surprisingly understudied. This is the case of Navarino Island (Chile), located south of Tierra del Fuego, the southernmost peatland areas globally. Our objective was to investigate the physiological, metabolomic, and genomic responses of *Polytrichum strictum* Menzies ex Brid., an ecologically significant moss found in bog environments on Navarino Island, to UV-B radiation under laboratory conditions. We aimed to compare these responses with those observed in populations of the moss from other latitudes. Moss samples isolated from Navarino Island were cultivated in plates containing growth medium and subjected to various UV-B treatments using lamps and filters. We assessed both UV-B-induced damage and the physiological, metabolic, genetic, and structural protective mechanisms adopted by the moss using a combination of destructive and non-destructive techniques. These included measuring chlorophyll fluorescence variables, gas exchange parameters, photosynthetic pigments, as well as non-destructive quantification of chlorophyll, carotenoids, and phenolic compounds. Additionally, we analyzed the levels of methanol-soluble and -insoluble UV-absorbing compounds, which are presumed to be located in different cell compartments and represent distinct forms of UV-B protection. Metabolomic analysis, specific phenolic compound profiling, assessment of oxidative damage, antioxidant capacity, DNA damage, transcriptomic analysis including examination of specific genes involved in the phenolic pathway, sclerophylly index, and growth parameters were also evaluated. Our findings will contribute to the understanding of the UV-B tolerance of *P. strictum* and elucidate the UV-B levels that trigger responses in this moss. This will aid in assessing the tolerance caused by ozone holes recorded in different years.

P.0114 Seedling functional traits along alpine environmental gradients

T. Maroto Gimena[1], C. Espinosa del Alba[2], E. Fernández-Pascual[2], B. Jiménez-Alfaro[2]

1 University of Oviedo, Asturias, Spain. 2 IMIB - Biodiversity Research Institute, Mieres, Spain.

Seedling establishment is the most vulnerable stage of plant regeneration, but little is known about seedling functional traits and developmental strategies. Seedling establishment is especially unknown in alpine environments with low temperatures, high solar radiation and short growing seasons. Additionally, the complex alpine topography creates sharp temperature and snowmelt gradients that may modulate plant regeneration at fine scales. Here we explore seedling trait functionality by focusing on 12 alpine specialists of grassland communities above 1800 m a.s.l. in the Cantabrian Mountains (Spain). To capture regional variability, we studied six species from the two major climates represented in the study area: Mediterranean and Temperate. We also selected species with ecological preferences in contrasting microclimatic conditions. Then, we measured a set of traits including emergence and establishment periods, above and belowground biomass, and seed mass. A Principal Component Analysis revealed consistent strategies across both climates varying in seed mass, shoot/root length ratio and cotyledon width/length ratio. The general gradient suggested a separation between acquisitive and conservative seedling strategies. When both climates were analysed separately, we found divergent trends. Trait variation in temperate species was mainly driven by relative growth rate, with species from colder and snow-persistent microclimatic conditions emerging and developing faster. Trait variation in Mediterranean species was mainly driven by radicle length, with species from warmer and less snowy sites having longer radicles. Our study confirms that seedling traits in alpine ecosystems show functional variability along macroecological and microclimatic gradients.

P.0115 Species diversity of vascular plants on periglacial moraines of Eastern Pamirs

Navruzshoev D[1]. Beknazarova Kh.A[1]

Pamir Botanical Garden, St. Kholdorov.1. Tajikistan, Khorog.

P.0116 Plant conservation in National Parks: vegetation checklist, biogeography and protected habitats (Sierra de las Nieves, Malaga, Spain).

Andrés V. Pérez Latorre[1], Federico Casimiro-Soriguer[1], Noelia Hidalgo-Triana[1], Baltasar Cabezudo[1]

1 Botany area. University of Malaga. Malaga. Spain.

A study of the plant communities that develop in the state protected natural area "Parque Nacional de la Sierra de las Nieves" (Andalusia, Spain) has been carried out. It is a very environmentally diverse area, with numerous and contrasting lithological types, mediterranean macro-bioclimate and 4 thermotypes, from thermo-mediterranean (150 m) to oro-mediterranean (1919 m). The park is included in three very different biogeographical sectors (Rondeño: dolomites/limestones, Bermejense: peridotites, Aljibico: siliceous substrates) belonging to the Western Mediterranean subregion and main refuge of *Abies pinsapo* among other endemic and relict species. The study was carried out using the updated phytosociological method, with inventories taken mainly during the years 2017-2023 and complemented with previous data (1996-1998). The syntaxonomic catalogue consists of 35 phytosociological classes, the richest in syntaxa being the classes Quercetea ilicis with 17 and Tuberarietea with 10, of which those of new description and novelties for the study area are highlighted. In the biogeographic aspect, the phytocoenological diversity and diversity per unit area in the 3 sectors was calculated. Of the total number of syntaxa, those considered as habitats of community interest (HIC), protected by the European directive 92/43 EU, have been identified, some of which are new for the study area or even at higher territorial levels. Due to their conservation interest, syntaxa considered as endemic or relicts were identified, on which appropriate management measures should be focused for their conservation.

P.0117 Roles of environmental and geographic distances from taxonomic to functional beta diversity of vascular plants in Pyrenean mires

Eulàlia Pladevall-Izard[1], Aaron Pérez-Haase[1], Josep M. Ninot Sugrañes[1]

1 University of Barcelona and IRBio, Barcelona, Spain.

In the Central Pyrenees, mires occupy small areas but contribute substantially to gamma diversity at landscape scale. Plant communities in mires have been broadly studied through ordination methods. Here we studied the contribution of beta diversity components (total, replacement and abundance differences) in 422 plots from 56 mire systems in the Central Pyrenees. Besides taxonomic beta diversity, we address phylogenetic and functional beta diversity. We analysed the entire plant communities –which implied over 250 species in total– and then plant assemblages of mire specialists –103 species. We found high rates of total taxonomic beta diversity, while phylogenetic and functional beta diversities were similarly lower. This result points to strong environmental filters that foster different plant communities to share phylogenetic plant relatives and similar ecological strategies. Beta diversity of specialist species showed almost the same results, denoting similar biogeographic patterns, but the abundance difference compartment was proportionally higher. We then related beta diversity indices with geographic distances and local and landscape environmental variables, carrying out variance partitioning analyses. Against expectation, the locality effect (i.e., the fact that two plots belonged to the same mire system) explained about 24% of the total beta diversity variance, while environmental variables and spatial distances showed secondary relevance for all beta diversity computations. This fact reveals the importance of dynamic immigration and successful settling processes in Pyrenean mires, which are characterized by constrained connectivity through landscape. There, the establishment of new species would be limited by niche occupancy by species with similar characteristics.

P.0118 Xylem conductivity response to temperature and not to rainfall relates to composition shift in a Macaronesian alpine dry community

Águeda M. González-Rodríguez[1], Beatriz Nievas-Valverde[1], Alicia Perera-Castro[1], Beatriz Fernández-Marín[2], Stefan Mayr[3], Jaime Puértolas*[1]

*1 Department of Botany, Ecology, and Plant Physiology, Universidad de La Laguna, La Laguna, Spain 2 Department of Biology and Ecology, Universidad del País Vasco, Leioa, Spain 3 Department of Botany, University of Innsbruck, Austria. *jpuertol@ull.edu.es.*

Climate change is having a strong impact in species distribution and composition of dry alpine environments of the Mediterranean and Macaronesian region, where both temperature and drought intensity are increasing. The two legume species (*Spartocytisus supranubius* and *Adenocarpus viscosus*) that dominated the summit scrub in Mount Teide National Park in the Canary Island of Tenerife a few decades ago, are being displaced by a formerly rare species, *Pterocephalus lasiospermus*. Increased herbivory pressure linked to increasing temperature and drought-related mortality has been suggested to explain the decline of the two legume species, but no ecophysiological comparison of the three species is available. In this study, we hypothesized that differences in water status and transport responses could explain the shift in species composition. In five campaigns distributed from November to September, we measured native stem xylem conductivity (*ks*), maximum xylem conductivity (*kmax*) and the percentage of native conductivity loss (*PCL*)of the three species in two locations within the National Park. Simultaneously, in the last four campaigns we measured stem water potential (Ψ_x). In general, Ψ_x remained constant and similar among species throughout the year. *PCL* peaked in winter in all species, coinciding with a minimum in *ks* and *kmax* This resulted in overall correlations between *ks* and averaged maximum temperature, which was not observed for rainfall, as *ks* continuously recovered over the dry spring-summer period. *PCL* was lower in *A. viscosus* throughout the year and, in winter, highest in *P. lasiospermus*, in particular in the coldest site. The results suggest that the recent success of *P. lasiospermus* might be related to the increase in winter temperatures, as xylem conductivity of this species seems the most sensitive to winter temperatures.

P.0119 Vegetation dynamics in the Gran Paradiso National Park through a remote sensing-based approach

Chiara Richiardi[1,2], Maria Adamo[3], Consolata Siniscalco[2]

1 Technology Laboratory for the Dynamics of Structures and Prevention of Seismic and Hydrogeological Risk, ENEA, Bologna, Italy. 2 Department of Life Sciences and Systems Biology, University of Torino, Turin, Italy. 3 Institute of Atmospheric Pollution Research (IIA), National Research Council (CNR), Interateneo Physics Department, Bari, Italy.

Climate change and human activities are widely recognized as the main driving forces of vegetation dynamics. Vegetation significantly affects the global material and energy flows, as well as carbon balance and climate stability at different spatiotemporal scales by changing the rates of plant photosynthesis, respiration, and soil organic carbon decomposition. In this context, alpine areas are facing deep changes as a result of the progressive abandonment of traditional agro-sylvo-pastoral practices, further exacerbated by climate change. Gran Paradiso National Park, established in 1922, represents a peculiar observatory because of the wide availability of studies conducted and data collected over time, although not continuous in time and space. Some questions still remain unanswered, such as the changes that have taken place and their timing at the landscape scale. The availability of long-term, high-resolution satellite remote sensing data has made it easier to obtain accurate information that can be used to study the role of vegetation, especially in remote and inaccessible areas, with high temporal and spatial resolution. This study, which is currently ongoing, aims at studying vegetation dynamics through a remote sensing approach. Time series of vegetation distribution maps will be extracted from Landsat satellite data. This will be achieved through the implementation of a land cover classification algorithm based on machine learning methods, which aims to take advantage of all the information that can be extracted from satellite images and available auxiliary data related to the distribution of plant communities. Subsequently, change maps will reveal the mechanisms of terrestrial ecosystem behavior, predicting future vegetation growth and, thus, informing environmental management and policies.

P.0120 Von Humbolt's Nightmare: effects of climate change on the vegetation of Chimborazo

Tuany Siqueira-Silva[1], Jesús López-Angulo[2], Pablo A. Martinez[1]

1 PIBi Lab – Laboratório de Pesquisas Integrativas em Biodiversidade, Department of Biology, Universidade Federal de Sergipe, São Cristóvão, Brazil. 2 Universidad Rey Juan Carlos, Móstoles, Spain.

Mountain plants are highly sensitive to the effects of climate change, and many species have shifted upwards and lost habitat as temperatures rise. The rich and endemic Tropical Andes have fascinated naturalists throughout history. Two centuries after Alexander von Humboldt and Aimé Bonpland's notorious expedition to Chimborazo (Ecuador), significant upward shifts have been detected on the mountain's vegetation due to climate change. Our main objective was to evaluate the effects of climate change on the vegetation of Chimborazo in the future (2061-80) under intermediate (SSP2-4.5) and pessimistic (SSP5-8.5) climate change scenarios. We built Species Distribution Models (SDMs) for 134 native species of Chimborazo using MaxEnt, WorldClim bioclimatic variables and GBIF occurrence points, and projected onto Chimborazo at a 1 second resolution. Through high accuracy SDMs for 102 species, we analysed richness patterns, phylogenetic diversity and potential area changes into the future. The plant richness on Chimborazo may shift upwards due to climate change, decreasing below 3,000 m and increasing above 3,500 m. Similarly, the phylogenetic diversity may decrease below 2,900 m, risking ecosystem functioning in these zones, and increase above 3,000 m, possibly due to the ascension of species with lower alpine specialization. Most plant species may lose potential habitat in the future, which has been reported for high elevation cold-adapted plants. However, other species (e.g., low elevation species) may gain significant amounts of potential area due to warming, expanding upwards. Chimborazo's vegetation may be significantly altered in the future, reinforcing the high sensitivity of mountain ecosystems to climate change.

P.0121 Climate and soil nutrients generate distinct diversity patterns across four elevational gradients within the same region

Zhongping Tian[1], Wenlong Chen[1], Mierkamili Maimait[1], Erfan Akberjan[1], Ming Ni[2], Bin Liu[1]

1 Xinjiang Key Laboratory of Special Species Conservation and Regulatory Biology, College of Life Science, Xinjiang Normal University, Urumqi, China. 2 Center for Ecological Dynamics in a Novel Biosphere, Department of Biology, Aarhus University, Aarhus, Denmark.

Numerous researchers have endeavored to discover a general explanation for elevational diversity gradients, but it remains unclear whether similar diversity patterns and driving factors exist for the same life-forms along different elevational gradients within the same region. In the Ili Valley of the Central Asia Biodiversity Hotspot, we selected four elevational gradients with similar species pools and evolutionary histories to assess the generalizability of elevational diversity gradients. Our findings indicate distinct patterns of species diversity along the four elevational gradients within the same region for the same life-forms. The species richness and abundance of woody plants are primarily controlled by climate-based factors (i.e., minimum temperature, temperature seasonality, mean annual precipitation, and potential evapotranspiration) along four elevational diversity gradients in the Ili Valley, while the species richness and abundance of herbaceous plants are primarily influenced by both climate and soil nutrients (i.e., soil organic carbon). In conclusion, our findings suggest that climate is an important driver of species diversity for woody plants, and that the driving mechanisms of herbaceous plant diversity along elevational gradients should consider both climate and soil nutrients.

P.0122 Climate-driven shifts in alpine plant persistence strategies: implications for adaptation to global warming

Margherita Tognela[1], Fiona J. White[1], Francesco Porro[1], Silvano Lodetti[1], Graziano Rossi[1], Marisol A. Saretto[1], Laura Amadeo[1], Andrea Mondoni[1,2]

1 University of Pavia, Pavia, Italy. 2 National Biodiversity Future Center, Palermo, Italy.

Climate warming in alpine biomes is increasing faster than the global average, altering the distribution, phenology and physiology of alpine plants. These effects have frequently been observed but, with limited exceptions, few studies have provided mechanistic explanations for these changes. In this context, differences in persistence strategies could play a key role in both plant population and community responses to climate change (CC). There are three alternative strategies for plant persistence in situ: (I) produce high quality and long-lasting seeds; (II) have an extended life span; (III) be highly clonal. The allocation of resources to vegetative growth leads to a reduction of regeneration by seed, resulting in a trade-off between seed persistence and clonality, along with extended life span. The prevalence of a particular strategy has been found to be habitat-related and elevation-specific, with low-altitude species allocating more resources to regeneration by seeds compared to higher-altitude species. Given the recent trend of upward migration driven by climate warming, persistence traits are expected to change in the future. Thus, we hypothesize that (I) global warming might favor species relying on regeneration by seeds and clonality, and that (II) persistence strategy is correlated to species response to CC. To explore these hypotheses, we investigated whether species with contrasting long-term population dynamics differ in their persistence strategies. Specifically, we correlated data on 20-yr population dynamics for 25 alpine species occurring in the Northern Apennines (Italy) with seed longevity, adult plant longevity and clonality, measured following standardised protocols and literature. Our results highlight a significant positive relationship between species abundance change and both seed longevity and mass; consequently, species with increasing abundance have larger and longer-lived seeds compared to decreasing species. These findings suggest that seed traits may provide valuable insights into the resilience or vulnerability of alpine species to climate change.

P.0123 Plant-pollinator interactions in a highly diverse Andean Paramo

Carolina Tovar[1], Carlos Martel[1], Laura Cifuentes[2], Emilia Ayala[2], Higor Antonio Domingues[1], Pavel Sanchez Flores[3], Laura Williamson[1], Jehova Lourenco[1], Liliya Draganova[4], Suzette Flantua[4], Francisco Cuesta[2]

1 Royal Botanic Gardens, Kew, Richmond, UK. 2 Grupo de Investigación en Biodiversidad Medio Ambiente y Salud-BIOMAS, Universidad de las Américas, Quito, Ecuador. 3 Departamento de Entomología, Museo de Historia Natural, Universidad Nacional Mayor de San Marcos, Lima, Perú. 4 Department of Biology, University of Bergen and Bjerknes, Centre for Climate Research, Bergen, Norway.

Plant-pollinator interactions are critical to sustain ecosystem functioning. Shifts in plant phenology, due to, for example, warming, could lead to asynchronies between plant flowering and pollinator availability, with negative consequences for plant reproductive success and/or local loss of pollinator species. So far, only a few studies have focused on plant-pollinator interactions in the Paramo, the high-elevation grasslands of the northern Andes, and whose flora is the most species rich among the tropical alpine ecosystems. Given the imminent changes in plant communities of this high elevation ecosystems it is of outmost importance to have a better understanding of the current diversity and complexity of the plant-pollinator interactions in the Paramo. This work is focused on the Paramos of Yanacocha, Ecuador (4,200 masl) and aims to 1) Characterise pollen diversity of dominant Páramo species, 2) Characterise pollinator diversity, 3) Build a preliminary plant-pollinator interaction network. We collected pollen samples from floral buds of 30 plant species and analysed them using light and electron microscopy. We also collected 133 floral visitor specimens that were classified into 23 morphospecies. In addition, we made observations of plant-pollinator interactions in June and October 2023. Our preliminary results show that the pollen diversity morphology is high (ornamentation, size), including marked differences between species within the same family. We also found that Asteraceae plants (*Monticalia peruviana*, *Chuquiraga jussieui*) are highly visited by an array of pollinators (bees, flies, butterflies). While most plant species from the paramos were recorded being visited and pollinated by different types of flies (with low representation of the family Syrphidae), dominant plant species were predominantly or even exclusively pollinated by the bumblebee *Bombus funebris*. Both flies and *Bombus funebris* are key pollinators and the best represented in the Paramo plant-pollinator networks.

P.0124 The response of Carex nigra to disturbance by trampling and herbivory

Paula Vicenç-Sabater[1], Eulàlia Pladevall-Izard[1], Aaron Pérez-Haase[1]

1 University of Barcelona and IRBio, Barcelona, Spain.

Fens are found in the boreal and subarctic climatic zones, and in Alpine mountains. Their soils are hypoxic and most often dominated by sedges and mosses. Most of these species have their European southernmost distribution limit in the Pyrenees, where they thrive in small fragmented and threatened fen patches. In the Pyrenees, and Alpine mountains in general, the most prominent threat is overgrazing, which alters the ecosystem functioning through the destruction of soil structure and changes in plant performance and fitness. Although mountain fens are highly diverse, the most frequent and dominant species is the ubiquitous sedge *Carex nigra,* a stoloniferous hemicryptophyte that reproduces vegetatively by rhizome elongation. Here, we aimed at assessing how livestock pressure modifies the performance of *C. nigra* from biomass allocation to vegetative reproduction and space occupancy, among other functional traits. Thus, we carried out a cultivation experiment in a factorial design for four months. We simulated herbivory and trampling (by soil-compaction and soil-pugging), under two water table levels (wet and flooded). Most of our results showed the negative effects of herbivory and trampling treatments on all organs. However, the structure of these organs changed according to the degree of soil disturbance. Herbivory was the most important factor, affecting the aboveground and belowground structures of the plants. The magnitude of herbivory was such that only the pugging was noticeable, in terms of biomass accumulation, whereas compaction cause no additive effect. In contrast, in the absence of herbivory, differences were observed between all trampling treatments. Besides, when trampling was also suppressed, flooding favoured the accumulation of biomass. Our analysis exemplifies the plasticity of Alpine fen plant communities. Further studies are needed to elucidate the disturbance responses of different plant functional groups, due to the known effect of competitive exclusion by gramineous forms in non-grazed fens.

S.012. AN UPDATE ON THE PHYLOGENY OF SEED PLANTS

P.0125 Relationships of Trichocereus with nearby genera of the tribe Trichocereeae-Cactoideae-Cactaceae and nomenclatural implications

Sofia Albesiano[1], Roberto Kiesling[2]

1 Departamento de Biología, Facultad de Ciencias, Universidad del Tolima, Ibagué, Colombia. asalbesianoh@ut.edu.co. 2 Instituto Argentino de Investigaciones en Zonas Áridas, CONICET, Mendoza, Argentina. rkiesling@mendoza-conicet.gob.ar

The genus *Trichocereus* belongs to the subtribe Trichocereinae and includes 58 taxa (38 species, 10 subspecies, 8 varieties and 2 forms), from the Andes of Ecuador, Peru, Bolivia, Argentina, Chile and one species introduced to southern Colombia. Some taxa are dominant and define phytogeographic provinces. The complexity and diversity of the genera of the tribe Trichocereeae, *Acanthocalycium*, *Chamaecereus*, *Echinopsis* s. str., *Hymenorebutia*, *Lobivia*, *Pseudolobivia*, *Soehrensia* and *Trichocereus*, it is possibly the problem of greatest interest at a generic level, at least for South American cacti. The intention of this work is to clarify whether *Echinopsis* in the broad sense of Friedrich and Rowley is correct, or if we must return to the traditional concept, of considering them three genus -*Echinopsis*, *Lobivia* and *Trichocereus*-, which are differentiated by the shape of the stems, size and hairiness of the flowers and by geographical distribution, in addition to solving nomenclatural problems. The study was carried out on the basis of anatomical, morphological and molecular characters. Phylogenetic relationships were examined in 17 species, based on 39 exomorphological characters and chloroplast DNA sequences, *trnL-F* and *rpl16*, and including other species of the tribes Hylocereeae, Notocacteae and Trichocereeae. Combined phylogenetic analysis recovered *Trichocereus* as monophyletic and supported by three synapomorphies. *Trichocereus* presents a close affinity with *Lobivia* by sharing two homoplasies, specifically with a group of species that had been transferred to the genus *Soehrensia*. As the main conclusions of the study, it is proposed that the genera *Trichocereus* and *Echinopsis* should be kept separate, while *Helianthocereus* should be considered in the synonymy of the former.

P.0126 A Systematic evaluation of the Ammi and Visnaga genera in Turkey

Miraç Ekici[1,2], Emine Akalın[1]

1 Faculty of Pharmacy, Istanbul University, Istanbul, Turkey. 2 Scientific Research Projects Coordination Unit, Istanbul University, Istanbul, Turkey.

The *Ammi* genus is represented by three species, while the *Visnaga* genus is represented by two species worldwide. In this study, the species *Visnaga daucoides* Gaertn. (synonym *Ammi visnaga* (L.) Lam.) and *Ammi majus* L., which are distributed in Turkey and are of great value medicinally, were subjected to a systematic evaluation (Al-Sanfi, 2013; Güner et al. 2012; IPNI, 2023). Plant materials are collected from various regions of Turkey. Analyses were carried out on both collected specimens and specimens in the ISTE herbarium. Morphological analysis included examination and measurement of fruit, basal and stem leaves, taking photographs and examination of fruit cross sections. The DNA was extracted from the specimens and the ITS gene region of the genomic DNA was amplified and sequenced for molecular analysis, followed by the construction of a phylogenetic tree. In addition, a chemotaxonomic evaluation was carried out. The coumarin and flavonoid contents of aqueous and ethanol extracts were quantified by LC-MS. Analyses were also carried out to quantify visnadine, which is important for the medicinal activity of the plants. The genera *Ammi* and *Visnaga* have been comprehensively analysed using multidisciplinary approaches. This analysis has resolved uncertainties and evaluated the taxonomic status of the genus in Turkey and worldwide.

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P.0127 Insights into the phylogeny of Sibbaldia L. (Fragariinae, Rosaceae) and close relatives, based on nuclear low copy gene sequences

Torsten Eriksson[1]

1 Department of Natural History, University Museum, University of Bergen, Norway.

Previous phylogenetic studies of Fragariinae and *Sibbaldia* have shown that plastid and nuclear (ribosomal) DNA sequences are partly incongruent regarding the relationships of the genera *Sibbaldia* (in the strict sense), *Sibbaldiopsis*, and *Sibbaldianthe*, here called the *Sibbaldia* group consisting of ca. 10-15 species. Some of these species have until recently been classified in *Potentilla*. As there are different ploidy levels involved, it has been suggested that allopolyploidy might have affected the evolution in this group. To investigate this, two low copy nuclear gene regions (DHAR, GAPCP1) were cloned, sequenced and analysed phylogenetically. The idea was that if allopolyploidy had been involved, clones from polyploids would join their respective parental species. The focus was the *Sibbaldia* group, and in addition, the close relatives *Comarum, Farinopsis* and *Alchemilla* were included with representatives from *Fragaria* as outgroup. The analyses indicated the *Sibbaldia* group to consist of two well supported subclades with *Farinopsis, Comarum* and *Alchemilla* as unresolved sisters. One of the *Sibbaldia* subclades consisted of the three diploid *Sibbaldia* species (*procumbens, parviflora*, and *cuneata*) together with clones from *Sibbaldiopsis* (sometimes treated as *Sibbaldia*) *tridentata, miyabei* and *cuneifolia*. The three latter are at least tetraploid. The other subclade contained clones from the two sampled species of *Sibbaldianthe* (*adpressa* and *bifurca*) also, like the first subclade, with clones from *tridentata, miyabei* and *cuneifolia*. The patterns of relationships are similar inside the two subclades. Folding the gene trees into a species tree involves postulating at least two reticulations between members of the two subclades. The connections between the two subclades favour classifying *Sibbaldia, Sibbaldiopsis* and *Sibbaldianthe* in one genus: *Sibbaldia*.

P.0128 Molecular phylogeny of Strobilanthes Blume species (Acanthaceae) from northern Western Ghats of India

Maria Cineola Fernandes[1], Krishnan Sellappan[1]

1 Goa University, Goa, India.

Strobilanthes is the second largest genus of the family Acanthaceae and grows naturally in the tropical regions of Asia. India harbours a centre of diversity of this genus in the Western Ghats and the North/Northeast regions of India with about 150 representative species. In this study, we have 10 species, including 1 unpublished taxon (*Strobilanthes* sp.) and 1 newly discovered variety from the northern Western Ghats to understand their evolutionary history using molecular phylogenetics. Nuclear ribosomal internal transcribed spacer (ITS), three chloroplast DNA (cpDNA) sequences *trn*L, *rbc*L, *mat*K and one mitochondrial DNA (mtDNA) sequence *mat*R have been sequenced. Overall, the northern Western Ghats species have a close relationship with other peninsular Indian species. The results indicate that the *Strobilanthes* species have origins indicating independent colonisation of their habitat in northern Western Ghats from southern Western Ghats or from Northeast India. This work provides the first phylogenetic understanding of the speciose genus *Strobilanthes* within India and will be further extended to unravel the evolution of this genus in the Indian sub-continent.

P.0129 The first Glossopteris flora occurrences in southeastern Brazil: evolutionary, phytogeographic and stratigraphic implications

Roberto Iannuzzi[1], Juliane, Marques-de-Souza[2], Mercedes M. di Pasquo[3], Neil P. Griffis[4], Fernando F. Vesely[5], Thammy Mottin[5]

1 Instituto de Geociências, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil. 2 Departamento de Ciências Biológicas, Universidade Estadual de Roraima, Boa Vista, Brazil. 3 Laboratorio de Palinoestratigrafía y Paleobotánica, CICYTTP (CONICET-ER-UADER), Diamante, Argentina. 4 Department of Earth and Planetary Sciences, University of California, Davis, USA. 5 Universidade Federal do Paraná, Centro Politécnico, Curitiba, Brazil

Glossopterids correspond to an enigmatic group of seed plants that emerged in Gondwana around the Carboniferous–Permian transition, flourished throughout the Permian and reduced drastically and/or became extinct during the end-Permian extinction event. This group of gymnosperms became famous because it was considered the first evolutionary step towards angiosperms, given the diversity and complexity of their reproductive organs. Recent studies on their reproductive biology have suggested that glossopterids may be more closely related to ginkgoaleans, cordaitaleans and some early conifers. However, many doubts still remain about where and how this group would have appeared. In recent years, some of the first occurrences of glossopterid-containing assemblages in the southern Paraná Basin (Rio Grande do Sul state, southern Brazil) have been radiometrically dated as earliest Asselian in age using high-resolution U–Pb zircon CA-TIMS methods. Currently, these correspond to the oldest well-dated records of this group throughout Gondwana. In these early assemblages, the fossil-genera considered evolutionarily as the most basal (less derived) female fructifications of glossopterids are present, i.e. *Arberia* and *Arberiopsis*, belonging to the Family Arberiaceae.

In addition, there is the first records of forms allied to the Dictyopteridiaceae (*Ottokaria*-like fructifications). Furthermore, this record gives evidences of how very simple reproductive structures can evolve into much more diverse (=distinct evolutionary lineages) and complex reproductive organs, drawing a distant parallel with the processes that occurred with angiosperms millions of years later. Given the abundance and diversity of forms related to Arberiaceae, as well as the occurrence of the oldest records in Gondwana, the region occupied by the Paraná Basin and surrounding areas becomes a probable center of origin for glossopterids. Finally, the appearance of glossopterids can be useful for biostratigraphic correlation purposes, as well as the successive first appearance of different types of their female fructifications over time.

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P.0130 Phylogenetic relationship of Cleyera and related genera of Pentaphylacaceae

Tetsuo Ohi-Toma[1], Hidetoshi Nagamasu[2], Shuichiro Tagane[3], Tetsukazu Yahara[4], Akiyo Naiki[5]

1 Nature Fieldwork Center, Okayama University of Science, Okayama, Japan. 2 The Kyoto University Museum, Kyoto University, Kyoto, Japan. 3 The Kagoshima University Museum, Kagoshima University, Kagoshima, Japan. 4 Kyusyu Open University, Fukuoka, Japan 5 Tropical Biosphere Research Center, University of the Ryukyus, Okinawa, Japan.

Cleyera is a genus of Pentaphylacaceae, consisting of 24 species that are disjunctly distributed in East and Southeast Asia, and Central America. However, some previous studies have classified the Central American species as either *Freziera, Ternstromeia,* or *Tristylium*. While some molecular phylogenetic studies indicated the monophyly of *Cleyera*, species from Central America were not included in those analyses. The current study aimed to elucidate the monophyly of *Cleyera* by conducting a molecular phylogenetic analysis based on ITS and ETS regions of six Asian species and two Central American species. The analysis also included several species of closely related genera, such as *Adinandra*, *Eurya*, etc. The resulting phylogenetic tree revealed that Asian *Cleyera* is a monophyletic group but is nested within *Adinandra*. *Cleyera integrifolia* and *C. theoides* in Central America form a sister group to the clade comprising Asian *Cleyera*-*Adinandra* clade and are not closely related to *Freziera*. Interestingly, one '*Adinandra*' species from Vietnam is separated from the Asian *Cleyera*-*Adinandra* clade and is close to the monotypic genus *Euryodendron*, which is endemic to China and closely related to *Eurya*. In the current classification, *Cleyara* is distinguished from *Adinandra* by the number of locules per ovary, ovules, and stigma. However, the Central American *Cleyera, C. integrifolia,* and *C. theoides* should be separated and placed in the formerly described genus *Tristylium*. *Adinandra* and Asian *Cleyera* should be treated as a single genus, *Cleyera,* based on the nomenclatural priority.

P.0131 A revision of the Juncaceae: Molecules and morphology in concert?

Jarosław Proćków[1], Lenka Záveská Drábková[2]

1 Department of Plant Biology, Wrocław University of Environmental and Life Sciences, Wrocław, Poland. 2 Botanica Nova, Mnichovice near Prague, Czech Republic.

Juncaceae is a cosmopolitan family belonging to the cyperid clade of Poales, together with *Cyperaceae* and *Thurniaceae*. These families have global economic and ethnobotanical significance and are often keystone species in wetlands around the world, with a widespread cosmopolitan distribution in temperate and arctic regions in both hemispheres. We reconstructed the molecular phylogeny of *Juncaceae* and cyperids based on selected regions of all three genomes, plastome, chondriome, and nuclear, by maximum parsimony, maximum likelihood, and Bayesian inference. The total evidence analyses included 542 taxa, separated analyses278-1032 taxa. The matrix contained ca. 6 kb per complete taxon. The resulting phylogenetic framework was used as the basis to interpret the evolution of key morphological character states and to revise the infrageneric classification of the group. Currently, *Juncaceae* comprises 14 genera: *Agathryon*, *Alpinojuncus*, *Australojuncus*, *Boreojuncus*, *Distichia*, *Juncinella*, *Juncus*, *Luzula*, *Marsippospermum*, *Oreojuncus*, *Oxychloë*, *Patosia*, *Rostkovia*, and *Verojuncus* (Proćków & Záveská Drábková, 2023a, 2023b; Brožová et al., 2022), however, not all relationships are clearly understood yet. The monophyly of the proposed new genera has been generally confirmed (Kenny et al., 2024). Special attention will be devoted to *Juncinella, Verojuncus,* and *Boreojuncus*. References: Kenny R., Záveská Drábková L., Potter D. (2024): Systematics of Juncaceae, phylogenetic relationships inferred from hyb-seq data. Abstracts, XX International Botanical Congress, 21st–27th July 2024, Madrid, Spain; Proćków J., Záveská Drábková L. (2023a): A revision of the *Juncaceae* with delimitation of six new genera: nomenclatural changes in *Juncus*. *Phytotaxa* 622 (1): 17-41; Proćków J., Záveská Drábková L. (2023b): Proposal on a new taxonomic rank, supergenus. *Taxon* 72(5): 1150; Brožová V., Proćków J., Záveská Drábková L. (2022): Toward finally unraveling the phylogenetic relationships of the *Juncaceae* with respect to another cyperid family, *Cyperaceae*. *Molecular Phylogenetics and Evolution* 177: 107588.

P.0132 Comparison of root structure in Chloranthaceae and implications for their systematics and evolution

Annika Rüdinger[1], Julien B. Bachelier[1]

1 Institute of Biology/Dahlem Center of Plant Sciences, Freie Universität Berlin, Berlin, Germany.

Chloranthaceae have one of the oldest and best documented fossil record among flowering plants. Dating back to the early Cretaceous and comprising both vegetative and reproductive structures and pollen, it suggests that they were a widespread and diverse lineage. However, they are represented today by only 4 genera and 75 species whose affinities with other flowering plant lineages have long remained unclear, and are now considered as sisters to the basal lineage of magnoliids. Previous comparative structural studies already showed some supports for such a relationship, but they focused solely on the aboveground parts, whereas their root system and structure are largely unknown. Using light and scanning electron microscopy, we compared the root system and anatomy in *Chloranthus* and *Sarcandra*, the two most closely related genera within the family. The root systems and anatomy of all 4 species studied here are all very similar to each other. They typically consisted of more or less branched adventitious roots with open meristems and typical common initials. Young roots also share a diarch central cylinder, but older roots showed evidence of some (incomplete/unusual) secondary growth and in the oldest roots, as many as 6 to 8 phloem poles around the central xylem plate. Our study demonstrates that roots of *Chloranthus* and *Sarcandra* share an unusual combination of typical monocots (such as adventitious, homorrhizous root system) and (eu)dicots (secondary growth) traits, and yet, have open meristems with common initials that are more similar to those found in gymnosperms and basal angiosperm lineages. Our study is not only the first to document the roots of Chloranthaceae, but also the first to show that their structure and anatomy provide good support for their potential affinities with angiosperm basal lineages.

P.0133 Addressing phylogeny and taxonomy of Betula L. genus using different approaches.

Andrii Tarieiev[1], Oliver Gailing[1]

1 Department of Forest Genetics and Forest Tree Breeding, Georg-August University of Göttingen, Göttingen, Germany.

The genus *Betula* L. is represented by common pioneer trees and shrubs of temperate and boreal zones in the Northern Hemisphere. Birches are characterized by high vegetative variability, phenotypic plasticity, a wide range of ploidies (from 2n=2x=28 to 2n=12x=168), and frequent hybridization (especially an introgressive one) between different species. That is why the phylogeny of this group is very complex and remains not well resolved. In the current study, we tried to infer the phylogenetic relationships between birch species in Europe using different approaches: (1) classical genetic markers: internal transcribed spacers, plastid genes; (2) a set of 20 newly developed COS-associated SSR markers; (3) complete plastid genome assemblies. Classical genetic markers could be helpful for distinguishing major well-established taxa and addressing some specific problems but in general lack resolution power. A newly developed SSR marker set is only helpful for the identification of the clusters of highly distinct taxa: *B. pendula* aggr., *B. nana*, *B. humilis* and *B. pubescens* aggr. It is not possible to resolve fine-scale phylogeny and to infer the phylogeny of polyploid complexes using these markers. Plastome-based phylogeny in the case of *Betula* L. genus provided significantly better resolution in comparison to previously used markers and therefore is useful for resolving complex groups of closely related taxa. However, some taxa remain unresolved/polyphyletic due to several potential issues: quality of assemblies and annotations, misidentification, chloroplast capture, etc. In addition, since plastids are maternally inherited, plastomes reveal only a part of evolutionary history and are not well-suited for detecting cases of hybridization. According to our estimation, the best possible approach to address birch phylogeny would be high-coverage whole-genome sequencing (preferably long-read with HiC to achieve a better assembly and also to infer epigenetic data) combined with other types of data (morphology, anatomy, "-omix" data, distribution, etc.).

P.0134 Complete plastid genome assembly for the critically endangered endemic birch species Betula klokovii Zaverucha

Andrii Tarieiev[1], Oliver Gailing[1]

1 Department of Forest Genetics and Forest Tree Breeding, Georg-August University of Göttingen, Göttingen, Germany.

In the current study, we assembled complete plastid genomes for the rare Ukrainian endemic species *Betula klokovii* Zaverucha, related species (*Betula pubescens* Ehrh. and *Betula pendula* Roth), and the potential hybrid *B. klokovii × pendula* from short-read low-coverage whole-genome sequencing data. *B. klokovii* was described as a separate species in 1964 by Borys Zaverucha, and is known only from two chalk hills (mt. Strakhova and mt. Maslyatyn) near Kremenets in the Ternopil region. It has a very low number of trees and small natural habitat. Consequently, it is protected at both local and state levels in Ukraine (its growing location is a part of the National Nature Park "Kremenets Mountains") and also included in the IUCN red list as a critically endangered species. *B. klokovii* has several distinctive morphological traits but its taxonomic position was questionable since ITS and SSR markers did not separate it from *B. pubescens*. To clarify the relations between these species we performed short-read low-coverage whole-genome sequencing from dried leaves. *B. klokovii* samples were collected in locus classicus. Plastid genomes were assembled (NOVOPlasty), annotated (GeSeq), aligned together with available birch plastome assemblies from NCBI GenBank representing 22 birch taxa (MAFFT), and used for phylogenetic reconstructions (Maximum Likelihood in RAxML-NG & IQ-TREE, and Bayesian Inference in MrBayes) according to the model suggested by ModelTest-NG. Plastome-based phylogenetic reconstructions revealed a clear separation between *B. klokovii* and *B. pubescens*, and therefore provide additional evidence that *B. klokovii* is a separate taxon. To infer more details about *B. klokovii* and estimate the level of its hybridization there is a need for sequencing more samples of this birch (ideally – the whole population), related species, and prospective hybrids from close locations. Also, it would be very beneficial to conduct reference-grade whole genome sequencing and assembly for *B. klokovii.*

S.013. APG V AND THE CHALLENGE OF TRANSLATING PHYLOGENY INTO CLASSIFICATION WHEN GENE TREES CONFLICT

P.0135 The Flowering Plants Handbook: a practical guide to the world's orders, families and genera

James Byng[1,2]

1 TU Delft Hortus Botanicus, Delft, The Netherlands. 2 Naturalis Biodiversity Center, Leiden, The Netherlands.

For over 250 years angiosperms were arranged in various classification systems based on their morphology and biochemistry. In the last 30 years the classification of angiosperms has changed dramatically with the accumulation of molecular data that is unravelling their evolutionary relationships. This has resulted in very few up-to-date, or even recent (<10 years), publications which can aid connecting the recent family and generic classifications to identifications in the field, herbarium and botanic gardens. The first edition of the book was published in 2014 following APG III. It was the first book in the APG era to comprehensively compile practical morphological characters of all recognised families and the vast majority genera for field identification. A second edition is close to completion (2025) and is fully revised and expanded. Diagnostic morphological characters of all angiosperm orders and families (following a future APG V) and all genera (following the most recent plant family literature). All families are represented with plates showing the full morphological range of diversity with detailed images of vegetative and reproductive characters. Approximately 70% of all recognised genera are visually represented. This work follows exhaustive literature review, extensive field work, study of cultivated plants in Delft, and supplemented with herbarium work. This poster showcases example pages, dealing with conflicting published studies and further details behind its compilation. The book will be a comprehensive and practical tool for botanists and other relevant fields interested in the identification of flowering plants using the most recent APG and infrafamilial classifications.

P.0136 The reticulate evolution of pawpaws: insights from nuclear and plastid genomes

Luiz Henrique M. Fonseca[1], Kate R. Goodrich[2], Lars W. Chatrou[1]

1 Systematic and Evolutionary Botany Laboratory, Department of Biology, Ghent University, Ghent, Belgium. 2 Department of Biology, Widener University, Chester, Pennsylvania, USA.

Asimina Adans. is the only temperate genus in Annonaceae, an otherwise tropical plant family containing fruit crops such as sugar apple and soursop. The genus has eleven recognized species distributed in eastern USA. The centre of diversity is peninsular Florida, where up to ten species can be found in their native habitats. Species limits in *Asimina* were traditionally determined using morphological traits. Flower traits are remarkably variable in *Asimina* with differences in colour, size, odour, and the shape and thickness of their petals. Species with intermediate floral morphology and scent composition are regularly observed in the field. The potential hybrid origin of some species suggests a complex evolutionary history for *Asimina* and increases the level of difficulty for determining phylogenetic relationships within the clade. Furthermore, hybridization also blurs species boundaries. Here we inferred the phylogeny of *Asimina* using 695 low-copy nuclear genes and 78 plastid genes obtained off-target. We also dated the tree using tools that take into account the effects of incomplete lineage sorting and introgression, two processes that probably shaped the evolution of *Asimina*. To assemble the targeted genes, we combined two available bait kits (i.e., Angiosperms353 and Annonaceae) creating the new Annonaceae799 bait kit useful for the entire family. We also evaluated the role of incomplete lineage sorting, hybridization, and introgression on the phylogeny of the clade. Overall, we recovered a monophyletic *Asimina.* Putative hybridizations/introgressions were inferred for the clade using model-based and the D-statistics. Hybrids hypothesized by morphology were also confirmed using molecular data and D-statistics. Phylogenetic results using plastome data also confirmed the intricate evolutionary history of the clade, with considerable incongruence between plastome and nuclear trees. The evidence obtained suggests a rather intricate and recent evolutionary history for *Asimina,* with most of its diversification occurring during the last million year in Florida peninsula.

P.0137 The character evolution of the genus Burmannia (Burmanniaceae)

Supakan Simachai[1], Saroj Ruchisansakun[1], Thaya Jenjittikul[1], Nicha Thawara[1], Vincent Merckx[2]

1 Department of Plant Science, Faculty of Science, Mahidol University, Bangkok, Thailand. 2 Naturalis Biodiversity Center, Leiden, The Netherlands.

Burmannia is a genus primarily mycoheterotrophic plants, with approximately 61 accepted species distributed in tropical and subtropical regions. The interaction between the genus *Burmannia* and mycorrhizal fungi has deep roots in their evolutionary history. This fascinating behavior is generally found among all sister genera in the Burmanniaceae family. The goal of this research is to understand the evolutions of mycoheterotrophic lifestyle and morphological shifts on *Burmannia* through phylogenetic approach. In this study we constructed phylogenies for 27 species, including nine species collected in Thailand and the remaining acquired from GenBank database. Bayesian and Maximum Likelihood trees were generated based on the DNA data of three sources: the internal transcribed spacer (ITS) region for nuclear data, and matK and rbcL genes for chloroplast data. The phylogenies established in BEAST2 for Bayesian inference and RaxML for Maximum Likelihood analysis. Subsequently, ancestral states of some morphological characters, e.g., the presence of rosette leaves, the colors of stem, flower shapes, outer and inner perianth shapes and colors, were reconstructed and mapped onto the phylogenetic trees using in RStudio.

P.0138 What is a genus? - taxonomic rank and name instability

Alan S. Weakley[1], Derick B. Poindexter[1]

1 North Carolina Botanical Garden (Herbarium NCU), University of North Carolina, Chapel Hill, USA.

A seeming increase in taxonomic change, with high levels of lumping and splitting at many taxonomic ranks, has generated significant concern. Decisions about ranks above genus do not involve changes in plant names, but are important (especially at family rank) in their sorting of finer taxa into groupings useful for learning and teaching and understanding broad evolutionary patterns and mechanisms. Lumping and splitting decisions at the rank of genus, and of course also at species and infraspecific ranks (variety and subspecies), also create name changes, and are perceived as particularly destabilizing by many users of plant taxonomy. The generation of phylogenetic trees has added additional bases for decisions on taxonomic rank. Even with a phylogenetic tree of a family that all taxonomists agree is "correct", there are many potential translations of that tree into the hierarchical taxonomy which we primarily use, and each of those different taxonomic translations is logically as correct as another. Frequently, authors of papers simply present their taxonomy as the "result of the tree", without addressing why they made the choices they did, and why they rejected an equally logical but alternate taxonomy. In developing a taxonomy, different taxonomists place different weights on a variety of factors, including pre-existing consensus taxonomy, tree topology, branch lengths, estimated divergence times, crossability, biogeography, presumed evolutionary history, morphological divergence, and other factors. Until and unless we come to a better community consensus on the criteria to be used and their weighting, and explicitly explain the choices we make, we will be doomed as a community to continued and essentially unresolvable instability in rank choices and the names resulting from those choices. We explore these issues through examples from the Flora of the Southeastern United States, a flora with 302 families, 2366 genera, and 11,101 species (or unique infrataxa).

S.014. APOCYNACEAE ON THE WAY TO A MODEL FAMILY

P.0139 The flowers of Heterostemma ficoides (Apocynaceae) fool fig-pollinating wasps with their olfactory and tactile resemblance to figs

Aroonrat Kidyoo 1*, Manit Kidyoo 1, Doyle McKey 2, Finn Kjellberg 2, Jean-Yves Rasplus 3, Martine Hossaert-McKey 2, Rumsaïs Blatrix 2, Magali Proffit 2

*1 Plants of Thailand Research Unit, Department of Botany, Faculty of Science, Chulalongkorn University, Bangkok, Thailand, *aroonratm@hotmail.com.*
2 CEFE, CNRS, Univ Montpellier, Montpellier, France.
3 CBGP, INRAE, CIRAD, IRD, Montpellier SupAgro, Univ Montpellier, Montpellier, France.

Unlike congeneric species, *Heterostemma ficoides* produces globose closed flowers that anyone can mistake for figs (syconia) of *Ficus* spp. (Moraceae). Could this 'anyone' include a fig wasp? Fig-fig wasp interactions are highly specialized mutualisms. The specificity of pollinator attraction is mediated by volatile organic compounds (VOCs) emitted by receptive figs. Pollinator access to the oviposition site inside the figs depends on passage through the fig's sole entrance (ostiole). Fig wasps should avoid non-host figs and even more non-*Ficus* flowers. However, inside receptive flowers of *H. ficoides* we have recurrently discovered several fig wasps, *Kradibia* sp. (Agaonidae, Hymenoptera), some of which carried a pollinarium on a leg. This *Kradibia* is the specific pollinator of *Ficus heterophylla* throughout Thailand. In two provinces, Chiang Mai (natural habitat of *H. ficoides*) and Bangkok (outside the plant's native range), we investigated the attraction of *Kradibia* wasps to the VOCs emitted by flowers of *H. ficoides* using Y-tube olfactometer tests. At both sites, *Kradibia* females were among the most frequent floral visitors and were strongly attracted by VOCs of *H. ficoides* flowers. Comparison of the chemical profiles revealed that receptive figs of *F. heterophylla* and flowers of *H. ficoides* share several of theirmajor VOCs, notably sesquiterpenes. Thus, floral odors of *H. ficoides* attract *Kradibia* females to their flowers. Then the insects are stimulated by the sutures at the corolla mouth, through which they force their passage into the flower as if they were passing through the ostiole of the fig. These results suggest that *H. ficoides* deceives *Kradibia* females by producing olfactory, tactile, and maybe also visual signals similar to those of the wasps' host plant, *F. heterophylla*. To assess whether this resemblance is adaptive for *H. ficoides*, the efficiency of the fig wasp as a pollinator remains to be determined.

P.0140 Style head in Apocynaceae: a very complex secretory activity performed by one tissue

Danielle Maximo[1], Diego Demarco[1]

1 Department of Botany, Institute of Biosciences, University of Sao Paulo, Sao Paulo, Brazil.

Nuptial glands are very diverse, being associated to different pollination mechanisms. The greater specificity in pollen transfer mechanism from anther to stigma, the greater the morphological elaboration of flowers and the functional complexity of the nuptial glands. In Apocynaceae, pollination mechanisms reached an extreme specificity, a fact that was only possible due to an extreme morphological synorganization and a profusion of floral glands. Although these glands are of different types, the vast majority have secretory cells only in the epidermis. In general, these epidermal cells produce many different compounds at the same time and previous studies demonstrate that in the style head, the functional complexity of epidermis has become even greater. To determine the secretory activity of this tissue, we analyzed the style head of *Blepharodon bicuspidatum* (Asclepiadoideae) during floral development. Our results demonstrate that epidermal cells produce distinct compounds at different developmental stages. Furthermore, cells positioned in different parts of the tissue also produce different compounds and this secretory activity occurs synchronously with the development and maturation of sporogenic tissues. After release the secretion, it hardens and acquires a specific shape, being moulded by the spatial constraints of the adjacent floral organs. This secretion, called translator, is formed by a rigid central portion with a central slit, which will adhere to the pollinator's proboscis or leg, and two caudicles that attach to two pollinia, forming the pollinarium. The morphogenesis of this gynoecial secretion is synchronized with the development of pollinia inside the anthers, being completed at the same time as anther dehiscence occurs. The translator has a distinct composition in its different parts. This difference is related to the movement of the caudicles after the pollinarium removal. With this movement, the pollinia assume the necessary position for their insertion into the stigmatic chamber of the flower, ensuring effective pollination.

P.0141 Selection of DNA barcode regions for species discrimination, genetic diversity assessment and molecular authentication of Rauvolfia L. (Apocyanaceae) from Southern Western Ghats of India

Nizam Ashifa[2], P.V. Swetha[2], T Anju[2], Kumar Ajay[2], Vadakkemuriyil Divya Nair[1]

1 Department of Plant Sciences, Central University of Himachal Pradesh, Shahpur Campus, Shahpur, Kangra District, Himachal Pradesh, India. 2 Deparment of Plant Sciences, Central University of Kerala, Tejaswini Hills, Periya, Kasaragod, Kerala, India.

Rauvolfia L. (Apocyanaceae) has long been considered a therapeutic herb. It is found all over the world, primarily on the continents of Asia and Africa, and is represented by 74 species with numerous synonyms. There are five species of *Rauvolfia* known to exist in India's Southern Western Ghats. Using a brief DNA sequence from a predetermined, standard location in the genome, DNA barcoding is a method for identifying speciesn as well as inter, and intr specific diversity assessment. Considering their capacity to distinguish between species and establish phylogenetic relationships between the accessions, we employed different markers to test the universality of thirty five accessions from various locations that belong to five *Rauvolfia* species: *R. serpentina*, *R. tetraphylla*, *R. micrantha*, *R. beddomei* and *R. densiflora* Due to the lack of distinct physical distinctions across species, two of the species are taxonomically challenging and so provide an excellent excellent candidate for DNA barcoding. During our field studies we have noticed that morphologically similar, easily available and medicinally poor quality plant species are using as adulterants for *Rauvolfia* species. It is observed that *Chassalia curviflora* (Wall.) Thwaites (Rubiaceae) and *Clerodendrum paniculatum* L. (Lamiaceae) are two species widely using as adulterants in industry. The effectiveness of barcode regions like, ITS, matK, rbcL, trnH-psbA, and ndhF –rpl32 in species discrimination, molecular authentication of *Rauvolfia* species from their adulterants and genetic diversity assessment of all the *Rauvolfia* species reported from Southern Western Ghats of India were examined in this work. Comparison of efficiency for discriminating species indicated that *mat*K is more effective in authentication of *Rauvolfia* species from its adulterant. Sequences generated by the amplification of rbcL regions were used for the genetic diversity assessment of different species studied.

S.015. APPLICATIONS OF SPECTRAL REFLECTANCE IN PLANT SYSTEMATICS AND EVOLUTION

P.0142 Identification of herbarium specimens using NIRS: ongoing research at CIRAD

Samantha Bazan[1,2], Morgane Dendoncker[3], Elodie Baby[1,2], Denis Bastianelli[1,2], Jennifer Mersni[1,2], Alexia Bennert[3], Mia Svensk[1,2], Simon Taugourdeau[1,2], Laurent Bonnal[1,2]

1 CIRAD, UMR SELMET, Montpellier, France. 2 SELMET, Univ. Montpellier, CIRAD, INRAE, Institut Agro, Montpellier, France. 3 Université Catholique de Louvain, Earth and Life Institute, Environmental Sciences, Louvain-la-Neuve, Belgium.

Near infrared spectroscopy (NIRS) is a promising tool for valorizing herbarium specimens as it allows to gather information on plants without damaging valuable and historical samples. The CIRAD herbarium is currently testing various approaches. One approach involves using NIRS as a tool for systematic discrimination. Assuming that intraspecific variations in the nir-infrared spectrum are smaller than the interspecific variations, it may be possible to identify herbarium specimens within some genus, using appropriate calibration. Preliminary testing was carried out on two *Pistacia* species and their hybrid, using some specimens dating back 150 years and others collected recently. Using these two datasets, we evaluate the ability of NIR models built on older collections to discriminate recent samples or, in opposite, the possibility of discriminating older samples with recent collections. We are also working on a dataset of *Combretum* genus from West and Central Africa. Some species are not easy to identify on herbarium specimen and many *Combretum* sp. remain undetermined in herbaria collections. We are applying NIRS on numerous specimens coming from different institutions (P, MPU, B, ALF...) with diverse geographic origins and years of collection. We are therefore proposing to present the preliminary results on the potential application of NIRS as a tool for species systematic discrimination on these two datasets.

P.0143 Seed morphology of genus Alysicarpus Desv. (Fabaceae, Desmodieae) from India: Identification of species and systematic significance.

Shantanu Y. Chavan[1], Rupali R. Taur[2]

1 Department of Botany, Sant Dnyaneshwar Mahavidyalaya Soegaon Dist Chhatrapati Sambhaji

Nagar, India. 2 Ambedkar Marathwada University Chhatrapati Sambhaji Nagar, India.

Studies on the genus *Alysicarpus* Desv. pertaining testatopography, surface pattern, exomorphic, & endomorphic character. The present study representing of 42 variants of genus *Alysicarpus*. Seeds of 42 variants of *Alysicarpus* were studied in respect to their length, width, seed index, shape, size, colour, surface structure, position of hylum, spermoderm pattern and anticlinal cell wall as well as periclinal cell wall. The occurrence of faveolate pattern in 13 taxa makes unique characteristic of the genus *Alysicarpus* in the family fabaceae. The Scanning Electron Microscopy revealed different types of spermoderm patterns and seeds size provide considerable as qualitative character that could be used to distinguish the section of this genus because the seeds characteristic support to specific and infraspecific classification. The SEM showed that the unique seeds coat morphology and combination of other seeds morphological and micromorphological characteristics permits a key for the identification of the investigated taxa based on seed characters is provided.

P.0144 Identifying species using spectra of the bark in standing trees: testing the Micronir for recognizing species in the Amazon field

Flavia Durgante[1,2]; Hilana Hadlich[2]; Caroline Vasconcelos[2]; Caroline Mallmann[3]; Ricardo Perdiz[2]; Jochen Schongart[2]; Maria Tereza Fernandes Piedade[2]; Florian Wittmann[1,2]

1 Department of Wetlands, IFGG, Karlsruhe Institute of Technology, Rastatt, Germany. 2 Botanical Post Graduate Course at National Institute of Amazonian Research, Manaus, Brazil. 3 Department of Geography, Federal University of Santa Maria, Santa Maria, Brazil.

Identifying species levels in hyperdiverse areas such as the Amazon Forest is a time-consuming, laborious process that is also prone to many errors. Developing fast and low-cost methods to support the species identification process in the field is fundamental for improving the quality of the inventories of the Amazon Forest. To meet this objective, we tested two spectrometers in the field, the ASD FieldSpec 4 (spectral range 350-2500 nm, weight 8 kg, cost $90,000) and the MicroNIR InnoSpec (spectral range 900-1700 nm, weight 300 g, cost $2,000) to recognize species field during the forest inventory of standing trees using the spectra of the inner bark and discriminant analysis. It was possible to determine that the MicroNIR device is not available to recognize species via spectra of the bark. The accuracy of the Micronir was less than 50%compared to the accuracy of the ASD FieldSpec, which was more than 90% for the same trees. The MicroNIR has a shorter wavelength and lower resolution than ASD FieldSpec, and the quality of the spectral information was insufficient. Recognizing the efficiency of a cheaper and smaller device in identifying species in the field with high precision can open up a range of possibilities for applying this tool in the scientific field and the timber industry, as well as by government agencies and Non-Governmental Organizations. However, it is necessary to conduct more tests with different equipment to find a cheap and smaller device to recognize tree species in the field.

P.0145 Assessing the role of interspecific and intraspecific plant-plant interactions in a mountainous Mediterranean forest

Angela Illuminati[1], David S. Pescador[1,2], Ana I. García-Cervigón[1], Sergio Núñez[1], Javier Pajares[1], P Castro Sánchez-Bermejo[3,4], Silvia Matesanz[1], Cristina Poyatos[1], Marcelino de la Cruz[1], Ana M. Sánchez[1], Adrián Escudero[1]

1 Área de Biodiversidad y Conservación. Universidad Rey Juan Carlos, Móstoles, Madrid, Spain. 2 Departamento de Farmacología, Farmacognosia y Botánica, Facultad de Farmacia, Universidad Complutense de Madrid, Madrid, Spain. 3 Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle, Germany. 4 German Centre for Integrative Biodiversity Research, Halle-Jena-Leipzig, Leipzig, Germany.

In the last decades, plant ecologists have increasingly focused their attention on intraspecific variability, as a key portion of diversity so far overlooked. Specifically, this component of diversity may be of interest for the study of coexistence processes in local communities, with special emphasis to plant

communities with a low number of species, where intraspecific competition may be notably high. In this context, we aimed to assess neighbourhood scale processes undergoing in a mountainous Mediterranean forest characterized by two tree species of the genus *Pinus*, where strong plant-plant interaction processes are expected both between and within species. We georeferenced and mapped all mature individuals (n = 965) in a 1.5 ha plot in a forest located in the Alto Tajo National Park (Guadalajara province, central Spain). This spatially explicit approach was combined with the phenotypic characterization of all adults in the forest, through the application of predictive models obtained by using near infrared spectroscopy techniques. Through this novel approach, we could identify the relative importance of both inter- and intraspecific interactions, thus giving a new perspective on key fine-scale coexistence processes driving plant community assembly in mountainous Mediterranean forests.

P.0146 Herbarium leaf spectroscopy and estimating functional traits from degraded specimens

Rykkar Jackson[1], Dominic Wood[2], Jordan Wilson-Morrison[2], Subbaiah Mechanda[2], Shan Kothari[3], Warren Cardinal-McTeague[1]

1 Department of Forest & Conservation Sciences, University of British Columbia, Vancouver, Canada. 2 Ottawa Research & Development Centre, Agriculture & Agri-Food Canada, Ottawa, Canada. 3 Département des sciences biologiques, Université de Québec à Montréal, Montréal, Canada.

The estimation of leaf functional traits using leaf spectroscopy is a novel and underutilized technique in biological collections. With ~400 million plant specimens being held in ~3,500 herbaria worldwide today, there is massive potential for the use of spectroscopy on dried leaf samples. Once models are developed to quantify the limits of leaf spectroscopy on degraded herbarium specimens, such as those which have been stored for decades or centuries, we will better know the extent to which we can use herbaria to estimate leaf functional traits through time. This research expands the application of collections-based leaf spectroscopy by quantifying the limits of specimen degradation in leaf spectral analyses. To do so, this project utilizes spectra from both fresh and dried leaves of *Ginkgo biloba*. Representative specimens were collected in 2022 from a hedgerow and pressed, dried for 48 hours, and assembled into the four treatments: one in a standard herbarium cabinet (control conditions) and three in growth chambers (18°C, 21°C, 24°C) to accelerate degradation. At this time, initial fresh-leaf spectral readings were conducted. In 2023, after 1 year within these treatments, the corresponding dried leaf spectra (350-2400 nm) were measured. These data will be used to analyze the effects of degradation on spectral analysis across treatment types by building an empirical model using multivariate techniques to estimate leaf functional traits via the use of least squares regression (PLSR). This research is among the earliest studies using PLSR modelling on intact dried leaves like those in herbaria, as previous models have been trained using the reflectance spectra of either fresh or ground, dried, but not intact, dried leaves.

P.0147 Association of leaf spectral variation with functional genetic variants

Cheng Li[1], Ewa A. Czyż[1], Rishav Ray[2], Rayko Halitschke[2], Ian T. Baldwin[2], Bernhard Schmid[1], Michael E. Schaepman[1], Meredith C. Schuman[1,3]

1 Department of Geography, University of Zürich, Zürich, Switzerland. 2 Department of Molecular Ecology, Max Planck Institute for Chemical Ecology, Jena, Germany. 3 Department of Chemistry, University of Zürich, Zürich, Switzerland.

The application of in-field and aerial spectroscopy to assess functional and phylogenetic variation in plants has led to novel ecological insights and promises to support global assessments of plant biodiversity. Understanding the influence of plant genetic variation on reflectance spectra will help to harness this potential for biodiversity monitoring and improve our understanding of why plants differ in their functional responses to environmental change. Here, we use a well-resolved genetic mapping population of the coyote tobacco *Nicotiana attenuata*, to associate genetic differences with differences in leaf spectra between plants in a field experiment in their natural environment. We analyzed the leaf reflectance spectra using a hand-held spectroradiometer on plants from 325 fully genotyped recombinant inbred lines (RILs) of *N. attenuata* grown in a randomized block design. We then tested three approaches to conducting Genome-Wide Association

Studies (GWAS) on spectral variants. We introduce a new Hierarchical Spectral Clustering with Parallel Analysis (HSC-PA) method. This method efficiently captured the variation in our high-dimensional dataset and allowed us to discover a novel association, between a locus on chromosome 1 and the 445-499 nm spectral range, which corresponds to the blue light absorption region of chlorophyll, indicating a genetic basis for variation in photosynthetic efficiency. These associations lie in close proximity to candidate genes known to be expressed in leaves and having annotated functions as methyltransferases, indicating possible underlying mechanisms governing these spectral differences. In contrast, an approach using well-established spectral indices related to photosynthesis, reducing complex spectra to a few dimensionless numbers, was not able to identify any robust associations with genotypes, while an approach treating single wavelengths as phenotypes identified the same associations as HSC-PA, but without the statistical power to pinpoint significant associations. HSC-PA approach offers an insightful, data-driven analysis of genetic factors in leaf spectral variation, aiding future research.

P.0148 Using spectral reflectance as a tool for species recognition in taxonomically complex groups: a case study in hawthorns (Crataegus)

Marc-Aurèle Vallée[1], Roman Ufimov[2], Roswitha Schmickl[3], Tim Dickinson[4], Étienne Lacroix-Carignan[1], Etienne Laliberté[1], Étienne Léveillé-Bourret[1]

1 University of Montreal, Montreal, Canada. 2 Austrian Research Centre for Forest, Vienna, Austria. 3 Charles University, Prague, Czech Republic. 4 ROM Green Plant Herbarium, Toronto, Canada.

The hawthorns (*Crataegus,* Rosaceae) are a taxonomically complex group of ca. 400 species, many of which reproduce by facultative apomixis, with relatively frequent production of hybrids. This remarkable diversity, coupled with an intricate breeding system and reticulate evolution, poses significant challenges for those attempting species identification. Consequently, hawthorns have garnered a reputation for being problematic within the botanical community and remain largely understudied. Yet, habitat degradation, changes in agricultural practices and the inability to relocate certain species suggests that many hawthorns may be in decline across North America. It is therefore imperative to develop new approaches that facilitate their identification, in order to facilitate detection and monitoring of wild and potentially threatened populations. We here test if leaf reflectance spectra (400-2,400 nm) can distinguish genetic clusters in hawthorns. We first inferred a phylogeny of North American hawthorns using data from hundreds of nuclear genes obtained with a Malineae-specific HybSeq probe set. We then acquired leaf-level reflectance data from dry hawthorn specimens deposited in herbaria, and tested whether classification models based on leaf spectra can identify clades inferred using the phylogenetic approach. Preliminary results obtained from more than 300 *Crataegus* accessions show that spectral reflectance is useful for infrageneric and species-level identification.

S.016. ASSESSING AND CLASSIFYING THE POSITIVE AND NEGATIVE IMPACTS OF ALIEN PLANTS

P.0149 Implications for the use of Parthenium hysterophorus as soil amendment to combat Macrophomina phaseolina causing disease in maize

Muhammad Akbar[1], Nazir Aslam[1], Tayyaba Khalil[1]

1 Department of Botany, University of Gujrat, Gujrat, Pakistan.

Allelochemicals from numerous plants have been reported to exert their effects in combating the fungal pathogens. Moreover, these allelochemicals have also been reported to affect the growth of recipient plants. Allelopathic activity of *Parthenium hysterophorus* have been well recognized as having effects on fungal pathogens like *Macrophomina phaseolina* as well as on plants but there are no reports that describe the allopathic effects of *P. hysterophorus* about *in vivo* control efficacy against *M. phaseolina* as well as its effects on the recipient plant. Herein, we reported that *P. hysterophorus* has allelopathic effects on the pathogen as well as on the crop. Treatments were included to estimate the effects of *P. hysterophorus* amendment into the soil on the growth, biochemical and physiological functions with or without pathogen at 3 concentrations. *P. hysterophorus* amended soil 0.5% (w/w) reduced the disease incidence, disease severity index, area under disease incidence progress curve and area under disease incidence progress curve to 40, 23, 38 and 35%, respectively over infested control. Moreover, this concentration increased shoot length, shoot dry mass, root dry mass, chlorophyll a, b and carotenoids by 15.9, 18.6, 29.4, 7.5, 19.3, and 10.1%, over infested control. This concentration also exerted minimum inhibitory effects on the defense related antioxidant enzymes (super oxide dismutase, peroxidase, and catalase), and physiological [Carbon assimilation rate (*A*), stomatal conductance (*gs*), transpiration (*E*), and internal carbon dioxide concentration (*Ci*)] functions of maize. Although, the higher concentrations (1 and 1.5%) of *P. hysterophorus* were more inhibitory on the pathogen, but these concentrations also caused significantly more deleterious effects on the maize plants. These results suggest to test the donor plants for having allelopathic effects on the recipient plants before testing the donor plants meant to combat the pathogens in the field crops.

P.0150 Mapping the invasive footprint of exotic plants: an analysis of garden-associated species in a high touristic municipality

Miquel Capó[1], Antoni Palerm[2], Joshua Borràs[2]

1 Plant & Animal Ecology Lab. Centro para la Conservación de la Biodiversidad y el Desarrollo Sostenible, Departamento de Sistemas y Recursos Naturales, Universidad Politécnica de Madrid, Madrid, Spain. 2 Research Group of Plant Biology under Mediterranean Conditions. Departament de Biologia, Universitat de les Illes Balears, Palma, Spain.

A great number of cultivated plants in private, business and public gardens in the Meditarranean Basin are exotic species. Among them, many have a high invasive potential, being a major threat to native species and natural landscapes. To prevent this, the early detection of invasive species and the assessment of propagule pressure is essential. Despite many studies have focused on the expansion of exotic species in Mediterranean regions, fine-scale analysis at local or regional level are scarce. This is contrary to what conservation management requires, as information at local level helps to design and personalize concrete elimination strategies. In this study, we used Son Servera municipality (Mallorca, Balearic Islands) as a local-study case because it comprehends a mix of touristic businesses, high-income residential housing and golf courses. There, we exhaustively explored the area collecting inventories of garden-associated exotic species found in the wild. Our study identified 68 garden-associated exotic taxa with a ca. 30% with great invasiveness potential. Moreover, only 8 species are considered invasive in Balearic Islands. We also detected that hotels and private gardens were by far the most used source of horticultural species, although garden plants were replaced and/or renewed after relatively long periods of time. The case of *Lantana camara* is alarming as it was the most frequent species found in the area. Fleshy berries probably dispersed by birds makes the area of propagation of *L. camara* far greater than other invasive species. We conclude that detecting the local expansion spots in the area, as the case of hotels and private gardens in this study, is the main priority to implement an optimum conservation plan. Also, detecting the species with the most invasive behaviour, as the case of *L. camara* in this study, will be useful to establish a priority scale when designing eradication programs.

P.0151 Understanding and predicting invasiveness in the native Australian flora using functional traits

Laurel Constanti Crosby[1,2], Ana Claudia Araújo[2], Neil A. Brummitt[2]

1 Centre for Biodiversity and Environmental Research, Department of Genetics, Evolution and Environment, University College London, London, UK. 2 Natural History Museum, London, UK.

Invasive species are well-recognised contributors to native biodiversity declines, prompting efforts to limit future invasions. To predict which species display the greatest invasion potential, an improved understanding of traits associated with invasiveness is necessary. It is expected that the same traits that confer a large range size will also predispose species to invasiveness by enabling them to become widespread in non-native regions, suggesting range size could act as a useful proxy for invasion potential. To date, studies examining plant traits associated with range size (or invasiveness directly) have focused primarily on European flora, and several traits, including reproductive morphology and leaf architecture, remain relatively unexplored in this context. In this study, trait information obtained from taxonomic descriptions was used to explore the association between 29 functional traits and the range sizes of a randomly-selected sample of 243 Australian angiosperms, determining the relative importance of significant traits for predicting range size. Native and total global (i.e., native plus introduced) range were measured using Extent of Occurrence and Area of Occupancy values. Functional traits encompassing a species' competitive ability (plant height, leaf area), pollination (flower architecture) and dispersal mode (fruit structure) are identified here as important determinants of range size differences, some of which are known to be key dimensions of plant ecological strategies. This study contributes to an improved understanding of the traits that make a species widespread across its native and total global range, indicating potential invasiveness traits and informing trait-based frameworks to predict species' invasion potential.

P.0152 Allochthonous plants in three green areas of Barcelona

Carles Burguera i Martín[1, 2], Francisco Javier Font Castell[1], Pere Fraga i Arguimbau[2]

1 Universitat de Barcelona, Barcelona, Spain. 2 Jardí Botànic Marimurtra, Blanes, Spain.

Barcelona is the second most populated city in Spain, with an area of 101.35 km² and a population density of 16.339 per sq Km. The city has green areas, parks and urban hills used for the citizens and tourists in many different activities. Three out of five largest areas, apart from Collserola mountain range, are the area known as the "three hills". These hills are *Turó de la Rovira* (0.42 km² and 262 m.a.s.l.), *Turó del Carmel* (0.3 km² and 266 m.a.s.l.) and *Parc de la Creueta del Coll* (0.17 km² and 245 m.a.s.l.). These natural areas did not have an active management by the city council, and most of them are semi wild natural, being a relict representation of the Mediterranean wild flora in the city. The presence of naturalized, escaped or persistent allochthonous plants, some of them reported for the first time for the city of Barcelona, makes noticeable these green areas as a hotspot for alien plants and a possible acclimatization zone. Most of the species are well known taxa in Catalonia (northeastern Spain), and the main part of them could have been introduced by public and private gardens or ornamental plants, as well as some persistent old tree plantations. In these work, we present an accurate list and distribution of the allochthonous plant taxa of the "three hills" of Barcelona, his naturalization category, corological distribution and the potential danger range as an alien species.

P.0153 Exploring nurseries as vectors for plant introductions: a deep dive into insights on plant contaminants

Carles Cardona[1 2], Pere M. Mir-Rosselló[2], Lorenzo Gil[2], Javier Fabado[3], Jaime Güemes[3] P. Pablo Ferrer-Gallego[4], Inmaculada Ferrando-Pardo[4], Emilio Laguna[4], Marcello Dante Cerrato[2]

1 Centre Forestal de les Illes Balears, Institut Balear de la Natura, Palma, Spain 2 Interdisciplinary Ecology Group, Department of Biology, University of the Balearic Islands, Palma, Spain. 3 Jardín Botánico de Valencia, Universidad de Valencia, Valencia. Spain. 4 Servicio de Vida Silvestre y Red Natura 2000 - Centro para la Investigación y Experimentación Forestal, Generalitat Valenciana, Valencia, Spain.

Plant species introductions pose a global threat to ecosystem conservation, with institutional nurseries playing a crucial role in habitat restoration and endangered species reinforcement. However, the substrates used in nurseries can inadvertently become a pathway for contaminant taxa. This study in Balearic Islands and Valencia assessed the risk of contaminant plant species in nurseries linked to conservation. Examining two nurseries dedicated to plant forestry and conservation projects and one to ornamental plants, the study identified 122 contaminant taxa. Among them, 22 species are first records for the European and Mediterranean region, and 12 are in only three or fewer places. Non-native taxa are notably, 90% for Valencia and 60% for Balearic Islands. Moreover, 60-70% of non-natives represent novelties for both regions. Taxonomically, the recorded species span 39 families, with varying prevalence of *Poaceae, Cyperaceae,* and *Asteraceae*. Only five taxa are common to all nurseries. Contaminated substrate, primarily from coconut peach (50-60%), serves as the main introduction pathway. Local contamination is relevant (20-40%), along with unknown origins, presumed to be the latter. Most species are annuals, with a bioclimatic preference for tropical or subtropical regions (70%) and being the remaining from temperate climates (30%). This aligns with the native ranges of many species, which range from paleotropical or broad distributed neotropicals (also present in the paleotropical), and euroasiatic to cosmopolitan. These results support nurseries as possible pathway for opportunistic species. And emphasize the importance of proper substrate use, plant control, and in situ contamination avoidance in nurseries. Although those species have a low probability of successful establishment in European nature, some of them have been found to be well established in various habitats and even to be invasive. It is vital to take strict measures, particularly concerning coconut peach substrate, to mitigate risks and safeguard delicate restoration efforts.

P.0154 Germination experiments on indehiscent two-seeded fruits of the invasive weed Xanthium spinosum

Miguel A. Copete[1], Elena Copete[1], Pablo Ferrandis[1], Alejandro Santiago[1], José M. Herranz[1]

1 Botanical Institute, University of Castilla-La Mancha, Albacete, Spain.

Understanding the germination ecology of invasive plants is crucial for comprehending their behavior and spread. In the case of *Xanthium spinosum*, a native of South America that has become a global menace, analyzing germination processes can aid in developing effective strategies for controlling its expansion. This study aims to evaluate optimal germination conditions for *X. spinosum*, specifically focusing on temperature and light factors. Fruits were collected from 10 plants, revealing no significant differences in fruit size or average number of viable seeds (1.74 viable seeds/fruit). Remarkably, 77% of the fruits contained two viable seeds, contributing to its potential dominance. Being indehiscent fruits, germination trials were conducted with intact fruits to simulate natural conditions, allowing the emergence of up to two seedlings per fruit. The thermoperiods analyzed represented the thermal conditions throughout the year in Mediterranean environments. Incubation temperatures of 5ºC and 28/14ºC resulted in the lowest radicle emergence. For other thermoperiods, radicles emerged in 65-71% of the fruits, with only 6.9% exhibiting germination of both seeds. Maximum germination of both seeds (22.5%) occurred at the 25/10°C thermoperiod. However, incubation temperature did not influence mean germination time (MGT). Additionally, light conditions had no impact on germination percentage, but it did affect MGT, with darkness promoting faster germination. After 9 months of desiccation in laboratory conditions, 2.1% of fruits still germinated. The low proportion of fruits with both seeds germinated indicates the accumulation of dormant seeds in the soil seed bank, emphasizing the need to study the mechanisms triggering their emergence from dormancy. This research provides valuable insights into the germination dynamics of *X. spinosum*, essential for developing targeted invasive plant management strategies.

P.0155 Avoiding the law: Clandestine invasive alien species in the evergreen cloudforest

Alberto de la Rosa Padilla[1], Victoria E. Martín Osorio[1], Wolf H. Wildpret Martín[2], Wolfredo Wildpret de la Torre[1]

1 Universidad de la Laguna, Tenerife, Spain. 2 Biodiversity, Macroecology & Biogeography Research Group. Faculty of Forest Sciences and Forest Ecology. University of Göttingen, Göttingen, Germany.

Since 2007 Spanish legislation prescribes the need to monitor exotic species with invasive potential (Law 42/2007, of December 13, on Natural Heritage and Biodiversity, article 61.4). From 2013 onwards, it is in the annex to the Royal Decree 630/2013, of August 2, which regulates the Spanish Catalogue of Invasive Exotic Species, where the territorial scope of application for these invasive alien species is detailed. After the study of species distribution in the evergreen cloudforest of the Anaga Rural Park (Biosphere Reserve), Tenerife, Canary Islands, 5 species have been identified and defined as sure introduced invasive (from Spanish; ISI); these occupy a considerable area but that for the moment remain outside the Spanish Catalogue of Invasive Exotic Species. These five clandestine species are: *Eucalyptus globulus* Labill., *Crocosmia* Planch., *Melinis repens* (Willd.) Zizka, *Crassula multicava* Lem. and *Anredera cordifolia* (Ten.) Steenis. In order to obtain these results, 82 exotic species have been inventoried using a geobotanical information system (GBOTIS). A total of 37 species were defined as sure introduced invasive. Five out of these 37 IAS were identified as having "greater impact" according to scientific and abundance/extension aspects of the taxon itself in situ, although remaining outside the law. Environmental and bioclimatic variables that affected their distribution were also studied to correlate these with the bioclimatic belts and occupied vegetation belts and then determine possible areas of expansion. In this way, it's possible that dispersion can be predicted and managed, and their advance stopped. Likewise, due to the environmental value of the study area and the increasing risk that the dispersion of these species would cause, their inclusion in the Spanish Catalogue of Invasive Exotic Species is proposed to guarantee the application of the corresponding regulations.

P.0156 Determination of the type of evergreen cloudforest most affected by the occupation of IAS in the Macizo de Anaga Biosphere Reserve

Alberto de la Rosa Padilla[1], Victoria E. Martín Osorio[1], Wolf H. Wildpret Martín[2], Wolfredo Wildpret de la Torre[1]

1 Universidad de la Laguna, Tenerife, Islas Canarias, Spain. 2 University of Göttingen, Göttingen, Germany.

This paper determines the area occupied by invasive alien species (IAS) in each of the four types of potential evergreen cloudforest relict vegetation of the tertiary present in The Macizo de Anaga Biosphere Reserve. A total of 1011 relevés were carried out using a geobotanical information system (GBOTIS), which allowed us to have information on the abundance/extension of the invasive taxa and on environmental variables. The percentage of potential cloudforest vegetation type occupied by IAS were: *Lauro novocanariensis-Perseo indicae sigmetum*: 51.11%; *Visneo mocanerae-Arbuto canariensis sigmetum*: 53.11%; *Ilici canariensis-Erico platycodonis sigmetum* 51.08%; *Diplazio caudati-Ocoteo foetentis sigmetum*: 71.05%. The latter, known as the "hydrophilous laurel forest", only presents its climax stage in 5,26% of the potentiality of its studied area, 15,79% corresponding to cultivated areas and the rest (78,95%) to other stages of substitution/degradation. The dominant thermotype is mainly Thermomediterranean (92.11%) and the most common bioclimatic belt, the subhumid pluviseasonal Thermomediterranean without trade-wind clouds (76.32%). Finally, ten of the thirteen introduced species have been classified as sure introduced invasive and eight of these appear included in the Spanish Catalogue of Invasive Exotic Species (Royal Decree 630/2013). *Arundo donax* L. is present in more than half of the relevés (52.63%) with an abundance index of 5. These values contrast with other studied species (*Ageratina adenophora* (Spreng.) R.M.King & H.Rob., *Cenchrus setaceus* (Forssk.) Morrone, *Erigeron canadensis* L., *Impatiens sodenii* Engl. & Warb., *Nassella neesiana* (Trin. & Rupr.) Barkworth) which, despite being able to reach abundance indexes of 4, do not exceed an occupancy rate of more than 5.26%. After the study, "hydrophilous laurel forest" is considered as the most disturbed kind of evergreen cloudforest. The priority control of *Arundo donax* is proposed due to the values obtained and, in addition, because it is a transforming species,which puts biodiversity and conservation at risk.

P.0157 Invasion degree of non-native plant species in the Alboran Sea: coasts of Malaga and Granada.

Estefany Goncalves[1], Federico Casimiro-Soriguer[1], Jaiver García-Caballero[1], Noelia Hidalgo-Triana[1].

1 Department of Botany and Plant Physiology, University of Malaga, Malaga, Spain.

The Iberian coastal environment of the Alboran Sea is characterised by a great diversity and richness of species and a high diversity of coastal habitats, many of them included as Habitats of Community Interest (HCI) in the Habitats Directive 92/43/EEC. These HCI are particularly relevant in the European context, although they are especially fragile, due to multiple factors that threaten their conservation. Among these threats, the increase in the presence of invasive non-native species emerges as one of the most significant problems. The aim of this study is to estimate the potential invasiveness of non-native species present in the coasts of Malaga and Granada, with the aim of identifying the most invasive species. To achieve this, we sampled the allochthonous species present in the study area and classified them in three categories (super, moderate and poor invaders) based on three criteria: species distribution or range, abundance and the number of habitats occupied by the species. We registered 97 allochthonous species, mostly from the Asparagaceae (12.5%), Asteraceae (8.3%) and Poaceae (8.3%) family. Of these species, 41.7% were classified as 'poor invaders', and 38.5% as 'moderate invaders'. Notably, a 19.8% of the allochthonous species were 'super invaders' occupying more than 20% of Habitats of Community Interest (HCIs). Some of these 'super invaders' are *Arundo donax* L., *Acacia saligna* (Labill.) H.L.Wendl., *Oxalis pes-caprae* L., *Carpobrotus edulis* (L.) N.E.Br., *Lantana camara* L. and *Eucalyptus camaldulensis* Dehnh. Because of this, we recommend establishing a more rigorous monitoring of these species due to their high invasiveness and establish them as priority management or eradication species.

P.0158 Multiple introductions of divergent lineages and admixture conferred the high invasiveness in a wide spread weed (Hypochaeris radicata)

Soo-Rang Lee[1]*, Tae-Young Choi[1], Dong-Chan Son[2]

1 Department of Biology Education, Chosun University, Gwangju, Korea. 2 Division of Forest Biodiversity and Herbarium, Korea National Arboretum, Pocheon, Korea.

Biological invasion consists of spatially and temporally varying stages accompanied by ecological and evolutionary changes. However, these changes are not straightforward, as the environmental barriers and coping strategies differ and are intertwined across the stages. Post-invasion shifts are particularly intricate, encompassing nearly all major determinants of invasion stages at metacommunity scale. Consequently, understanding the post-invasion dynamics provides critical information on the rate and direction of invasion. Here, we used genomic data and model-based approaches to characterize the post-invasion dynamics of Hypochaeris radicata L., a noxious weed in Korea. Genetic diversity and assignment patterns were investigated using 3,563 SNPs on 283 individuals sampled from 22 populations. We employed a coalescent-based simulation method to estimate demographic changes for each population and inferred colonization history using both phylogenetic and model-based approaches. Our data suggested that H. radicata has repeatedly been introduced to Korea from multiple genetic sources within the last

50 years experiencing subsequent population bottlenecks. Genetic diversity was relatively well-maintained for an invasive herb with a recent invasion history and rapid demographic shifts. Collectively, the results demonstrate the potential for further range expansion, particularly in the presence of anthropogenic impacts. Our study is the first population-level genomic research documenting the post-invasion dynamics of the successful invader, H. radicata, outside of Europe. The integrated approach employed in our study can widely be applied to other invasive species within their novel ranges.

P.0159 Prioritizing management actions for emergent invasive alien plants through expert-based knowledge and Species Distribution Models

Vanessa Lozano[1,10], Flavio Marzialetti[1,10], Alicia T. R. Acosta[2], Iduna Arduini[3], Gianluigi Bacchetta[4], Gianniantonio Domina[5], Valentina L. A. Laface[6], Valerio Lazzeri[7], Chiara Montagnani[8,10], Maria C. Musarella[6], Gianluca Nicolella[8], Lina Podda[4], Giovanni Spampinato[6], Gianmarco Tavilla[9], Giuseppe Brundu[1,10]

1 Department of Agricultural Sciences, University of Sassari, Sassari, Italy. 2 Department of Science, University of Roma Tre, Rome, Italy. 3 Department of Agriculture, Food and Environment, University of Pisa, Pisa, Italy. 4 Department of Life and Environmental Sciences, University of Cagliari, Cagliari, Italy. 5 Department of Agricultural, Food and Forest Sciences, University of Palermo, Palermo, Italy. 6 Department of Agriculture, Mediterranean University of Reggio Calabria, Reggio Calabria, Italy. 7 Natural History Museum of Rosignano Marittimo, Livorno, Italy. 7 Department of Earth and Environmental Sciences, University of Milano-Bicocca, Milan, Italy. 8 Acta Plantarum ODV, Genova, Italy. 9 Department of Biological, Geological and Environmental Sciences, University of Catania, Catania, Italy. 10 National Biodiversity Future Center, Palermo, Italy.

Innovative tools for rapid and efficient prioritization lists of emergent invasive alien plants (IAPs) are essential to support cost-effective management strategy. In this context, Species Distribution Models (SDMs) are a sound tool for predicting current and future suitable areas for new IAPs. Within this work, we firstly provided the European and Mediterreanean Plant Protection Organization (EPPO) with a list of emergent IAPs for Italy, and after applied a methodological framework that combined SDM, clustering and ordination in order to produce a prioritization management list for emergent IAPs at the national scale (Italy). The identification of emergent IAPs was achieved by members of the Italian Botanical Society (SBI). Occurrences of each IAP were retrieved from GBIF. Current and future suitable areas of each IAP were identified using MaxEnt and bioclimatic variables retrieved from the Chelsa database. After, we estimated the current and future suitability percentage in each Italian bioregion, and we calculated future suitability changes caused by climate change. The suitability percentages were the data to define prioritization list combining cluster analysis, non-metric multidimensional scaling (NMDS) ordination analysis and classification of IAPs. The list of emergent IAPs included 36 species invading or potentially invading at least one of the three biogeographical (Mediterranean – M, Continental – C, Alpine – A) regions of Italy. Overall suitability models showed excellent predictive performances (AUC > 0.945, BCI > 0.786), and most IAPs were classified with high and very high suitability class in M and C regions. Three clusters showing different suitability for the Italian bioregions were identified by cluster analysis, and the three NMDS estimate the cluster internal variability, current distribution pattern of IAPs and classification in the prioritization list. The proposed prioritization framework has proved efficient, fast and reproducible procedure in order to indicate management actions for emergent IAPs in Italy.

P.0160 Field demonstrations for water chestnut (Trapa spp.) management – Year 1

Lynde Dodd[1], Ryan McIntyre[2,3], Kristina Hellinghausen[2,4], Nancy Rybicki[3], Christopher Mudge[1], Benjamin Sperry[1]

1 U.S. Army Engineer Research and Development Center, USA. 2 Oak Ridge Institute for Science and Education, Oak Ridge, USA. 3 Department of Environmental Science and Policy, George Mason University, USA. 4 University of North Texas, Denton, USA.

Collaborative applied research conducted under the U.S. Army Corps of Engineers' Aquatic Plant Control Research Program is currently developing management strategies of introduced water chestnut species, *Trapa natans* and *T. bispinosa* var. *iinumai*. While much information exists on management in the U.S., specifically targeting *T. natans*, knowledge gaps exist in translating management strategies from one congener to another, and whether currently employed strategies are successful in reducing impact and spread of this invasive aquatic plant. Demonstrations and lessons learned from Year 1 of a 2-year project work focus on determining what management approach works best in an operational setting to control two water chestnut species. While not all known strategies are reviewed, those currently being implemented and recent findings from greenhouse and mesocosm studies were demonstrated during the summer of 2023 at field sites in New York for *T. natans*, and in Virginia and Maryland for *T. bispinosa*. Preliminary results indicate that foliar herbicide applications work well to reduce biomass for both species of water chestnut, but that biomass harvesting strategies employed for *T. natans* will need further investigation for implementation large-scale for *T. bispinosa* control. Findings from this 2-year study will be used to refine water chestnut management strategies.

P.0161 Annona glabra L. invasion in wetlands of kannur district of Kerala, India

P. Sreeja[1]

1 PG Department of Botany and Research Centre, Sir Syed College, Taliparamba, Kerala, India.

Wetlands seems to be vulnerable to invasions. Furthermore, many wetland invaders form monotypes, which alter habitat structure, lower biodiversity (both number and “quality” of species), change nutrient cycling and productivity (often increasing it), and modify food webs. In Kannur district recently it was found that an invasive species namely *Annona glabra*, commonly called pond apple spreading in the mangrove rich wetlands. Through this study an attempt was made to understand its distribution, stress tolerance ability and other adaptive features of *Annona glabra*, make them a successful invader. For this study frequent field visits conducted in all the parts of mangrove rich as well as other riverside and coastal wetlands. Samples were collected from different sites and interview was carried out with some stake holders. Microscopic sections of leaf, stem and root was analyzed for studying anatomical features. Stomatal index was determined by taking the epidermal peels of leaves collected from study sites. Pond apple is a semi deciduous woody tree, typically grow 30 to 40 feet tall and 10 to 20 feet wide. The clusters of seedlings produce and appears to be tightly packed multi-stemmed trees. Twigs are spotted with reddish brown, warty, raised projections called lenticels. The striking fact recognised by the socio-economic survey is that most of the local people are not bothered about the impacts of *Annona glabra* L. In other words, they are not recognizing the’ slow poison’ effect of *Annona glabra*. The present study was an attempt to familiarize the negative impacts of this invasive species to the society.

P.0162 Impact of the invasive alien macrophyte Ludwigia hexapetala on freshwater ecosystems: evidence from field data

Emanuele Pelella[1]

1 Department of Science, University of Roma Tre, Rome, Italy.

Biological invasions are a serious threat to biodiversity conservation, especially in freshwater ecosystems. The American macrophyte *Ludwigia hexapetala*, which colonizes both the aquatic and bank habitats of lakes, rivers, and canals, is invading many waterbodies in Europe, becoming an increasingly worrisome threat in several European countries, including Italy. However, only fragmentary information is available on the actual impact of its invasion in these habitats. This study aims to collect field data, including plant cover and environmental variables, from various freshwater habitats in central and northern Italy, to assess the possible impact of *L. hexapetala* on the environmental parameters and plant biodiversity of the invaded habitats. The results show that in aquatic habitats, dense floating *L. hexapetala* populations reduce the light levels and dissolved oxygen available in the water, significantly altering water quality and consequently limiting the growth of other aquatic plants. Indeed, *L. hexapetala* populations negatively affect aquatic plant diversity, as an increase in *L. hexapetala* cover corresponded to a decrease in Simpson’s diversity index. This suggests that aquatic plants, being the first to face the alien species in its colonization phase, are more susceptible to its invasion. In contrast, in bank habitats, *L. hexapetala* has no significant impact on plant diversity. Evidence suggests that some native species, such as *Phragmites australis*, which generally form compact populations along the banks, effectively counteract the invasion of *L. hexapetala,* hindering the establishment of its propagules arriving from nearby invaded aquatic areas. This information may prove valuable for the environmental managers of those freshwater habitats where L. hexapetala invasion needs to be addressed and controlled.

P.0164 Habitat suitability of invasive alien Populus alba L. in South Africa

Dikonketso Tlaamela[1], Lourens Swanepoel[1], Milingoni Tshisikhawe[1], Sebataolo Rahlao[2]

1 University of Venda, Limpopo Province, South Africa. 2 Ezemvelo KZN Wildlife, Kwazulu Natal Province, South Africa.

Invasive alien plants cause negative environmental and socio-economic impacts. *Populus alba* L. is amongst the woody alien invasive species present in South Africa. *Populus alba* is native to Europe, North Africa, and Asia; and has been introduced to South Africa for ornamental purposes. It poses threats to native biodiversity through competition and reduction of surface water runoff. Its suitable habitats remain unknown in the country, which present challenges for management measures. This study reports the habitat suitability of *P. alba* in South Africa using the species distribution models. An ensemble model was developed using Maximum Entropy, Generalised Additive Model and Random Forest algorithms. Furthermore, a species response curve was generated to assess the change in species probability of occurrence along each environmental variable. The accuracy of the models was measured by calculating the area under the received operator curve and Pearson Correlation Test. The performance accuracy evaluations of Maxent, Generalised Additive Model and Random Forest projected a more realistic and practical method, with mean performance of 0.49, 0.52 and 0.62 respectively. Based on the models, suitable habitat conditions for *Populus alba* are present in Gauteng, Free State, Mpumalanga and Western Cape provinces.

P.0165 Suppressing the invasive common milkweed (Asclepias syriaca L.) saves soil moisture reserves

Benedek Tóth[1], Csaba Tölgyesi[2], Zoltán Bátori[1], Alida Anna Hábenyczus[1], Kata Frei[1], Viktória Tóth[1]

1 Department of Ecology, University of Szeged, Szeged, Hungary. 2 MTA-SZTE 'Momentum' Applied Ecology Research Group, University of Szeged, Szeged, Hungary.

Common milkweed (Asclepias syriaca L.) is a widespread invasive alien forb in dry sandy habitats of Central Europe. It affects native plant and animal communities in many ways, but its ecosystem-level effects, particularly on moisture regime, are little known. Since milkweed has an extensive, deep root system and large, broad leaves, we assumed a negative effect on the soil moisture content of the hosting ecosystem. In seven partially invaded sandy grasslands of Hungary, we compared the soil moisture content of the top 120 cm of the soil under milkweed stands to that of non-invaded reference parts of the grasslands. To prove the causal role of milkweed in soil moisture differences, we treated half of the milkweed stands in the second year by mechanically removing all above-ground biomass of milkweed and continued the comparative soil moisture measurements started in the first year. We found that milkweed stands had significantly drier soils compared to reference grasslands during the growing season, but the soil under milkweed stands recharged to the level of the non-invaded references in autumn and winter. However, the amount of moisture needed for this was lost from deeper percolation to ground water. Milkweed removal efficiently prevented the depletion of soil moisture during the growing season and could lead to the retention of 21.6 l m-2 of soil moisture on average. Our results reinforce the importance of milkweed suppression in invaded grasslands, even if it does not lead to a complete eradication of the species and/or the full recovery of the native flora and fauna. The reduction of milkweed density, even if it is temporary following herbicide application or other more nature-friendly methods, can promote groundwater recharge, which is particularly important in the dry regions of Central Europe, currently facing severe aridification due to climate change and unfavourable land use trends.

P.0166 Cytogeography of invasive Solidago taxa in Europe: what is the origin, fate and role of new cytotypes?

Katarína Skokanová[1], Barbora Šingliarová[1], Stanislav Španiel[1], Michaela Murgašová[2], Kristína Pulišová[1,3], Judita Zozomová-Lihová[1]

1 Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovakia; judita.zozomova@savba.sk. 2 Department of Biology, Ecology and Environment, Faculty of Natural Sciences, Matej Bel University, Banská Bystrica, Slovakia. 3 Department of Phytology, Faculty of Forestry, Technical University in Zvolen, Zvolen, Slovakia.

Invasive alien species have a negative impact on biodiversity and are one of the major threats to native ecosystems. It has been repeatedly shown that evolutionary processes such as genome duplication and hybridization can form new, more-invasive genotypes. We investigated the karyological variation and cytogeography of invasive *Solidago* species in Central Europe by analysing nearly 4800 plants from 800 sampled sites using flow cytometry and chromosome counting. Our results are consistent with previous reports, with the diploids of *S. canadensis* and the tetraploids of *S. gigantea* dominating the invasive range. However, we also found rare cytotypes for the first time – triploids of *S. canadensis* and pentaploids of *S. gigantea*. The triploids were scattered within diploid populations, and probably arose from a fusion of reduced and unreduced gametes. The origin of the *S. gigantea* pentaploids is more obscure; we recorded hundreds of plants in the invasive range, although only one pentaploid has been reported so far from the native range. To assess the true extent of the threat these new cytotypes pose to nature (comparable or greater than their already successful counterparts?), the origin of the newly discovered polyploids and their invasive potential were further investigated using an integrative approach combining screening of relative DNA content, assessment of population genetic structure by ddRADseq and measurements of reproductive potential and fitness parameters (fertility, mode of reproduction, karyology of progeny, extent of clonality). First findings indicate that pentaploids of *S. gigantea* produce reduced but unbalanced gametes that enter into mating with co-occurring tetraploid plants. This is reflected in the production of viable seeds with a relative DNA content ranging from 4x to 5x in both tetraploid and pentaploid maternal plants. Pentaploids have a greatly reduced seed production and probably reproduce mainly clonally. Acknowledgments: The study was supported by the grant VEGA 2/0024/23.

S.017. ASSESSING THE INTERPLAY BETWEEN GENETIC AND NONGENETIC MECHANISMS CONTRIBUTING TO PHENOTYPIC VARIATION AND ADAPTATION OVER TIME

P.0167 Evolution of pollen grain traits in Malpighiaceae is strongly correlated with type of habit and chromosome numbers

Higor Antonio-Domingues[1], Marco Octávio de Oliveira Pellegrini[1], Isa L. de Morais[2], Rafael Felipe de Almeida[1,2]

1 Royal Botanic Gardens Kew, Richmond, UK. 2 Universidade Estadual de Goiás, Quirinópolis, Goiás, Brazil.

Pollen grain morphology is an important morphological character for aiding the systematics of flowering plants. For Malpighiaceae, just a single unpublished palynological study has comprehensively sampled ca. 60 from this family's 75 currently accepted genera. To test the evolutionary relevance of pollen morphology in the face of current phylogenetic evidence for this family, we tested the correlation between pollen traits related to axis and aperture (length, number, position, and type) with habit types and chromosome numbers. We sampled all 75 currently accepted genera of Malpighiaceae as ingroups and two genera of Elatinaceae as outgroups. Pollen grain, plant habit, and chromosome number traits were retrieved from different sources of the literature, scored and coded into six traits and mapped into the most recent generic molecular phylogeny of Malpighiaceae using maximum likelihood criteria. The patterns of pollen grain evolution evidenced by our results showed that all pollen traits showed a strong correlation with the evolution of different habits and chromosome numbers in Malpighiaceae. Pollen grain axis mean values steadily increased in all phylogenetic clades, from the oldest (80 Mya) to the earliest (10 Mya) groups arising throughout the geological time. Our results evidence that even though the pollen traits of Malpighiaceae are somewhat homogeneous for the four largest lianescent clades (Hiraeoid, Malpighioid, Tetrapteroid, and Stigmaphylloid) with larger chromosome numbers, a greater variability in pollen traits was recorded in the six early diverging, shrubby to tree lineages of this family showing smaller chromosome numbers. Additionally, all pollen traits studied showed a great taxonomic potential in circumscribing most of the ten molecular phylogenetic clades resolved in this family and will be properly and widely tested in future studies by us.

P.0168 A field study of the molecular response of brown macroalgae to heavy metal exposure: an (epi) genetic approach

Rita García-Seoane[1], Christina L. Richards[2], Jesús R. Aboal[3], J. Ángel Fernández[3], Marc W. Schmid[4], M. Teresa Boquete[3]

1 Instituto Español de Oceanografía (IEO-CSIC), A Coruña, Spain. 2 University of South Florida, Tampa, USA. 3 CRETUS, Ecology Unit, Universidade de Santiago de Compostela, Spain. 4 MWSchmid GmbH, Glarus, Switzerland

Our understanding of the relative contribution of genetic and epigenetic mechanisms to organismal response to stress is largely biased towards specific taxonomic groups (e.g., seed plants) and environmental stresses (e.g., drought, salinity). Here, we investigated the molecular basis of the response of the brown macroalgae *Fucus vesiculosus* to heavy metal (HM) exposure. This species can accumulate and tolerate high concentrations of HMs, yet the molecular mechanisms underlying the response are poorly understood. We reciprocally transplanted living thalli of *F. vesiculosus* between two polluted (P) and two unpolluted (UP) sites on the Galician coast for 90 days. We determined initial (before transplantation) and final (after transplantation) concentrations of HMs in the thalli and characterized their genetic (single nucleotide polymorphisms) and epigenetic (cytosine DNA methylation) variability using epigenotyping by sequencing (epiGBS). Distance based redundancy analyses of genetic, epigenetic and phenotypic pairwise distance matrices showed that: **(i)** all populations differed in their HM content profiles before transplantation (origin explained 98% of the variation in phenotypic distances). After transplantation, they clustered by exposure site regardless of origin (exposure explained 60% of the variation in phenotypic distances); **(ii)** all populations were genetically differentiated; **(iii)** epigenetic differentiation was not significant before transplantation and, when accounting for genotype effects, it was not significant either after transplantation; **(v)** macroalgae from UP sites transplanted within and outside their origin sites showed a higher proportion of individual cytosine methylation changes than those from P sites. Albeit we could not find a consistent epigenetic response to transplantation, potentially due to the environmental differences across all study sites, we found differences in the amount of point methylation changes between macroalgae originated from P and UP sites. Hence, although genetic mechanisms seem to prevail, we cannot completely rule out a potential contribution of epigenetic mechanisms to macroalgal response to HMs.

P.0169 Taxonomic exploration of diatoms in saline wetlands of the Ebro Basin, NE Spain, integrating conventional and molecular approaches

María Borrego Ramos[1,2,*], Saúl Blanco[1,2], Raquel Viso[1], Carmen Castañeda[3], María Tierra[3]

*1 Diatom Lab, University of León - Universidad de León, León, Spain. 2 LIMNO Group, University of León - Universidad de León, León, Spain. 3 Estación Experimental de Aula Dei (CSIC), Zaragoza, Spain. *mborr@unileon.es*

Saline wetlands, renowned for their uniqueness in the Iberian Peninsula and very scarce in Europe, represent intricate lacustrine systems inhabited by dense periphytic algal communities. This study presents results from characterizing diatom populations in diverse saline wetlands of the Ebro Basin (NE Spain), included among Natura 2000 sites and the International RAMSAR list of wetlands. For sample collection, artificial substrata consisting on polypropylene ropes were set over a 6-week period to gather diatoms adhering to their surfaces. Subsequently, samples from each wetland underwent analysis using both optical microscopy and molecular DNA metabarcoding. A short segment of the rbcL gene was sequenced using Illumina MiSeq High-Throughput Sequencing (HTS) techniques to generate Amplicon Sequence Variants (ASVs) via the DADA2 pipeline, taxonomically assigned using the Diat.Barcode database. This work, part of the 'Assessment of the sustainability of agriculture regulated by the CAP in the basins of protected saline wetland' (AGROWET) project, represents the first taxonomic exploration of diatom communities in these wetlands, integrating both methodologies. The incorporation of molecular techniques allows for the detection of species not identified by classical methods. This significantly contributes to understanding diatom ecology in saline and hypersaline environments, emphasizing their pivotal role in the dynamics of these ecosystems. The findings have crucial implications for the management and conservation of these distinctive habitats, offering enhanced insight into how diatom communities respond to extreme environmental conditions. This combined approach opens novel perspectives for aquatic biology research, highlighting the necessity to address the conservation of saline wetlands comprehensively, considering the microscopic diversity that supports these unique ecosystems.

P.0170 Unlocking the potential of epigenetic engineering for sustainable forests

Hans Hoenicka[1], Susanne Bein[1], Marta Starczak[2], Daniel Gackowski[2]

1 Thünen Institute of Forest Genetics, Grosshansdorf, Germany. 2 Department of Clinical Biochemistry, Faculty of Pharmacy, Collegium Medicum in Bydgoszcz, Nicolaus Copernicus University in Toruń, Bydgoszcz, Poland.

Forest trees play a vital role in maintaining biodiversity and providing ecosystem services. However, they are increasingly facing environmental stressors such as drought, heat, and pests, which threaten their survival and resilience. Epigenetic modifications offer a promising, yet complex and still developing approach to potentially enhance the stress tolerance of forest trees over time. Further research is needed to fully understand the mechanisms involved and ensure safe and effective application. This study investigated the effects of 2-aminobutyric acid (BABA), an amino acid with epigenetic-modulating properties, on the growth, physiology, and epigenetic parameters of around 600 field elms (*Ulmus minor*) under normal and drought stress conditions. Epigenetic modifications were assessed in both DNA and RNA using UPLC-MS. The results demonstrated that BABA treatment significantly improved the growth, and chlorophyll content in field elms. Moreover, BABA induced extensive epigenetic alterations in both DNA and RNA. These epigenetic changes were linked to enhanced stress tolerance in field elms, as evidenced by improved resistance to drought stress. The findings highlight the potential of BABA and other epigenetic modifiers to enhance the resilience of forest ecosystems to environmental stressors. Additionally, our institute is conducting long-term field trials to evaluate the persistence of epigenetic modifications induced by BABA. Epigenetic changes provide a unique advantage over genetic methods for adaptation to rapidly changing environmental conditions. Unlike genetic changes, which under natural conditions require multiple generations, epigenetic changes can be induced relatively rapidly and can be reversed or modified in response to changing environmental cues. In conclusion, this study demonstrates that epigenetic modification can be a powerful tool for enhancing stress tolerance in forest trees. Epigenetic engineering offers a promising alternative to genetic methods and holds potential for faster improving the resilience of forest ecosystems to environmental stressors.

P.0171 Lactuca sativa L. seedlings under doses of Lithothamnium calcareum

Talys Oliveira[1], Edlén Bonela[1], Sara Arantes[3], Diego Aguiar[3], Giuseppe Polonini[3]

1 Federal University of Espírito Santo, São Mateus, Brazil. 3 Capixaba Institute of Research, Technical Assistance and Rural Extension, Linhares, Brazil.

Lettuce (*Lactuca sativa* L) is a typically leafy vegetable with a wide reach for consumers, being the main ingredient in most salads due to its pleasant flavor and easy preparation. Biostimulants, *Lithothamnion* *calcareum* have been objects of study to be applied to plants to increase nutritional efficiency, improve tolerance to abiotic stresses and/or the inherent qualities of crops. The production of seedlings is crucial to the success of the lettuce production system, which is why the objective of this work is to investigate the combined effects of different substrates and doses of the biofertilizer Lithothamnium calcareum on the production of seedlings of this vegetable. The experiment was conducted at the Instituto Capixaba de Pesquisa, Assistência Técnica e Extensão Rural do Espírito Santo (INCAPER). The experimental design was in randomized blocks in a 6x2 factorial scheme, with six doses of Lithothamnium calcareum (0, 2, 4, 6, 8 and 10 kg m^{-3}) and two types of substrate, Carolina Soil® (CA) and Tropstrato HT® (HT). A variety of Stella lettuce was used. The variations tested were number of leaves, leaf area, stem length, stem diameter and root length. For the number of leaves, the HT substrate was superior to CA at a dose of 10 kg m^{-3}. For leaf area, the HT substrate was superior to CA at a dose of 2 kg m^{-3} and the CA substrate was superior to HT at a dose of 10 kg m^{-3}. For root length, the HT substrate was superior to CA at doses of 2, 4, 6, 8 and 10kg m^{-3}. References: Ramos, Elmo Pereira et al. Lithothamnion sp. as biostimulant in plant cultivation. **Pesquisa Agropecuária Tropical**, v. 53, p. e76273, 2023.

P.0172 How diversity facets of functional traits affect to multifunctionality and ecosystem services in drylands worldwide?

Joaquín Moreno[1], Yoann Le Bagousse-Pinguet[2], Fernando T. Maestre[3], Nicolas Gross[4]

1 Miguel Hernández University of Elche, Elche, Spain. 2 Institut Méditerranéen de Biodiversité et d'Écologie Marine et Continentale, Marseille, France. 3 Multidisciplinary Institute for Environmental Studies, Alicante, Spain. 4 Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement, Clermont-Ferrand, France.

Drylands are the largest set of biomes on Earth (c. of 41%), being home to more than 38% of the world's population. These ecosystems are very vulnerable to climate change and land use alterations, which impact plant communities by altering their composition and diversity. The distribution of the diversity and abundance of functional traits within a plant community affect multiple ecosystem processes and ecosystem services (ES). A key aspect of functional diversity is phytochemical diversity, which affects the adaptation and resistance of plants to abiotic and biotic stress, and affect ecosystem functioning. We evaluated how functional diversity facets of plant traits affect multifunctionality (M) and ES across global drylands. To do so, we used the BIODESERT database, considering 21 morphological and phytochemical traits surveyed *in situ* in 326 plots from 25 countries. A principal component analysis (PCA) was performed to determine the trait-syndromes along the global aridity gradient surveyed. Besides, we calculated the functional dominance (CWM) and functional dispersion (CWV) of the obtained trait-syndromes. These diversity facets were used to perform linear models and to assess their effect on M and ES in drylands worldwide. According to our results, the two trait-syndromes obtained were driven by specific leaf area, N, P, K, leaf dry matter content (PC1), and Cu and by C, phenolics, Na and Zn (PC2). CWM-PC1 had a significant positive effect on M, erosion control and C stocks, whereas CWV-PC1 had a significant positive effect on soil fertility and decomposition. Besides, CWM-PC2 had a significant negative effect on soil erosion, while CWV of PC2had a significant negative effect on M, soil fertility, decomposition, and productivity. Finally, CWV-PC2had a significant positive effect on erosion control. These results provide information about how plant functional diversity responds to changes in aridity conditions and impact ecosystem functioning across drylands worldwide.

P.0173 Megafauna affects the genetic structure and demographic history of a megafruit palm in Africa

Yuanshu Pu[1,2], Laura Méndez[1,2], Lesego Malekana[4], Michelle Greve[5], William Baker[6], Renske E. Onstein[2,3]

1 Univeristy of Leipzig, Leipzig, Germany (yuanshu.pu@evobio.eu). 2 German Centre for Integrative Biodiversity Research, Halle-Jena-Leipzig, Leipzig, Germany. 3 Naturalis Biodiversity Center, Leiden, the Nethrelands. 4 University of the Free State, South Africa. 5 University of Pretoria, Pretoria, South Africa. 6 Royal Botanic Gardens, Kew, United Kingdom.

The largest animals in ecosystems (megafauna) can feed on mega-fruited plants (fruits diameter > 4 cm) and disperse massive loads of large seeds across long distances, thus playing a vital role in maintaining biotic connectivity and population structures of mega-fruited plants. However, it remains unclear how the global extinction of most megafauna since the late Quaternary affected mega-fruited plant populations. Here, we hypothesize that the loss of specialized megafaunal seed dispersers led to dispersal limitation of mega-fruited plants, resulting in high population genetic structure and decreases in population sizes and migration rates that coincided spatially and temporally with the decline and extinction of co-occuring megafauna. We focus on the megafaunal palm *Hyphaene coriacea,* which naturally occurs in savannas in Madagascar (where all seed-dispersing megafauna have gone extinct) and mainland Africa (where more intact elephant populations are still functioning as seed dispersers of *H. coriaceae*).Using RAD-seq from 22 populations and 151 individuals, we found that *H. coriaceae* population structure is shaped by extant and extinct fruit-eating and seed dispersing animals (frugivores), and we detected signatures of population size declines and migration rate disruption in both Malagasy and mainland African populations. This suggests that current and past interactions with megafauna have left signatures in the genome of mega-fruited plant populations, and reduced seed dispersal may have led to a loss of biotic connectivity and population size declines. Furthermore, alternative dispersal mechanisms, such as human-mediated dispersal and dispersal by surface runoff, may have substituted dispersal functions by past megafauna, explaining the persistence of *H. coriaceae* in Madagascar. These results provide important insights in the role of frugivores in maintaining seed dispersal and population structure of African plants, and how mega-fruited plants have been able to persist since the late Quaternary extinction of most primary seed dispersers.

P.0174 Phenotypic plasticity modulated by hormonal and epigenetic modifications compensates detrimental effect of herbivory in Erodium cicutarium

Javier Puy[1], Mónica Medrano[1], Ruben Martín-Blazquez[1], Conchita Alonso[1]

1 Estacion Biológica de Doñana. CSIC, Sevilla, Spain.

Epigenetic mechanisms enable plants to adjust their phenotype to the environment, promoting local adaptation. Although generally overlooked at a broad scale, biotic interactions such as herbivory, are considered key factors for local population establishment and phenotypic divergence. In the natural populations of *Erodium cicutarium*, ungulate grazing is unpredictable and could be highly detrimental to individuals. In this study, we quantify the magnitude of the adaptive plasticity of this species, and we explore to what extent it is hormonally and/or epigenetically mediated. In order to do so, we conducted an experiment where full-sib individuals of *E. cicutarium,* half demethylated with *5-azacytidine,* were grown experiencing simulated artificial herbivory or not. The results show that herbivory heavily affected leave and root morphological traits as well as the hormonal composition of the individuals towards a higher competitive performance (i.e. fast growing and more resource adsorptive-acquisitive phenotypes) which compensated the detrimental effect of the biomass removal on their fitness. More interestingly, we found that the phenotypic and hormonal adjustments of demethylated individuals in response to herbivory were much smaller than the control ones, suggesting that adaptive phenotypic plasticity was modulated via epigenetic changes. Furthermore, the transcriptomic analysis supports these results, finding genes differentially expressed by herbivory and demethylation treatments.

P.0175 Bioinformatic analysis of the conservation of Amaranth-specific miRNA target genes in different species

Daniela Arrieta Flores[1], Vladimir Flores Benavides[1], Magali Ruiz Rivas[2], Marcelino Martínez Nuñez[3], Valeria Lemus Castillo[1], Abigail Flores Peréz [1], Flor de Fátima Rosas Cárdenas[1]

1 Instituto Politécnico Nacional, Centro de Investigación en Biotecnología Aplicada, Tlaxcala, México. 2 INIFAP, Morelia, Michoacán, México. 3 Colegio de Postgraduados Campus Montecillo, Texcoco, México.

PPR proteins have RNA-binding motifs with specific affinity, which allow interaction with mRNA, participating in post-transcriptional gene regulation. Some mutated PPR proteins produce defects in photosynthesis, pigmentation, growth-development, embryogenesis, sensitivity to ABA or tolerance to abiotic stress conditions (Wang et al. 2021). In 2021, a specific miRNA in Amaranthus hypochondriacus (miRXXX1) with multiple target genes containing the pentantricopeptide repeat domain involved in Mitochondria and Chloroplast biogenesis was reported (Martínez Núñez et al. 2021). In this analysis by bioinformatics approaches, we demonstrated that multiple predicted white genes in amaranth, tobacco, tomato, and Arabidopsis are orthologous genes in all four species. The function of the target genes was performed with the information available for Arabidopsis in the following platforms: BAR, GENEmania, UNIPROT, Phytozome and STRING. We found genes with functions in ABA metabolism, chlorophyll biosynthesis, carbon metabolism and regulators of plastid biogenesis. This suggests that the regulation of these genes by miRXX1 confers to the plant a greater adaptation to heat, drought and salinity stress conditions.

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P.0176 Genetic transformation of amaranth, selection and analysis of microRNA overexpressing lines

Daniela Arrieta Flores[1], Vladimir Flores Benavides[1], Magali Ruiz Rivas[2], Marcelino Martínez Nuñez[3], Valeria Lemus Castillo[1], Abigail Flores Peréz[1], Flor de Fátima Rosas Cárdenas[1]

1 Instituto Politécnico Nacional, Centro de Investigación en Biotecnología Aplicada, Tlaxcala, México. 2 INIFAP, Morelia, Michoacán, México. 3 Colegio de Postgraduados Campus Montecillo, Texcoco, México.

Amaranth is a plant tolerant to different types of abiotic stress, which also exhibits high phenotypic plasticity, allowing for plants ranging from 0.1 to 2 meters. Therefore, interest in these processes has led to the search for transformation strategies that help elucidate key molecules in abiotic stress and other processes associated to climate change. Hence, it is necessary to develop a strategy that allows a high efficiency transformation. In this study, overexpressing constructs of microRNAs (miRX1, miRX2, and miRX3) were used to establish the efficiency of genetic transformation. The modified floral dip method was employed for transformation. Selection, phenotypic, and molecular analysis of transgenic lines were conducted. The results demonstrate the viability of the method used and provide us with tools for amaranth transformation for sustainable agriculture.

P.0177 Effect of soil properties on the phenology of a grapevine collection in Southern Spain

Jesús J. Soriano[1], Enrico Cretazzo[2], Juan F. Aguiar[1], Rocío Gutiérrez-Escobar[2], Raúl Ochoa-Hueso[1], Nerea Pereira[1], Inmaculada RodríguezTorres[2], José L. Blanco-Pastor[1]

1 Departamento de Biología, Instituto de Investigación Vitivinícola y Agroalimentaria, Campus de Excelencia Internacional Agroalimentario, Universidad de Cádiz, Puerto Real, Cádiz, Spain. 2 Grupo de viticultura y enología, Instituto de Investigación y Formación Agraria, Pesquera, Alimentaria y de la Producción Ecológica (IFAPA), Centro Rancho de la Merced, Carretera Cañada de la Loba. Jerez, Cádiz, Spain.

Identifying the effect of soil properties on plant agronomical traits offers the possibility to manage crops more efficiently and sustainably. We investigated the associations between the physicochemical and microbiological parameters of the soil and the phenological characteristics (budding and flowering) of a grapevine collection of 386 varieties in replicated experimental plots located at the IFAPA Centro Rancho de la Merced (Jerez, Spain), in the southern limit of the cultivated grapevine distribution in Europe. We took soil cores of 20 cm depth at multiple points using a regular sampling scheme to measure pH, electrical conductivity (salinity indicator), redox potential (soil aeration indicator), as well as variables related to the biological activity of soil microbial communities (eight enzymatic activities linked to the biogeochemical cycles of carbon, nitrogen, phosphorus, and sulfur). We interpolated these data using the Kriging method to generate distribution maps of soil properties. At the same time, precise dates for the budding and flowering of all grapevines in the plots were recorded. With the data obtained, we performed regression analyses to identify associations between the individual soil properties and the phenological traits of the grapevines. Identifying associations between soil parameters and grapevine phenological traits can help to implement alternative management strategies in specific areas of the crop/field. It could also allow the identification of optimal grapevine varieties or soil types for a desired phenological behavior. Finally, monitoring the effect of soil properties on the phenotypic traits of a grapevine collection is useful for including correcting parameters in quantitative genetic analyses.

P.0178 Functional evolution of PLETHORA genes in root development in cacti

Eduardo Torres-Flores[1,2], Luis F. Cisneros-Lemus[1,2], Michael D. Purugganan[3], Ulises Rosas[1]

1 Botanical Garden, Institute of Biology, Universidad Nacional Autónoma de México, Mexico City, Mexico. 2 Graduate Program in Biological Sciences, Universidad Nacional Autónoma de México, Mexico City, Mexico. 3 Center for Genomics and Systems Biology, New York University, New York, USA.

In arid ecosystems the main limitation for plant growth is the availability of water. Cacti are a family of plants that have radiated in these kinds of environments, and much of this success is probably due to the architecture of their roots. The growth of the primary root in most cacti is determined shortly after the seedling has germinated, and with this the formation of lateral roots begins. This allows the seedling to form a root network to take advantage of water from the most superficial part of the soil. The *PLETHORA* (*PLT*) genes of the model plant *Arabidopsis thaliana* encode AP2-domain transcription factors that maintain the indeterminate state of the primary root and are involved in early stages of lateral root formation. Multiple mutants of members of this gene family exhibit short root (e.g., *plt1 plt2*) and lack of lateral roots phenotypes (e.g., *plt3 plt7*). These phenotypes suggest PLTs as potential transcription factors involved in the signaling underlying root development in cacti. To test this hypothesis, using *Mamillaria san-angelensis* as a model, the genome of this cactus was sequenced with PacBio technology and using the Basic Local Alignment Search Tool (BLAST, NCBI), the homologous genes of *PLT1*, *PLT2*, *PLT3*, *PLT5* and *PLT7* were bioinformatically identified in *M. san-angelensis*. Remarkably, *PLT4* was not found in this genome. Now we intend to corroborate these bioinformatic predictions experimentally to make constructions to carry out genetic complementation analysis by cloning mutant plants in *PLT* genes of *A. thaliana* with the CDS region of *M. san-angelensis*' *PLT* genes, to analyze the morphological changes that could arise in the root development of *A. thaliana*, hoping to provide a genetic explanation of the evolutionary novelties of cacti roots.

P.0179 Comparative epigenetic and genetic spatial structure in Mediterranean mountain plants: a multispecies study

Javier Valverde[1,2], Mónica Medrano[1], Carlos M. Herrera[1], Conchita Alonso[1]

1 Estación Biológica de Doñana, Consejo Superior de Investigaciones Científicas, Sevilla, Spain. 2 Departamento de Biología Vegetal y Ecología, Universidad de Sevilla, Sevilla, Spain.

DNA methylation provides an additional layer of plant variation that contributes to the evolutionary potential of plant populations. Part of epigenetic methylation can respond to the environment, thus the spatial distribution of epigenetic variation might reflect the spatial heterogeneity of environmental conditions in which a plant grows. In this study we hypothesize that, in narrow endemics associated to specific habitats, epigenetic variability should be less structured in space than in their widespread congeners growing under broader environmental conditions. We tested this hypothesis at the within-population scale in seven pairs of congeneric plant species inhabiting the Cazorla Mountains (SE Spain). The narrow endemics studied inhabit very specific and scattered microhabitats, whereas widespread species can grow in a more diverse type of habitats. We analysed three populations per species and >20 individuals per population, and used AFLP and methylation-sensitive AFLP markers to characterise the Spatial Genetic Structure (SGS) and Spatial Epigenetic Structure (SEGS) of populations, respectively. As hypothesised, epigenetic variation was more homogeneous across space than the background genetic variation (SEGS < SGS) in most populations of narrow endemics. This decoupling between SEGS and SGS was further supported by a lack of correlation between epigenetic and genetic information in narrow endemics. Our findings suggest that in Mediterranean plants the relevance of environment-responsive epigenetic variation depends on their niche breadth and highlight the need to address spatial genetic and epigenetic variation to better understand the evolution of plant endemics.

S.018. ATYPICAL SUBSTRATES AS ENGINES FOR PLANT AND LICHEN EVOLUTION I: GYPSUM SOILS

P.0180 Analysis and representativeness of gypsophytes in the province of Toledo (Spain).

Beatriz Cervigón Recuero[1], Álvaro Mayoral Medina[1], Arianna Michell Torres Morán[1], Juan Manuel Martínez Labarga[1], Santiago Sardinero Roscales[2]

1 Unidad de Botánica: Departamento de Sistemas y Recursos Naturales, E.T.S.I. de Montes, Forestal y del Medio Natural. Universidad Politécnica de Madrid, Madrid, Spain. 2 Área Botánica: Departamento de Ciencias Ambientales. Instituto de Ciencias Ambientales-Facultad de Ciencias del Medio Ambiente. Universidad de Castilla-La Mancha, Toledo, Spain.

Gypsophyte vegetation is a relevant part of our Natural Heritage due to the large number of endemisms belonging to this particular lithology and its widely representative abundance in Spain; especially in the middle basin of the Tagus river and its near exclusive distribution regarding European scales. Reasons mentioned above led to the inclusion of this habitat in Directive 92/43/EC as a priority (1520* - Iberian gypsophilous vegetation (Gypsophiletalia)). In Toledo, gypsum outcrops have particular importance due to their abundant presence of considerable extent. The objective of this work is to expand further knowledge in the distribution area and flora of these outcrops; to verify its legal protection by either legislative figure such as the Natura 2000 Network; and develop impact evaluation. In order to elaborate this study, a UTM grid of 10x10 km is superimposed over the lithological cartography of the area. On the grids where there is presence of gypsum outcrops, the present vegetation is analyzed through the provided field data (Martínez Labarga, 2014; Sardinero, 2024) and compared with the species proposed on the checklist (Mota et al, 2009); in addition to local expert criteria suggestions. Once the data processing is concluded, the result gives the required cartographic outputs, displaying the results into the study area.

P.0181 Unveiling the complex ecology of gypsum soils in Iran: Gypsophyte reclassification calls for holistic ecological studies

Hossein Rahmaninia[1], Hamid Ejtehadi[1], Farshid Memariani[2,3*], Mehdi Abedi[4], Sara Palacio[5]

1 Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran. 2 Department of Range and Watershed Management, Faculty of Natural Resources and Environment, Ferdowsi University of Mashhad, Mashhad, Iran. 3 Herbarium FUMH, Department of Botany, Research Center for Plant Science, Ferdowsi University of Mashhad, Mashhad, Iran. 4 Department of Range Management, Faculty of Natural Resources and Marine Sciences, Tarbiat Modares University, Noor, Iran. 5 Instituto Pirenaico de Ecología (IPE-CSIC), Huesca, Spain.

Gypsum soils play a critical role in plant distribution. The Irano-Turanian region has been reported as rich in gypsophile species. Despite this richness, the ecological and floristic studies focusing on gypsum soils in Iran remain scarce. Building upon the research conducted by Pérez-García *et al.* (2018) using the floristic data who reported 301 gypsophyte and gypsocline species from the Iranian territory, our study delved into the distribution of specific species listed in the 2018 checklist, examining their distribution in northeastern Iran through the utilization of existing data in the literature and also field investigation on their distribution and soil physical and chemical properties. Our findings challenge the classification of certain endemic species, including *Anabasis firouzii*, *Atraphaxis intricata*, *Colutea gifana*, and *Psephellus galactochrous*, previously categorized as gypsoclines or gypsophytes, which are not observed in the gypsum soils and they are mainly calciphytes. We have also classified certain species based on their distribution into gypsovags, including species such as *Astragalus citrinus*, *Astragalus podolobus*, *Krascheninnikovia ceratoides*, *Matthiola farinosa*, *Astragalus verus*, *Dendrostellera lessertii*, and *Euphorbia bungei*, previously identified as gypsoclines. Additionally, species like *Sclerorhachis platyrachis*, *Hedysarum monophyllum*, and *Cleome turkmena*, which were introduced as gypsophytes, have also been found in other non-gypsum soils with high abundance. Given Iran's remarkable species and habitat diversity, we strongly advocate for more extensive and precise studies in this field. It is crucial to note that most of these species are endemic and specific to certain regions. Therefore, undertaking comprehensive ecological studies is essential to revise the classification of gypsophytes in Iran and gain an in-depth understanding of the intricate nature of gypsum soils, ultimately facilitating the conservation and restoration efforts for these complex ecosystems.

P.0182 Genetics, morphometrics and ionomics evidence of hybridization between Limonium estevei and Limonium cossonianum in Playa Macenas

Lucía Miranda Hernández[1], M. Encarnación Merlo[1], María Jesús Fernández Cobo[1], Carlos Salazar Mendías[2], Antonio J. Mendoza Fernández[3], Fabián Martínez Hernández[1], Francisco J. Pérez García[1], Julio Peñas de Giles[3], Esteban Salmerón Sánchez[1], Juan F. Mota Poveda[1]

1 University of de Almería, Almería, España. emerlo@ual.es. 2 University of Granada, Granada, España. 3 University of Jaén, Jaén, España.

Limonium Mill. is a cosmopolitan genus, mainly diversified in the Western Mediterranean region. Its species colonize reduced and isolated areas with saline, gypsum or arid substrates. *Limonium cossonianum* Kuntze and *Limonium estevei* Fern. Casas, two representatives of the genus, coexist sympatrically in Macenas (Mojácar, Almería). While the former is widely distributed throughout the Spanish Levant, the latter is a local endemism critically endangered due to coastal urban development. Hybridization between these two species has been mentioned, but it hasn't been formally described. With this in mind, the present research has focused on the genetic, morphometric and nutritional characterization of the potentially parental species and their putative hybrid. Leaf material and the corresponding soil samples were collected from five individuals of each taxon in Macenas, as well as from three individuals of *L. cossonianum* in six additional localities. Three chloroplastic regions (*rbcL*, *trnL-F* and *matK*) along with a nuclear region (ITS) were sequenced and ribotypes with additivities were isolated by cloning PCR products. Also, twenty-nine quantitative morphological characters were measured in plant vouchers of each taxon. In addition, the nutritional differences between taxa were established by means of a simple ANOVA applied to the foliar and soil composition analysis. Genetic and morphometric results confirmed hybridization between these two Macenas species, as well as retro-hybridization events. Regarding the biochemical niche, *L. estevei* exhibited less significant differences with the hybrid than with *L. cossonianum*. Unlike expected, retro-hybridization only involves hybrid forms and *L. cossonianum*. It doesn't seem to be a gene transference to *L. estevei* that would compromise the continuity and identity of this species as a result of introgressive hybridization. The extreme edaphic conditions in which this local endemism develops are apparently an insurmountable barrier that minimizes the risk of genetic assimilation.

P.0183 Vascular flora of the gypsum islands: Who can be a tenant?

Francisco J. Pérez García[1], Encarna Merlo[1], Fabián Martínez Hernández[1], Antonio J. Mendoza Fernández[1], Esteban Salmerón Sánchez[1], Agustín Lahora[1], Juan F. Mota[1]

1 University of Almeria, Almeria, Spain.

The geoedaphic properties of the gypsum deposits show significant differences with respect to those of surrounding areas. These differences have an effect on the vascular flora. Gypsum outcrops have been identified as areas where is hindered water use, constituting true "dry-islands". This disruption makes the gypsum outcrops appear to be like islands in an archipelago, but located within the mainland. Nine gypsum outcrops of highly variable size were studied. All of them were located in the province of Almería, under a semi-arid Mediterranean climate. Different subsets of the whole flora were studied in order to test MacArthur & Wilson model. Specifically, the linear regressions in the Species vs. Area equation, from Arrhenius, taking into account the adjustment values (R^2) and the slope of the line (z). The subsets were established based on what biotype they had, on their ecological behaviour, or what plant community they characterized. A total of 484 taxa were counted. The whole flora clearly fit an insular pattern ($z = 0.292$; $R^2 = 0.8171$). By ecological behaviour, high z-values, which indicate great isolation, were observed in species characteristic of siliceous ($z = 0.4036$), sandy ($z = 0.3619$) and pebbly ($z = 0.2986$) environments, along with species from the maquis ($z = 0.3653$). While low z-values, which indicate great permeability, were recorded as halophiles ($z = 0.1413$) and gypsophiles (z = P.757). This shows the importance of environmental filters in the colonization of outcrops, so that it is not enough to arrive, what is really important is the establishment and persistence. By biotypes, therophytes showed little isolation in the outcrops (z = P.707), while geophytes ($z = 0.4093$) and hemicryptophytes ($z = 0.3541$) show the opposite behavior. This could be linked to the fact that an ephemeral life-cycle is an ideal strategy for arid environments.

P.0184 Resolving phylogenetic relationships of gypsum endemic species of Teucrium L. (Lamiaceae)

Esteban Salmerón Sánchez[1], Krista Grabski[2], Delia Aguilar-Ramos[1], Encarna Merlo[1], Michael J. Moore[3], Jaime Güemes[4], Pedro Sánchez-Gómez[5], José L. Canovas-Rubio[5], Fabián Martínez Hernández[1], Antonio J. Mendoza Fernández[1], Francisco J. Pérez García[1], Juan F. Mota Poveda[1]

1 Department of Biology and Geology, University of Almería, Almería, Spain. 2 Department of Biology, John Carroll University, University Heights, USA. 3 Department of Biology, Oberlin College, Oberlin, USA. 4 Botanic Garden, University of Valencia, Valencia, Spain. 5 Department of Plant Biology, University of Murcia, Murcia, Spain.

The genus Teucrium exhibits a Subcosmopolitan distribution, comprising 434 taxa. The Mediterranean region and its surrounding floristic areas serve as the primary center of diversity, hosting approximately 90% of the total Teucrium species worldwide. Predominantly, species within the Polium section are concentrated in the western Mediterranean region of north-west Africa and south-west Europe. Polium section, encompasses the majority of species of the genus, is subdivided into four subsections: Polium, Simplicipilosa, Pumilum, and Rotundifolia. Of particular interest within this genus is the subsection Pumilum, as most of its constituent species exhibit clear gypsophily and represent prime examples of “shipwrecked on the rock” phenomena, characterized by schizoendemic or endemic distribution due to fragmentation. This subsection comprises up to six species: T. balthazaris, T. lepicephalum, T. libanitis, T. pumilum, T. carolipaui, and T. turredanum. Furthermore, some populations of T. balthazaris, in Topares, in the north of the province of Almería, and of T. pumilum in La Malá, in the province of Granada, exhibit distinct traits and characteristics deviating from other populations. The focus of the current study is to test the circumscription and phylogenetic position of the species within the section, in order to determine if the current subsections are confirmed as congruent with the molecular data and whether the mentioned deviant populations can be considered with their own taxonomic rank. To achieve this goal, molecular phylogenetic analyses, including individuals from all taxa in the Pumilum subsection and representative species from other related sections. Preliminary molecular analyses, using nuclear and plastidial markers did not support the currently proposed subsections of Polium section. On the other hand, the proposition of a new species for la Malá, was supported. This work is a first step to explore molecular characters to support future work aiming to solve the taxonomic problems within Teucrium.

P.0185 Study and identification of new gypsophilous taxa of the genus Limonium Mill. in the inner outcrops of Andalusia (SE Spain)

M. Jesús Fernández-Cobo[1], Esteban Salmerón Sánchez[1], Carlos Salazar Mendías[2], Lucía Miranda Hernández[1], M. Encarnación Merlo[1], Juan F. Mota Poveda[1]

1 Department of Biology and Geology, University of Almería, Almería, Spain. 2 Department of Animal Biology, Plant Biology and Ecology. University of Jaén, Jaén, Spain.

The genus Limonium, which belongs to Plumbaginaceae family, with a cosmopolitan distribution, includes more than 500 species, and its main diversification centre in the Western Mediterranean region, growing on gypsum or saline outcrops. The taxonomical study of this genus is challenging because of its recent diversification and the intraspecific variability due to frequent interspecific hybridization. In the province of Jaén (Andalusia, SE. Spain), Limonium quesadense, an endemic species present on gypsum outcrops, shows a high morphological variability. The objective of this study focused on the genetic and morphological characterization of L. quesadense throughout its geographical distribution as well as some related species like L. alicunense and L. supinum, present in the area. Molecular analyses were carried out with the aid of nuclear ribosomal (ITS1 and ITS2) and plastid (matK, trnL-F and rbcL) sequences. In order to differentiate the presence of different ribotypes, ITS regions were also studied with the aid of molecular cloning techniques. Regarding the morphological analysis, 120 herbarium vouchers belonging to the different taxa studied were analyzed. The results showed hybridization events between analyzed species, with the exception of the populations that were considered to be the westernmost area of distribution of L. quesadense. In these populations, molecular and morphological studies showed that there are significant differences that allow us to consider the proposal of a new species for the genus. According to these evidences, Limonium vallei sp. nova is proposed. In addition, the taxonomic rank of L. alicunense is questioned due to the absence of genetical and morphological differences between this species and L. quesadense. Our results would suggest the possibility of the existence of a singameon, composed by different species with sympatric distribution among which genetic flow seems to exist or has existed. This scenario could have important implications for the conservation of the species.

S.019. ATYPICAL SUBSTRATES FOR PLANT AND LICHEN EVOLUTION II: ULTRAMAFIC SOILS

P.0186 Orchids of serpentine areas of the Central Balkans: patterns of species richness and composition in relation to vegetation types

Vladan Djordjević[1], Spyros Tsiftsis[2], Ksenija Jakovljević[1], Dmitar Lakušić[1]

1 University of Belgrade, Faculty of Biology, Institute of Botany and Botanical Garden, Belgrade, Serbia. 2 Department of Forest and Natural Environment Sciences, International Hellenic University, Drama, Greece.

Habitats found on serpentine bedrocks are known for stressful physico-chemical conditions, such as low concentrations of macronutrients, high concentrations of Fe, Mg, Ni, Cr, wide range of diurnal temperature fluctuations and poor water-retaining capacity. It is insufficiently known whether serpentine habitats are suitable for the growth and development of terrestrial orchids and which vegetation types are particularly rich in orchids on such substrates. The main objectives of this study were to determine the total richness of orchid taxa in the serpentine areas of the Central Balkans and to determine their richness and composition in relation to vegetation types. The data on the occurrence of orchids and vegetation types were collected in Serbia in the period between 1995 and 2023. A total of 34 orchid species and subspecies, classified into 16 genera, were found in the study area and their phytocoenological affiliation was analysed. Orchid taxa were recorded in plant communities belonging to 11 classes, 15 orders and 20 alliances. Most orchid taxa grow in the following vegetation types: dry grasslands (Festuco-Brometea, Brachypodietalia pinnati, Chrysopogono-Danthonion calycinae); wet meadows (Molinio-Arrhenatheretea, Molinietalia caeruleae, Molinion caeruleae, Deschampsion cespitosae and Calthion palustris); pine forests (Erico-Pinetea, Erico-Pinetalia, Erico-Fraxinion orni); oak forests (Quercetea pubescentis, Quercetalia pubescenti-petraeae); beech and oak-hornbeam forests (Carpino-Fagetea sylvaticae). Five statistically significant groups of vegetation orders and five statistically significant groups of vegetation alliances are distinguished. The following orchid taxa have particularly large populations on serpentine areas of the Central Balkans: *Anacamptis morio*, *Gymnadenia conopsea*, *Neotinea ustulata*, *Dactylorhiza sambucina*, *D. maculata* subsp. *transsilvanica* and *Platanthera bifolia*. This study emphasises the important role of the serpentine areas of the Central Balkans for the occurrence of terrestrial orchids and indicates that they could be considered as potential orchid reserves due to the lower agricultural use compared to the surrounding non-serpentine areas.

P.0187 Neglect of limestone enclaves in Extremadura: necessity and importance of protecting them

Sheila Galindo-Ortiz [1,2], Tomás Rodríguez-Riaño [2], Ana Ortega-Olivencia [2]

1 University of Salamanca, Salamanca, Spain. 2 University of Extremadura, Badajoz, Spain.

Extremaduran flora is fundamentally acidophilic due to the predominance of the siliceous substrate; however, there are few limestone outcrops, in which a greater number of plant species inhabit compared to the surrounding substrates. These enclaves are not governed by any protective regulation in Extremadura; therefore, we are facing a potential loss of them due to agro-livestock overexploitation and other land uses (e.g., construction of roads, pathways, urban developments, or power lines installation), leading to a decrease in biodiversity. Our main aim was to carry out a floristic study of one of these limestone enclaves adjacent to the Hinojales stream (Badajoz). The results indicated a total of 39 families, 122 genera and 152 species and subspecies, of which 17 are basophilic and out of the 135 edaphic indifferent 21 prefer the basic substrate in our region. In addition, two are Iberian endemisms and seven Ibero-North Africans, highlighting *Galium talaveranum* from the first group, which has here its type locality. The data from the UNEX herbarium and previous publications about the area recorded 62 taxa, of which 35 have not been collected again in our study period (September 2021 to July 2022). The Digital Photo Library of the National Geographic Institute and our own observations indicate that this limestone enclave has been greatly modified by human in the last 50 years with a considerable reduction in its size, due to agricultural overexploitation in the surrounding lands, the creation of roads and power lines. The loss or severe deterioration of these limestone enclaves could cause a great reduction in the Extremadurian floristic diversity since these enclaves are scarce. Therefore, we propose establishing the figure of "Flora Microreserve" in Extremadura to protect small habitats that are important for their biodiversity and for hosting type localities of one of our Iberian endemisms or rare species.

P.0188 A comparative study on CSR strategies in two closely related Cousinia species endemic to the serpentine soils of Northeastern Iran

Elaheh Tabasi[1], Hamid Ejtehadi[1], Farshid Memariani[2,3*], Hossein Rahmaninia[1]

1 Department of Biology, Faculty of Science, Ferdowsi University of Mashhad, Mashhad, Iran. 2 Department of Range and Watershed Management, Faculty of Natural Resources and Environment, Ferdowsi University of Mashhad, Mashhad, Iran. 3 Herbarium FUMH, Department of Botany, Research Center for Plant Science, Ferdowsi University of Mashhad, Mashhad, Iran.

Serpentine soils host a large number of endemic species and contribute to the turnover of community composition. The infertility of the soil strongly influences the species and functional composition of serpentine environments. Plant communities in environmentally harsh habitats such as serpentine soils may demonstrate unique responses to environmental change, via the mediating role of their functional traits. The Khorassan-Kopet Dagh floristic province located in the northeastern region of Iran has a high level of plant endemism due to its biogeographical position as well as the large extent of calcareous, gypsum, and ophiolitic soils. To gain a better understanding of the impact of environmental conditions on serpentine plant communities in the area, we sampled 44 relevés using the Braun-Blanquet method at two sites dominated by two threatened, endemic and phylogenetically closely related *Cousinia* species (*Cousinia* sect. *Argenteae*) in serpentine soils of NE Iran, i.e., *Cousinia kadereitii* and *C. argentea*. The adaptive strategies of two *Cousinia* communities were investigated according to Grime's competitor/stress-tolerator/ruderal (CSR) model. While both plant communities occupied similar habitats ecologically and converged on the stress-tolerator strategy, *C. kadereitii* exhibited functional divergence from C- to S-selected, however, *C. argentea* showed functional convergence on the S-selected strategy. Understanding the strategies employed by different species can give us valuable insights into the resilience and survival of plant communities in challenging environments. This knowledge is crucial for biodiversity conservation efforts in serpentine habitats.

P.0189 Lessons on ecology and evolution from the study of edaphic specialization

Nishanta Rajakaruna[1,2]

1 Biological Sciences Department, California Polytechnic State University, San Luis Obispo, United States. 2 Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa.

Edaphic islands, characterized by sharp abiotic and biotic gradients, mosaic landscapes, patchiness and isolation, and harsh environments, offer exceptional opportunities to test macroecological and evolutionary theory, and conservation and restoration practices. Edaphic islands are often distinguished by unique biotic communities with high proportions of rare and endemic species. These communities, often restricted to fragmented islands of harsh substrates, are model settings to investigate the factors and mechanisms contributing to regional and global patterns of diversity and spatial ecology, including metapopulation and metacommunity theory, as well as cross-kingdom interactions. They also provide model organisms for investigating the drivers of adaptive evolution, including the genetic bases for and architecture of traits conferring adaptation and reproductive isolation. Additionally, they offer opportunities to explore cross-adaptation, which is when a trait that evolved for tolerance to one harsh substrate becomes effective as an adaptation for another, allowing species to show cross-tolerance to multiple harsh substrates characterized by a suite of common stressors (*i.e.*, stress resistance syndrome), including habitat bareness, drought, pH, ionic strength, and specific ions. Biota of harsh and nutrient-poor substrates are especially prone to stressors associated with climate change, including atmospheric deposition of nitrogen. Much of the research on harsh substrate-biota relations has focused on plants of ultramafic and other metal-enriched rock outcrops or saline soils. Recent research on biota of gypsum and other chemically 'harsh' substrates can help reexamine the biota-harsh soil relationship, especially commonalities and differences across distinct biota-soil type associations, both within and across biomes. Such efforts will also provide opportunities for productive collaboration across research groups with expertise on edaphically distinct communities (e.g., serpentine vs gypsum) or tools of investigation (e.g., ecophysiological vs phylogenomic) relating to key questions on drivers of diversity and community assembly, ecological and evolutionary theory, and conservation and restoration practices.

P.0190 Plant traits, flowering phenology and phylogenetic signal in the ultramafic flora of Tuscany: preliminary results

Federico Selvi[1], Andrea Coppi[2], Elisa Carrari[1], Cristina Gasperini[1]

1 University of Florence, Department of Agriculture, Food, Environment and Forestry, Florence, Italy. 2 University of Florence, Department of Biology, Florence, Italy.

The specialized floras of ultramafic outcrops worldwide are rich in endemic species and distinct ecotypes with adaptive traits to the harsh soil conditions of these edaphic "islands". Many of the morpho-anatomical characteristics that contribute to the fitness of these plants are well known and collectively indicated as "serpentine syndrome". For many ultramafic floras, however, the investigation of the plant functional traits that are currently used to predict species responses to environmental changes and their influence on key properties of communities and ecosystems is still at its infancy. Accordingly, we started a study of a set of traits and the flowering phenology of a pool of species of the ultramafic flora of Tuscany (Italy). The aim is to test the hypothesis that traits reflecting competitive ability like plant height and specific leaf area are linked to the flower timing, as suggested for other floristic components. In addition, we aim at examining the relationships between species phylogenetic position and traits, quantifying the signal of each trait across our floristic sample. To this purpose we set up a permanent plot in an ultramafic site with typical vegetation, including twenty obligate or facultative serpentinophytes (annual and perennial herbs and grasses, small shrubs, shrubs); the plot was equipped with an air temperature datalogger to record T variation over the next years. Flowering phenology was monitored in 2023 and 2024 (part) by field visits every ca. 15 days. Leaf traits, plant height stem density and other traits, measured on 3-5 individuals per species, were widely variable. Interspecific variation in flowering time ranged from February (Juniperus oxycedrus) to October (Artemisia alba), with several late-flowering species Preliminary results suggest that vegetative height is positively related to flowering timing, but not specific leaf area. Based on Blomberg K statistics, trait evolution appears largely independent of phylogeny.

S.020. BACK TO BASICS: USING MICROMORPHOLOGY, ANATOMY AND HISTOLOGY TO INVESTIGATE EVOLUTION IN BRYOPHYTES

P.0191 Species delimitation of hornworts from Madagascar: a spores morpho-morphometrical approach

Dejonghe Quentin[1], Reeb Catherine[1]

1 Muséum national d'Histoire naturelle Institut de Systématique, Evolution, Biodiversité, Paris, France.

Hornworts, constituting a group of terrestrial plants encompassing 11 families and approximately 220 species (Frangedakis et al., 2023), are integral components within the broader Bryophytes sensu lato, alongside mosses and liverworts. Their phylogenetic positioning and distinct morpho-anatomical features render hornworts pivotal in elucidating the evolutionary trajectories of terrestrial plant lineages. Despite their significance, hornworts remain understudied, particularly within the Afro-Malagasy region, where species delineation and characterization pose notable challenges. With similar morphology and characterized by thalloid structures, hornworts display few distinguishing morpho-anatomical traits for species delimitation. Additionally, extracting DNA from hornworts is challenging due to the mucus in their thalli, which contains inhibitors (Villarreal, pers. comm.). The key feature for identifying hornworts is their spores, which vary significantly in morphology between genera. To clarify taxonomic uncertainties and improve systematic classification, we propose combining morphological and morphometric analyses. Using morphometric techniques is a new approach in hornwort research and shows potential for distinguishing between at least genera. We will present our preliminary findings derived from employing this method, which could serve as a valuable tool for species delineation in cases where molecular approaches prove inadequate.

P.0192 Diversity of liverworts and hornworts in India

Shuvadeep Majumdar[1]

1 Department of Botany, Scottish Church College, Kolkata, India.

A new rank Superphylum "Monosporangiophyta" was proposed to accommodate three phyla, viz. Marchantiophyta, Bryophyta s.str. and Anthocerotophyta under Kingdom Plantae. Among land plants, pteridophytes, gymnosperms and angiosperms together are grouped under Superphylum "Polysporangiophyta" (Majumdar, 2020). India has rich diversity of liverworts (Marchantiophyta) and hornworts (Anthocerotophyta). Presently, rich bryodiversity of India includes 979 taxa belonging to 147 genera, 61 families, 17 orders, and four classes from two phyla. Of these, 881 species, 18 subspecies, 39 varieties, and two forma belonging to 141 genera in 57 families of liverworts and 39 species representing seven genera in four (Anthocerotaceae, Dendrocerotaceae, Notothyladaceae, Phymatocerotaceae) families of hornworts (Majumdar & Dey, 2024 unpub.). After, Majumdar and Dey (2021) six genera, viz. *Barbilophozia*, *Dinckleria*, *Diplasiolejeunea*, *Gymnocolea*, *Mesoptychia* and *Saccogyna* of liverworts and a genus namely *Phymatoceros* of hornworts was added to the liverwort and hornwort flora of the country. Two families one each from hornwort (Phymatocerotaceae) and liverwort (Saccogynaceae) was recorded for the first time in India.

References: Majumdar, S. 2020. New Superphylum -Monosporangiophyta for grouping Marchantiophyta, Bryophyta s.str. and Anthocerotophyta. Phytotaxa 451(2): 175–178.; Majumdar, S. and Dey, M. 2021. Present status of Liverworts and Hornworts in India. Annals of Plant Sciences 10(3): 4162–4166.; Majumdar, S. and Dey, M. 2024. Updated Diversity of Liverworts and Hornworts in India. (unpublished)

P.0193 Seed micromorphology in Crocus pallasii: a tale of papillar diversity

Rachel Mollman1, Almıla Çiftçi[2], Levent Şık[3], Bilge S. Kaleli[1], Ceyda Yazici[1], Osman Erol[4]

1 Istanbul University, Istanbul, Turkey. 2 Leibniz Institute of Plant Genetics and Crop Research, Gatersleben, Germany. 3 Manisa Celal Bayar University, Manisa, Turkey. 4 Istanbul University, Institute of Science, Istanbul, Turkey.

Molecular and morphological evidence increasingly indicates that the widespread and variable *Crocus pallasii* Goldbl. in Turkey may harbor several distinct taxa, some of which have already been described as separate species or infraspecific taxa, although their status remains unresolved. The results of SEM micromorphological investigations into 20 populations of this group and its close relatives in Series *Crocus* across Turkey indicates that this group has highly variable seed surface micromorphology, consisting of dense papilla in a variety of forms and sizes, as in other *Crocus* species. We noted the papilla shape, length, posture and surface texture of both the main seed coat and the raphe, finding that the populations in Trakya (Turkey-in-Europe) have distinctive bulbous-based papillae and relatively stable seed surface characteristics easily separating them from the much more variable populations scattered across Anatolia, which have long, dense and variably shaped and postured papilla. These observations corroborate the results of morphological and molecular investigations we carried out in parallel as part of our ongoing investigations (istanbul University Scientific Research Projects Unit Grant No. 38,022) into this species complex in Turkey. However, the diversity of papilla types across Series *Crocus* populations in Anatolia tells a more complex story about the variability of the widespread and systematically complex *C. pallasii,* its infraspecific taxa and some of its closest relatives.

P.0194 Western Ghats: a heaven for bryophytes, unveiling their distribution

Manju C.N. [1], K.P. Rajesh [2]

1University of Calicut, Kerala, India, manjucali@gmail.com. 2 The Zamorin's Guruvayurappan College, Kerala, India.

The Western Ghats are a mountain range located along the western coast of India. They are home to a rich biodiversity of plants and animals, including a large number of bryophytes. Bryophytes are found throughout the Western Ghats, from the lowlands to the high mountains. They are most common in moist, shady habitats, such as forests and along streams. A total of 1,220 bryophytes distributed among 822 species including 8 subspecies and 44 varieties of mosses under 257 genera, 20 species of hornworts including one subspecies under 4 genera and 379 species including 6 subspecies and 6 varieties of liverworts under 80 genera were recorded. Among these 79 species are endemic to the Western Ghats. Bryophytes play an important role in the ecology of the Western Ghats. They help to regulate the water cycle, provide habitat for other organisms, and contribute to the soil formation. Bryophytes are also indicators of environmental health. Their presence or absence can be used to assess the quality of the air and water. Bryophytes are threatened by a number of factors, including habitat loss, pollution, and climate change. Habitat loss is the most serious threat to bryophytes in the Western Ghats. As forests are cleared for agriculture and other development, bryophytes lose their homes. Pollution from industrial and agricultural activities can also harm bryophytes. Climate change is also a threat to the bryophytes, as it can lead to changes in temperature and precipitation patterns that can make it difficult for bryophytes to survive.

P.0195 Distribution of the genus Riccia L. (Ricciaceae: Marchantiophyta) along altitudinal and latitudinal gradients in the Western Ghats

Manju C.N.*[1], Mufeed B.[1]

*1 Department of Botany, University of Calicut, Kerala, India. *manjucali@gmail.com.*

Riccia L. of the family Ricciaceae is a widely distributed genus in the world. Its pattern of distribution was examined in the Western Ghats of Peninsular India and its environs. In the area, the quality of vegetation cover and climatic features improves as moves from the low to high altitudes. The lower reaches are largely man-modified, losing its original vegetation. The distribution of Bryophytes in the area shows an increasing trend, lowlands to the less disturbed uplands. However, *Riccia* shows a different pattern. A total of 26 species are known in the area distributed mainly in the low-altitude and disturbed areas, rather than pristine forests of upper reaches. High-altitude montane wet temperate forests, wet evergreen forests and semi-evergreen forests of the Western Ghats are devoid of *Riccia* species. The absence of *Riccia* species in these vegetation types may be attributed to the genus' reproductive adaptations, favouring disturbed habitats. The distribution of *Riccia* in the Western Ghats is complex and is influenced by a number of factors, including altitude, latitude, and longitude.

P.0197 Testing the molecular and morphological variability of the moss Physcomitrium pyriforme (Hedw.) Brid. in the Iberian Peninsula

Diego Rodríguez-Hernández[1], Bernard Goffinet[2], Rafael Medina[1]

1 Universidad Complutense de Madrid, Madrid, Spain. 2 University of Connecticut, Storrs, USA.

Compared to vascular plants, bryophytes have simple architectures and limited morphological spaces. In highly reduced taxa, matching molecular phylogenetic evidence with morphotypes can be challenging, and cryptic species (those that are morphologically indistinguishable) may be overlooked. An example of this scenario is shown by the subcosmopolitan moss *Physcomitrium pyriforme* (Hedw.) Brid. (Funariaceae, Bryophyta), a very variable morphospecies with a complex phylogenetic structure in North America. Here we test the homogeneity of *P. pyriforme* in the Iberian Peninsula under morphological and molecular criteria. We have studied a sample of 21 herbarium specimens from BCB, CONN, MA, MACB, VAL, and VIT identified as *P. pyriforme* plus four additional samples of other Funariaceae such as *Physcomitrium eurystomum* Sendtn. and *Entosthodon fascicularis* (Hedw.) Müll. Hal. We prepared semipermanent microscopic slides to score morphological characters such as exothecium and leaf areolation, spore size and ornamentation, seta length, or capsule shape. We extracted DNA of the suitable samples and amplified via PCR the sequence of two single-copy nuclear genes (4780 and 7379), the ITS regions, and the plastidial *atp*B-*rbc*L spacer. Our preliminary results show that despite its morphological plasticity, the taxon *P. pyriforme* does not include a heterogeneous assemblage of lineages, as it was found in North America. Notably, a specimen morphologically congruent with the *P. pyriforme* complex shares the molecular signature of the allopolyploid species *P. eurystomum*. Our study has been limited by a scarce number of available specimens, mostly collected many years ago and from just a few localities. Improving the knowledge on the diversity of this taxon would benefit from an increased sampling effort spanning a higher number of localities within the Iberian Peninsula.

P.0198 Re-delimitation of the liverwort species Cyathodium aureonitens (Marchantiophyta, Marchantiales)

Nilobon sevanakun[1], Cécile Gueidan[2], D. Christine Cargill[2, 3], Sahut Chantanaorrapint[1]

1 Division of Biological Science, Faculty of Science, Prince of Songkla University, Songkhla, Thailand. 2 Australian National Herbarium, Centre for Australian National Biodiversity Research (a joint venture between Parks Australia and CSIRO), Canberra, Australia. 3 Australian National Botanic Gardens, Canberra, Australia.

The thalloid liverwort species *Cyathodium aureonitens* is characterized by a large fan-shaped thallus up to 2–3 cm wide, hairy involucres, spinate spores, and dioicous sexuality. It is mainly found in the Sino-Himalayan region and extends to mainland Southeast Asia. A significant variation in the morphology of gametophytes and sporophytes has previously been observed in this taxon, suggesting that it might in fact include several species. This study aims at refining the delimitation of species within *Cyathodium au-*

reonitens based on morphological observations and molecular data inferred from five chloroplast (*psb*A, *psb*T, *rbc*L, *rpoC1*, and *rps4*) and two mitochondrial (*nad1* and *nad5*) markers. The phylogenetic analyses show that all material identified as *Cyathodium aureonitens* form a monophyletic group with strong support and sister to a clade of tuberous species (*C. mehranum* and *C. tuberosum*). Within this monophyletic group, three species are recognized: *C. aureonitens*, and two phylogenetically distinct and well-supported undescribed species differing from *C. aureonitens* by their involucre rim color and the length of the spines of their spores.

P.0199 Transition of the division plane of apical cell and anisotropic cell wall growth leading to species-specific phyllotactic angle

Ryuya Hirashima[1], Kazuhiro Muraoka[1], Taiki Kaneguchi[1], Naoya Kamamoto[1], Koichi Fujimoto[1], Masaki Shimamura[1]

1 Graduate School of Integrated Sciences for Life, Hiroshima University, Hiroshima, Japan.

Phyllotaxis in vascular plants is produced at a multicellular meristem, whereas bryophyte phyllotaxis emerges directly from a single apical cell (AC) that is embedded in a growing tip of the gametophyte. The AC is asymmetrically divided into itself and a single 'merophyte', producing a future leaf and a portion of the stem. We examined three moss species, *Tetraphis pellucida*, *Physcomitrium patens*, and *Niphotrichum japonicum*, which exhibit 1/3 (120 degree), 2/5 (144 degree), and 3/8 (135 degree) spiral phyllotaxis, respectively and have indicated that the transition of the division plane of the AC that occurs at a certain rotation angle roughly coincides with the species specific phyllotactic angle. Rearrangement of organelles inside AC predicts the direction of the rotational cell division of AC. Furthermore, in order to clarify the developmental process that ultimately establishes the correct phyllotactic angle, we compared cell division patterns of merophytes, changes in cell wall components, and changes in the external shape of merophytes as they grow between the three moss species. In Tetraphis, where there is no difference between the rotation angle of the division plane of the apical cell and the degree of phyllotaxis angle, merophytes grow isotropically. On the other hand, in *Physcomitrium* and *Niphotrichum* that form larger phyllotactic angles (144 and 135 degrees), merophytes show anisotropic growth and elongate greatly in the direction of rotation of the phyllotactic spiral. In the early merophytes surrounding the apical cell, in the region where the merophyte external shape changes anisotropically, the cell wall is rich in callose, suggesting a plastic nature to the cell and merophyte outline, influencing the modulation and convergence of the phyllotaxis angle.

S.021. BARK STRUCTURE: EVOLUTIONARY, FUNCTIONAL AND ECOLOGICAL IMPLICATIONS

P.0200 A tentative key for macroscopic and microscopic bark identification of European trees and shrubs

Alan Crivellaro[1]

1 Forest Biometrics Laboratory, Faculty of Forestry, "Stefan cel Mare" University of Suceava, Suceava, Romania.

Despite the various roles performed in living plants and the abundance of preserved archaeobotanical remains, bark identification has rarely been undertaken today. Therefore, I designed a combined macroscopic and microscopic bark identification key for the most common European trees and shrubs. The resulting bark identification key suggests a step-by-step process that only applies easy-to-observe macroscopic characters that require no sampling. Then, the identification key aims at the most accurate level of identification reachable, including targeted microscopic features. The key underlies the limits of the process and suggests possible solutions.

P.0202 Phloem activity drives xylogenesis in Abies religiosa in a high mountain forest in Mexico

Teresa Terrazas[1], Lauro López-Mata[2], Marco V. Alvarado[1]

1 Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, Mexico. 2 Posgrado en Botánica, Colegio de Postgraduados, Montecillo, Mexico.

The inner bark (secondary phloem) is responsible for the mobilization of photosynthates woody plants. The outer bark, on the other hand, provides protection to the vascular system against biotic and abiotic factors. It is known that in gymnosperms the formation and activity of inner bark may be or not coupled with xylogenesis. The aims of this study were to study the seasonal changes of the secondary phloem and its dynamic related to growth in *Abies religiosa* (Kunth) Schltdl. & Cham. Sampling and observations were carried out for 24 months in four trees at a high mountain fir forest (19º 26′ 02″ N, 98º44′56″, 3441 masl) in Mexico. The samples were removed with a Trephor, fixed and processed. Transverse-sections revealed that reactivation of phloem is not simultaneous with xylem. The conducting phloem is recognized by thin-walled sieve cells separated by two or more discontinuous bands of parenchyma cells (0.4-0.6 mm in width). These parenchyma cells proliferate near vascular cambium where also few solitary sclereids were seen. The non-conductive phloem is distinctive by the wavy-rays and abundant clusters of sclereids and resin cells, both expanding towards the inner periderm. The non-conductive phloem represents 5 or 6-folds of the conductive phloem (> 2 mm in width). The increase in the number of cells of the conducting phloem begins in early February when the vegetative buds swell. The conducting phloem is reduced at the beginning of October, when cambial activity ceases. We conclude that the reactivation of the phloem sends the corresponding signals to activate vegetative growth and xylem development.

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S.022. BENEFICIAL PLANTMICROBE INTERACTIONS.

P.0203 Plant-soil feedback as a key of competitors' coexistence

Ezequiel Antorán-Pilar[1], Jaime Madrigal-González[2], Joaquín Calatayud[1]

1 Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, Móstoles, Madrid, Spain. 2 EiFAB-iuFOR, Universidad de Valladolid, Soria, Spain.

Understanding species coexistence is not only about exploring the classic paradigm of competitive exclusion but also considering the role of other ecological mechanisms. In plants, plant-soil feedback (PSF) has been identified as a relevant factor influencing plant performance and population dynamics, but its role in the coexistence of competing species is still poorly explored. This study explores how PSF mediated by microorganisms, may regulate or impact coexistence mechanisms of two competing species. Rather than relying exclusively on direct competition, we hypothesized that population dynamics and distribution of species could be driven by PSF. A common garden experiment was conducted involving two species, *Cistus ladanifer* and *C. laurifolius*. Performance measures, focusing on root and shoot biomass, were recorded under experimental conditions. We used soils dominated by each of the two species, conducted a cross-experimental approach that used sterilized soils and soil microorganism inoculum from both species. This separation aimed to discern the effects of soil physic-chemical properties and living microorganisms. We found that the interaction of soil properties and microorganisms drive early growth of both species. Both species grow better in richer soils where only one species prevails. Yet, this only occurs when plants are experiencing microorganisms from their own soil. Consequently, our findings suggest that PSF play a key role in regulating population dynamics of competing species, challenging the conventional understanding dominated by direct competition.

P.0204 Isolation and characterization of beneficial soil microorganisms from Mediterranean regions to use in agroecosystems.

Cesaro Patrizia[1*], Campana Daniela Cristina[1], Massa Nadia[1], Todeschini Valeria[1], Zouitane Ilham[2], Derraz Khalid[3], Gamalero Elisa[1], Novello Giorgia[1], Hammami Sofiene[4], El Ghachtouli Naïma[2], Meddad-Hamza Amel[5], Labidi Sonia[4], Lingua Guido[1]

1 Università del Piemonte Orientale, Alessandria, Italy. 2 Laboratory of Microbial Biotechnology and Bioactive Molecules, Sciences and Technology Faculty, Sidi Mohamed Ben Abdellah University, Fez, Morocco. 3 Laboratory of Functional Ecology and Environment, Sciences and Technology Faculty, Sidi Mohamed Ben Abdellah University, Fez, Morocco. 4 Institut National Agronomique de Tunisie, Tunisia. 5 Université Badji-Mokhtar Annaba, Algeria.

Unsustainable management practices and climate changes are threatening the natural capital of soils, particularly in the Mediterranean region where increasing population, rapid land-use changes and associated socio-economic activities are imposing high pressures on soils. In this context a rational use of indigenous beneficial soil microbiota can firmly increase the resilience of these systems. Under field conditions plants interact with a multitude of microorganisms. Among them plant growth-promoting bacteria (PGPB) and arbuscular mycorrhizal fungi (AMF) represent a fundamental component of soil fertility through their role in plant growth, health and productivity. The main aim of the PRIMA project titled "Promoting soil fertility, yield and income in small holder agriculture of semiarid and arid Mediterranean regions by management of beneficial soil microbiota, conservation agriculture and intercropping", is the improvement of small farmer agronomic practices through the promotion of the rational use of beneficial soil microbiota and consequent positive effects on productivity of inter-cropped perennial and short-term species. In this work, the authors report the isolation, the molecular identification and the physiological characterization of rhizospheric bacteria from three Morocco sites differing for their climatic conditions (humid, semi-arid and arid) as well as the isolation and the molecular identification of AMF spores from Algeria and Tunisia. To find good PGPB candidates that will be later applied in field conditions, different assays on the bacterial strains, such as growth compatibility test and germination and *in vivo* tests using sorghum plants, have been carried out. Finally, the AMF spores have been propagated to obtain a pure inoculum that will be tested individually or *in consortium* on different plant species.

P.0205 Endozoochory by woolly monkeys (Lagothrix lagothricha) and burial condition: Impacts on the seed-associated fungal microbiome

Felipe Cruz-Suárez[1], Pablo R. Stevenson[1], Emma C. Solano-Flórez[2], Adriana Bernal[3], Carolina Sarmiento[4,5], Paul-Camilo Zalamea[4,5]

1 Laboratorio de Ecología de Bosques Tropicales y Primatología, Departamento de Ciencias Biológicas, Facultad de Ciencias, Universidad de Los Andes, Bogotá, Colombia. 2 Escuela de Ciencias Básicas y Aplicadas, Universidad de La Salle, Bogotá, Colombia. 3 Department of Biological Sciences, Universidad de Los Andes, Bogotá, Colombia 4 Department of Integrative Biology, University of South Florida, Tampa, Florida, USA. 5 Smithsonian Tropical Research Institute, Panama City, Republic of Panama.

Lagothrix lagothricha is recognized as an efficient seed disperser in the neotropics because they transport high quantities of seeds without negatively impacting their viability after passing through its digestive tract. However, there is a possibility that this mechanism is more intricate, involving the colonization by endophytic microorganisms that promote plant growth. Biologically, when the seeds are released, they come into contact with the soil, allowing colonization by microorganisms that impact seed viability. Therefore, with this approach the dynamics of seed dispersal would be completely evaluated. Our study aimed to understand how *L. lagothricha* endozoochory and burial affect the germination, viability and diversity of endophytic microorganisms in seeds of *Cecropia peltata* and *Ficus dendrocida*. We worked in the plains foothills in the Rey Zamuro Reserve, San Martín, Meta, Colombia. By feeding *L. lagothricha* with seeds of the selected species, we obtained fecal samples and consumed seeds. Subsequently, we buried the seeds for two months in the native forest soil and evaluated the percentage of germination, viability, germination time and diversity of endophytic fungi in dispersed (D), buried (B), dispersed-buried (D+B) and control seeds (C). Our results indicate that endozoochory and burial are the main sources of colonization in seeds by microorganisms, revealing that no endophytic fungi were isolated in the control seeds. Additionally, endozoochory does not negatively affect the germination, germination time, and viability of dispersed seeds for both species. However, burial significantly reduced all of these processes. Dispersed seeds seem to resist burial better than buried seeds and control, this is directly correlating with changes in the composition and diversity of endophytic fungi, which can establish mutualistic, antagonistic, or commensalistic relationships. Finally, endozoochory could provide mutualistic fungi, while burial provide antagonistic fungi that affect seed persistence, highlighting the importance of this dynamic in the maintenance of neotropical forests.

P.0206 Soil and oak roots interactions under urban gradient: a case study using targeted enzyme activity imaging

Anna Gillini[1], Nataliya Bilyera [2], Dalila Trupiano [1], Iryna Loginova [2], Michaela A. Dippold[2], Gabriella S. Scippa[1]

1 University of Molise, Pesche, Italy. 2 University of Tübingen, Tübingen, Germany.

The urban environment is one of the most vulnerable ecosystem, due to the current pollution and climate change however its integrity and stability are critical for the global ecosystems. Various interactions including enzymatic hydrolysis of soil organic matter occur within urban soil between its (a)biotic components and plant roots, which are important for biogeochemical element cycles and resilience of urban ecosystems. To investigate these interactions and their changes to increasingly urban context, a controlled experiment was set up to assess enzyme activity. The experiment was performed in the rhizoboxes, where oak (Quercus cerris) seedlings were grown in three different urban soils collected in Campobasso city (Italy). These soils were chosen based on a specific gradient of urbanization and vegetation fragmentation. After two weeks, the spatial distribution of activity for three enzymes - acid phosphatase (P-cycle),β-glucosidase (C-cycle), and leucine aminopeptidase (N-cycle) - was mapped using a 2-D soil zymography technique. We detected the area of enzymatic hotspots and enzyme activities in a bulk soil and rhizosphere. The zymography showed that the levels of enzymatic activity and the area of hotspots varied along the urbanization gradient, with the more urbanized soil exhibiting the highest levels of both. These variations can be explained by two related factors: soil organic pollutants (SOPs) and stress conditions, both of which seem to follow the urbanization gradient. In bulk soil, SOPs can act as a substrate for microorganisms, resulting in significant enzyme activity. At the same time, SOPs can put oak under stress, which is why, in the rhizosphere, oak produces greater exudates and enzymes to support these conditions. To better understand these processes, more in-depth analyses are currently underway.

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P.0207 Comparative Analysis of PGPR impact on plant growth: ANOVA vs. machine learning approaches

Chih Tao Hsu[1], Günter Neumann[2], Jer-Ming Hu[3], Torsten Müller[4]

1 Institute of Ecology and Evolutionary Biology, National Taiwan University, Taiwan. 2 Institute of Crop Science. University of Hohenheim, Germany. 3 Institute of Ecology and Evolutionary Biology, National Taiwan University, Taiwan. 4 Institute of Crop Science. University of Hohenheim, Germany.

This study aims to investigate the effect of microbial fertilizer (CFB) on plant growth under different soil conditions. Plant growth data from different treatment groups were analyzed using both ANOVA and machine learning (Random Forest and PVC) methods, comparing the effect of CFB as well as the differences in evaluating the effects of CFB between these two approaches. The ANOVA analysis focused on exploring statistically significant differences in growth parameters between different treatment groups, while the machine learning analysis concentrated on assessing feature importance and the predictive capability of the model.

P.0208 Ethylene-inhibiting rhizobacteria regulated genes in creeping bentgrass associated with drought tolerance and post-stress recovery

William Errickson[1], Bingru Huang[1]

1 Department of Plant Biology, Rutgers University, New Brunswick, USA.

Drought stress has negative impacts on the growth and quality of cool season grasses such as creeping bentgrass (*Agrostis stolonifera).* The use of plant growth promoting rhizobacteria (PGPR) that produce the ACC deaminase (ACCd) enzyme to reduce stress-induced ethylene in plants has emerged as a novel and sustainable approach to improving drought stress tolerance and post-stress recovery upon re-watering. This study explored a transcriptome analysis of creeping bentgrass plants inoculated with a novel strain of ACCd-producing *Paraburkholderia* bacteria under three different drought stress regimes (well-watered, 35 days of drought stress, and 15 days of post-drought recovery) in order to understand which key genes are regulated by ACCd bacteria to promote drought stress tolerance and post-stress recovery. ACCd bacteria inoculation resulted in differential expression of 122 genes under well-watered conditions, including up-regulation of genes involved in root growth, water dynamics, and antioxidant production (OTS1), cell wall modification (PMEI25), anti-senescence (S3H), and reduced ROS (ADH2), as well as down-regulation of genes associated with abiotic stress response (AAO5). Inoculation also resulted in differential expression of 15 genes under drought stress, including upregulation of OTS1 and ADH2. After 15 days of post-drought re-watering, inoculated plants demonstrated differential expression of 13 genes, including up-regulation of RAD6, which is associated with DNA repair, and D10, which is associated with tiller development. These findings help to explain the mechanisms associated with ACCd-bacteria mediated drought stress tolerance and post-drought recovery in cool season turfgrass.

P.0209 NOOT1 remodeling underground lateral organ ontogeny is regulated by NIN and availability of nitrogen

Liying Lan [1], Ertao Wang [1]

1 Center for Excellence in Molecular Plant Sciences, Institute of Plant Physiology and Ecology, the Chinese Academy of Sciences, Shanghai, China.

Nod factor-induced nodule organogenesis is a prerequisite for sufficient nitrogen-fixation symbiosis between legume and rhizobia. This type of symbiosis is supposed to have undergone a conversion from actinorhizal-type symbiosis established between the *Frankia* and some of non-legume plant in Nitrogen Fixation Clade (NFC). The absence of co-transcriptional factor *NODULE ROOT1/2*(*MtNOOT1/2*) has been reported to reverse this conversion in *Medicago truncatula*. Here, we found MtNOOT1/2 can interact with the transcription factor MtNF-YA1 which is a pivotal positive regulator for nodule organogenesis. Over-expression of *MtNOOT1/2* decreased root nodule number, which is opposite to the over-expression of *NF-YA1*. Surprisingly, the nodule number is not impacted in mutant of *MtNOOT1/2* in early stage, but significantly increased after 35d post inoculation than wild type R108. We also found that the decreasing of lateral root in *Mtnf-ya1* mutant as well as the increasing of LR number in *noot1noot2* mutant are both depended on the availability of nitrogen. Furthermore, we discovered NIN-binding motif in the promoter of *MtNOOT1* through bioinformation analysis and verified the transcriptional up-regulation of *MtNOOT1* by *MtNIN in vivo*. And the expression of *MtNOOT1* is upregulated under low nitrogen conditions. As NF-YA1 uniformly distributed in the nucleus, we observed that MtNF-YA1 being constrained in phase-separated droplets formed by MtNOOT1/2 by which NOOT1/2 might inhibit the transcriptional activity of NF-YA1. In conclusion, our results suggest that NOOT1/2 remodeling root nodule ontogeny by antagonizing NF-YA1 to fine tune root architecture and root nodule ontogeny.

P.0210 Do ectomycorrhizal fungi enable the productivity of oaks in inhospitable environments of the tropical montane cloud forest?

Sara Moledor[1,2], Oscar J. Rocha[2], Maritza Guerrero-Barrantes[3], Andrew Eagar[1,2], Margaret Campbell[2], Jorge A. Leiva-Sanabria[4], Marvin Castillo-Ugalde[3], Christopher Blackwood[1,2]

1 Michigan State University, East Lansing, USA. 2 Kent State University, Kent, USA. 3 Tecnológico de Costa Rica, Cartago, Costa Rica. 4 Universidad de Costa Rica, San José, Costa Rica.

The mechanisms by which species withstand stresses are critical to study because of the importance of species migration in ecosystems threatened by climate change. Tropical montane cloud forests are generally characterized by conditions inhospitable to tree growth - excessive moisture, cool temperatures, excessive UV radiation, and slowed decomposition. This gives rise to an organic nutrient pool inaccessible to most trees, driving nutrient limitation. Counter to typical Krummholz adaptations in such conditions, the oak trees of the Talamanca Mountain Range in Costa Rica are unexpectedly tall, productive, and dominant on the landscape. One possible mechanism that may relieve the trees of these environmental constraints is their partnership with particular ectomycorrhizal fungi. Most mycorrhizal fungi capture and supply inorganic nutrients, but some species of ectomycorrhizal fungi can acquire *organic* nutrients, granting tree hosts access to this high-demand nutrient pool that is otherwise unavailable to other vegetation. This would represent a significant advantage that could explain the unexpected survival and great productivity of oaks in these inhospitable regions. We sampled and sequenced soil and root fungi along an established elevational transect (2,400 – 3,100 meters) dominated by *Quercus salicifolia, Q. bumelioides*, and *Q. costaricensis* to characterize these ectomycorrhizal systems. Because increases in elevation are associated with increases in the stressors described above, we expect to see decreased overall abundance and diversity of ECM fungi at the highest elevations. Further we expect that mycorrhizal fungal relative abundances will shift in favor of organic-acquisitive taxa at higher elevations, suggestive of selection for this trait that should provide greater benefit to high-elevation host trees. Our project illustrates the complex relationships between trees and soil fungi at high altitude ecosystems and the role they may play in permitting or hindering range shifts and informing management strategies in light of a changing climate.

P.0211 Molecular characterization of potential plant growth promoting bacteria isolates from the central region of Puerto Rico.

Hirelys M. Montes-Jiménez1, Sharelys M. Montes-Jiménez[1], Yairelys Rosa-Morales[1], Christopher A. Sambolín-Pérez[1], Ramón E. Rivera-Vicéns[1]

1 Institute of Sustainable Biotechnology, Inter American University of Puerto Rico, Barranquitas, Puerto Rico.

Chemical fertilizers are one of the most used strategies to improve the yield and production of agricultural crops. However, the excessive use of these substances has caused negative consequences with direct impact on the environment, agriculture, and human health. An alternative strategy, the use of Plant Growth-Promoting Bacteria (PGPB) as biostimulants, have gained interest due to their ability to address the problems of chemical fertilizers. Therefore, our study aimed to characterize isolated bacteria from the central region of Puerto Rico at a molecular, biochemical, and morphological level to evaluate their potential biostimulant capacity in several plants species. Spread plate and serial dilutions were used to isolate bacterial communities present in the soil rhizosphere. Three bacterial strains were purified and characterized by Gram staining, Scanning Electron Microscopy (SEM), biochemical test, motility, and DNA barcoding of 16S rRNA gene. Results at the molecular level showed a preliminary identification of isolates for the species *Staphylococcus* spp., *Peribacillus* spp., and *Bacillus paramycoides.* Additionally, biostimulant capability was evaluated using model plant *Solanum lycopersicum* from phenology stage v2 to v5. Although no statistically significant changes were obtained (P >P.5), some biological variability corresponding to the *Peribacillus* treatment, when comparing positive and negative controls, was observed in terms of number of leaves, root size, and change of size.

The findings of this research, together with new experiments being carried out, would contribute to the scarce literature on native microorganisms in Puerto Rico and their application as biostimulants, promoting sustainable agriculture in Puerto Rico and other tropical and sub-tropical countries.

P.0212 Testing interactions in fungal endophyte communities of the model liverwort Marchantia polymorpha

Jessica Nelson[1]

1 Natural History Museum, University of Oslo, Oslo, Norway.

Plants harbor diverse communities of microbes on their surfaces and within their tissues. These microbiomes, composed of fungi, bacteria, archaea, and other eukaryotic organisms, are key in plant health and success. Interactions with microbial symbionts can contribute to plant nutrient uptake, immunity, competitive ability, and hormonal regulation. Interactions between members of plant microbiomes can significantly impact the outcome for the host overall, for example when certain symbionts can fight a pathogen or block the colonization of a mutualist. Untangling such dynamics within plant microbiomes and their impacts on hosts requires a variety of study types, from network analyses of environmental microbiome sequencing data, to controlled laboratory experiments. For the later type of study, systems using sterile plants and known microbiome members are necessary. These kinds of experimental systems ideally use model plant hosts so that the molecular mechanisms behind the host outcomes can also be studied. This work has already begun with synthetic communities of bacteria and fungi from the *Arabidopsis thaliana* microbiome. The study presented here brings this methodology into a bryophyte model, the liverwort *Marchantia polymorpha.* This study presents a series of experiments using wild-collected fungal endophytes of *M. polymorpha* to investigate principles of microbiome community interactions. The experiments address (1) pairwise interactions between fungi in the host, (2) relatedness among interacting endophytes, (3) priority effects when two fungi are inoculated at different times, and (4) interactions between groups of four or five endophytes. These experiments reveal a variety of interactions between endophyte community members that impact the health of the plant host.

P.0213 Native vs. non-native arbuscular mycorrhizal fungi inoculation for dry habitat restoration

M. Pérez-Redondo[1], M.J. Jaizme-Vega[1], A. Montesinos-Navarro[2], L. Díaz-Jimenez[3], J.A. Reyes-Betancort[1], A.M. González-Rodríguez[3]

1 Instituto Canario de Investigaciones Agrarias, San Cristóbal de La Laguna, Spain. 2 Centro de Investigaciones sobre la Desertificación-CSIC. Valencia, Spain. 3 Universidad de La Laguna, San Cristóbal de la Laguna, Spain.

Arbuscular mycorrhizal fungi (AMF) are mutualistic symbionts of most plant species, playing a key role in facilitating plant establishment in natural terrestrial ecosystems. Their integration into restoration projects is becoming increasingly important, particularly in arid environments where plant development faces greater threats. These organisms play a fundamental role in enhancing plant nutrition and tolerance to biotic and abiotic stresses, especially under harsh environmental conditions. The aim of this work is to assess the impact of native versus non-native AMF inoculants on the functional response of native species from the Macaronesia region for the restoration of arid areas in the Canary Islands. Chlorophyll content, anthocyanins, flavonoids, and gas exchange parameters were evaluated in five native plant species inoculated with native and allochthonous mycorrhizae, after six months of growth under greenhouse conditions. Additionally, parameters such as shoot/root ratio and shoot dry weight were analysed. The species of interest were *Coronilla viminalis, Asteriscus intermedius, Echium decaisnei, Phalaris coerulescens* and *Bituminaria bituminosa.* The physiological behaviour of the studied species exhibited variations depending on the origin of the inoculum. *Coronilla viminalis* demonstrated a positive response (with higher shoot/root ratio and shoot dry weight) when inoculated with native AMF, exhibiting elevated chlorophyll content and lower levels of antioxidants (anthocyanins and flavonoids). This work contributes to the advancement of nature-based restoration strategies by highlighting the efficacy of using native AMF inoculants specific to the study area. The findings show the beneficial effects of native AMF inoculants on certain plant species, emphasizing the need for further research in this direction.

P.0214 Discovery and bioengineering of natural products from Streptomyces to improve plant stress resistance

Yijun Qiao[1], Zhijie Yang[1], Naga Charan Konakalla[2], Emil Strøbech[1], Pernille Harris[1], Gundela Peschel[3], Miriam Agler-Rosenbaum[3], Tilmann Weber[4], Erik Andreasson[2], Ling Ding[1]

1 Technical University of Denmark, Kgs. Lyngby, Denmark. 2 Swedish University of Agricultural Sciences, Alnarp, Sweden. 3 Leibniz Institute for Natural Product Research and Infection Biology - Hans Knöll Institute, Jena, Germany. 4 Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Kgs. Lyngby, Denmark.

Greater challenges have been aroused with the increasingly serious environment and climate change issues, such as drought and excessive salinity in soil. Innovative and environmentally friendly solutions for improving agriculture are on call to meet the United Nations Sustainable Development Goals 2 and 15. According to the literature, microorganisms and their secondary metabolites that are beneficial to plants can correspondingly provide strategies for this goal. So that our project was proposed, based on previously discovered microbial natural products, pteridic acids, which were produced by *Streptomyces* and can promote plant growth as well as improve stress resistance at the concentration of 1 ng/mL. Our main purpose is to find more bioactive natural analogues, confirm their modes of action, and obtain enough amount for application in agricultural production to improve yield, reduce water usage, and enhance plants stress resistance. To achieve the goals, this project is ongoing, carried out through a series of research, combining the technology of microbiology, natural product chemistry, biotechnology with plant sciences. Firstly, we're trying to discover new pteridic acids and investigate their structure-activity relationship by genome mining, high throughout chemical determination, molecular networking and genetic editing. Secondly, we've tested the effects of pteridic acids on different plants, such as *Arabidopsis*, wheat and mung beans. Meanwhile, we've tried to elucidate the mode of action of pteridic acids by transcriptome analysis. Finally, genetic editing and media optimization have been used to improve the production of pteridic acids from *Streptomyces*. The anticipated outcome is to provide biostimulants and strategies to help in dealing with environmental and climate threats, as well as assisting develop environmentally friendly and sustainable green agriculture.

P.0215 Characterization of Puerto Rico Musa spp. resistance gene candidate against Fusarium oxysporum f. sp. *cubense*

Christopher A. Sambolín-Pérez[1], Ramón E. Rivera-Vicéns[1], Rosalinda Aybar-Batista[1], Juan A. Negrón-Berríos[1]

1 Institute of Sustainable Biotechnology, Inter American University of Puerto Rico, Barranquitas, Puerto Rico.

The species of Musa are an important food source worldwide and possess a big role in the economy of underdeveloped countries. Bananas and plantains are the most important member of *Musa* spp. due to their nutritional composition and value. *Musa* spp. are commonly affected by harmful diseases caused by phytopathogens, including black sigatoka and fusarium wilt. Moreover, the lethal strain of *Fusarium oxysporum* f. sp. *cubense* tropical race 4 (FOC-4), have been reported in various places in Central America and currently there is a warning in Venezuela. If this deadly phytopathogen arrives to Puerto Rico, it will affect the whole economical and agricultural sector due to the severe phytopathology of this fungal disease. Previous work reported in some *Musa* spp. wildtypes have found several Nucleotide-binding-and-Leucine-rich-repeat (NB-LRR) type resistance (R) genes that can provide immunity against FOC-4. However, there is no characterization and detection of such genes in Puerto Rico local *Musa* spp. varieties. Our research aims to employ molecular tools (PCR, qPCR, Sanger sequencing, and RNA-Seq) in local *in-vitro Musa* spp. (Dwarf, Maiden, and Maricongo varieties) to detect the candidate resistance gene and elucidate their abundance and regulation. This project has a vital role for protecting Puerto Rico food crops, by saving potential losses of products of the farmers cultivating banana and plantains. Preliminary, diagnostic PCR and qRT-PCR results shows the presence of *Musa* spp. resistance gene analog against FOC-4 and high transcripts abundance on Dwarf variety. Resistance gene was sequenced using Sanger method and results shows high similarity with candidate resistance gene suggested in the literature. Detecting and understanding the functionality of such genes will provide an insight into the molecular defense mechanisms of local *Musa* spp. varieties against FOC-4 and perhaps, have preventive strategy for its control.

P.0216 Understanding the environmental drivers of root-associated fungal communities in a West Carpathian endemic Daphne arbuscula

Zuzana Gajdošová[1], Miroslav Caboň[1], Zuzana Kolaříková[2], Radka Sudová[2], Jana Rydlová[2], Ingrid Turisová[3], Peter Turis[3], Jaromír Kučera[1], Marek Slovák[1,4]

1 Plant Sciences and Biodiversity Centre of Slovak Academy of Sciences, Bratislava, Slovakia. 2 Institute of Botany of the Czech Academy of Sciences, Průhonice, Czech Republic. 3 Matej Bel University in Banská Bystrica, Banská Bystrica, Slovakia 4 Charles University, Prague, Czech Republic.

Rocky outcrops function as ecological islands, hosting an extraordinary biodiversity characterized by numerous rare and endemic species. These habitats impose challenging abiotic conditions, necessitating adaptive responses from rock plants. The fitness and long-term survival of these plants are intricately linked to diverse mutualistic and antagonistic interactions with the surrounding mycobiome. Despite the complexity of this ecosystem network, it still needs to be explored and demands further scrutiny. In our investigation, microscopic observations and metabarcoding analyses (amplicon sequencing) were employed to unravel the diversity of root-associated fungi in *Daphne arbuscula* (Thymelaeaceae), a rock specialist and West Carpathian narrow endemic shrub. Our findings unveiled extensive colonization of *D. arbuscula* roots by a diverse array of taxonomic and ecological fungal groups, predominantly comprised of plant pathogens, dark septate endophytes (DSE), and arbuscular mycorrhizal fungi (AMF). Our results suggested that the observed diversification in the fungal spectrum was likely triggered by environmental variables: sites with warmer microclimates exhibited a prevalence of plant pathogens, while colder sites demonstrated a dominance of DSE. This implies that *D. arbuscula* populations in warmer areas may be more susceptible to fungal infections, especially during abrupt climatic shifts associated with ongoing climate change. Conversely, an increased abundance of DSE in colder areas may mitigate biotic and abiotic stresses. Establishing a nuanced equilibrium between beneficial and detrimental interactions between rock-dwelling plants and the surrounding microbiome emerges as a pivotal factor for the enduring survival of this endemic species. Acknowledgments: This work was supported by the Slovak Research and Development Agency (APVV-22-0365), the Scientific Grant Agency of the Ministry of Education, Science, Research, and Sports of the Slovak Republic and the Slovak Academy of Sciences (VEGA 2/0098/22 and VEGA 2/0050/22), the Grant Programme for Slovak Academy of Science PhD students (APP0361), and the institutional project RVO 67985939.

P.0217 There's Azolla lot more to Azolla: insights from the California Conservation Genomics Project

Michael J. Song[1], Carrie Tribble[2], Forrest Freund[3], Fay-Wei Li[4], Carl Rothfels[5]

1 Skyline College, San Bruno, USA. 2 University of Washington, Seattle, USA. 3 Bureau of Land Management, USA. 4 Boyce Thompson Institute and Cornell University, Cornell, USA. 5 Utah State University, USA.

Our chromosome-level assembly of *Azolla microphylla* and the resequencing of hundreds of Azolla samples across the state of California shed light on how many species there are in the state, patterns of co-diversification with its main endosymbiont and many newly discovered leaf-pocket associated bacteria, and population genomics.

P.0218 Interaction between Rhizopogon himalayensis ectomycorrhiza and Cedrus deodara root during mantle development

Gunjan Thakur[1], Kulraj S. Kapoor[1], Ashwani Tapwal[1]

1 Himalayan Forest Research Institute Conifer Campus, Panthaghati, Shimla, Himachal Pradesh, India.

The myobiont, *Rhizopogon himalayensis* is only understood to exclusively exist in ectomycorrhizal association with *Cedrus deodara* in Himachal Pradesh, India. The current research is the first attempt at understanding this plant–mycobiont interaction in a framework of the developmental and physiological processes that underscore the colonization and morphogenesis of ectomycorrhiza. For this, 6-month-old *C. deodara* seedlings tailored with the mycobiont *R. himalayensis* were harvested from the nursery bags and the excised root tips were examined under a light microscope at 100x, 400x, and 1000x power to progressively examine the steps leading to complete encasing of roots by mantle hyphae. It was observed that the ectomycorrhiza emerged as a lateral outgrowth from the mother root, exhibiting two distinct root morphologies. The fungal colonization involved a series of steps including fungal hyphae aggregation around the root hair, suppression of root hair development, twisting and collapsing of the root hair, and eventually complete encasing of the root tips by the fungal mycelium. Understanding the development of the mantle and the interactions between *R. himalayensis* ectomycorrhiza and *C. deodara* root is crucial for comprehending the establishment and functioning of this mutualistic association. Results from this experiment provide valuable insights into our understanding of the mechanisms underlying ectomycorrhizal symbiosis and potentially aid in the development of sustainable forestry practices by improving the establishment and growth of *C. deodara* trees through the enhancement of ectomycorrhizal associations.

P.0219 Unraveling leaf host-microbial interactions: do intraspecific, intraindividual, and temporal variations in functional traits matter?

Xiangbo Yin[1,2], Susanne Walden[1], Eric Martiné[1], Lars Opgenoorth[1], Maaike Y. Bader[1]

1 Philipp University of Marburg, Marburg, Germany.
2 National Institute of Scientific Research, Quebec City, Canada.

Functional traits offer mechanistic insights, precise metrics, and predictive capabilities for assessing the physiological status, fitness, and even broader ecosystem processes and responses of plants. Leaves, comprising both the phyllosphere (exterior) and endosphere (interior), represent a widespread and diverse habitat for microbiota. Those microorganisms in leaves not only promote host fitness and nutrient acquisition, but also play important roles in global biodiversity and biogeochemical cycles. However, understanding the relative contributions of host-associated and environmental factors in determining host microbial community composition as well as the primary mechanisms within a host that mediate host-microbe interactions, remains a challenge in microbial ecology. To address the questions, the common oak (*Quercus robur* L.),a main forest-forming species in European forest ecosystems, was chosen to determine and quantify the interaction between leaf functional traits and microbial community structure and functions. Both field and greenhouse experiments weredesigned to focus on intraindividual (e.g., canopy position, leaf sides), intraspecific (e.g., site-specific conditions), and temporal variations (e.g., growth stages) as potential drivers of functional trait-microbial interactions. Morphological (e.g., specific leaf area and dry mass), physiological (e.g., photosynthetic rates and surface wettability) and chemical properties (e.g., nutrient concentrations, metabolite production) were measured to represent the leaf functional traits. Furthermore, to determine potential influence of global changes on leaf functions, we will design experiments to evaluate how these properties change under drought and heat. This project aims to unravel the complex interaction between plant functional traits and leaf microbiota, thereby informing potential mitigation strategies to safeguard plant fitness and ecosystem stability to global changes. We will present the concepts used in this project as well as the preliminary results.

P.0220 Variety-specific effects of Trichoderma application on wheat germination, early growth, and biomass

Mehrdad Zarafshar [1], Olivier Besnard [2], Gaëlle Vincent[3], Stéphane Bazot[3]

1 Department of Forestry and Wood Technology, Faculty of Technology, Linnaeus University, Växjö, Sweden 2 Biophytech Research and Development Company, Paris, France 3 Ecology Systematique Evolution, Institute for the Diversity, Ecology and Evolution of the Living World, University of Paris-Saclay, CNRS, AgroParisTech, Gif sur Yvette, France.

This study investigated the varietal-specific impact of *Trichoderma* application on wheat germination, early growth, and biomass. The experiment was conducted within a controlled chamber, employing three distinct Trichoderma treatments with six replications: a coating application method applied by carboxymethyl cellulose, liquid application method, and a series of control groups, with each treatment applied to both sterilized and non-sterilized soil samples. The research concentrated on assessing how these Trichoderma treatments influence the germination process, early growth stages, and overall biomass of wheat plants. Seed germination in the Archashon wheat variety exhibited a decline when subjected to Trichoderma applications. In contrast to the control group, where seed germination reached approximately 77%, the application of Trichoderma in liquid form led to a remarkable increase in seed germination for the Cell wheat variety, with rates reaching as high as 90%. Similarly, the Shrek variety exhibited a parallel trend, further emphasizing the variety-specific impact of Trichoderma application on seed germination. While Trichoderma applications had a notable impact on plant height in the Archashon and Shrek wheat varieties, the Cell variety displayed remarkable stability in this regard, showing no significant shift in plant height in response to our treatments. Specifically, for Archashon and Shrek, Trichoderma applications were associated with a decrease in plant height. Regarding shoot biomass, no considerable change was observed in all varieties following Trichoderma applications. However, a very slight increase was noted after employing the seed sticking method. Finally, we measured root extrication biomass, and the data reveal a promising impact of Trichoderma application in terms of stimulating root growth of wheat plant. In conclusion, our initial experiment exhibited a promising impact of Trichoderma as a biostimulator. We are currently extending our research to real field conditions, and future data will provide a more comprehensive understanding of its practical application.

S.023. BEYOND BIOGEOGRAPHY: ADAPTATION AND DIVERSIFICATION ACROSS THE INDOPACIFIC

P.0221 Understanding the diversity of Begonia sect Baryandra in the West Indo-Pacific using phylogenomics and machine learning

Mark Angelo C. Bucay[1,2], Li-Wei Tsai[1], Danilo N. Tandang[1,2,3], Hong-Wun Chen[1],,Hao-Chun Hsu[1], Rosario R. Rubite[4], Kuo-Fang Chung[1]

1 Academia Sinica, Taipei, Taiwan. 2 National Taiwan Normal University, Taipei, Taiwan. 3 National Museum of the Philippines, Manila, Philippines. 4 University of the Philippines, Manila, Philippines.

The Western Indo-Pacific is a crucial laboratory of plant evolution wherein the very diverse floristic assemblage is scattered across islands. This study focuses on identifying speciation of *Begonia* sect *Baryandra* based on its ancestry and morphology. *Baryandra* is a monophyletic plant group that has a very diverse leaf morphology centrally distributed in the Philippine archipelago and reaches islands of Taiwan, Japan and Malaysia. The project, with the help of local institutions, implemented one of the most comprehensive *Begonia* samplings in the Philippines to date. Forty species were collected in the year 2023 alone, around half of which are potentially new to science. This collection is further combined with the past collections deposited in Academia Sinica in Taiwan. Combined collections accounts for ~90% of all described *Baryandra* species to date, representing almost all major islands of the known species range. To study this vast collection, the project is integrating two approaches to determine their phenotypic and genotypic diversity– machine learning and phylogenomics. Machine learning (ML) will utilize leaf images from the field to quantify diversity of these plants' foliage. Given their immense leaf variations, ML aims to eliminate human perception bias on morphological characterization. Phylogenomics will utilize both nuclear DNA (through hybrid capture of known *Begonia* markers) and whole plastid DNA (through genome skimming) to see ancestry and hybridization patterns across different islands. The quantified leaf diversity will then be integrated into the phylogenomic lineages to see phylogenetic signals and infer possible inter- and intra-island species relationships in this portion of the Pacific. It is anticipated that there are corresponding patterns between *Baryandra* lineages and how these leaves look like across the species' range. It will show the speciation patterns of these plants in the archipelago, further shedding light to understand how the planet's botanical diversity evolves in island settings.

P.0222 Examining phylogenetic relationships of Barringtonia taxa in the Indo-Pacific using herbarium samples and ethnobotanical records

Else Demeulenaere[1], J. Gordon Burleigh[2], Tom Schils[3], Stefanie M. Ickert-Bond[4]

1 University of Guam Center for Island Sustainability and Sea Grant, University of Guam, UOG Station, Mangilao, Guam. 2 Department of Biology, University of Florida, Gainesville, USA. 3 Marine Laboratory, University of Guam, UOG Station, Mangilao, Guam 4 UA Museum of the North Herbarium and Department of Biology and Wildlife, University of Alaska Fairbanks, Fairbanks, USA.

Barringtonia J.R.Forst. & G.Forst. (Lecythidaceae) is a genus of flowering plants known for its showy flowers and peculiar fruits. The genus is found in the Indo-Pacific region. Indigenous peoples from these regions use various parts of these plants for medicine, food, fish poison, and other uses. In addition to inferring the first molecular phylogeny based on broad geographic sampling (22 out of 72 species), we are aiming to explore the genetic variation of two widespread taxa *Barringtonia asiatica* (L.) Kurz and *Barringtonia racemosa* (L.) Spreng as well as the genetic and ethnobotanical relationship with other taxa in the region. *Barringtonia asiatica* and *B. racemosa* have the widest distribution range among all *Barringtonia* species, stretching from eastern Africa to the Pacific Islands and Australia. Our analysis incorporates 12 samples of *B. asiatica* and 14 samples from *B. racemosa* from different islands and mainland areas in the Indo-Pacific region. *Barringtonia asiatica* forms a well supported monophyletic clade, while the *B. racemosa* clade receives lower support. Our phylogeny also includes samples of 20 other *Barringtonia* species from different geographic regions. Prance in the latest monograph of the genus identified three centers of biodiversity in 2012, Peninsular Malaysia, Borneo, and New Guinea. Taxa belonging to these areas form biogeographic clusters in our analysis. In addition, our data identified a well supported cluster of closely related Melanesian taxa. Another part of our study focuses on identifying nodes based on plant properties and ethnobotanical uses, which we can compare with our phylogeny.

P.0223 Revision of the Cranfillia vulcanica (Blechnaceae, Polypodiopsida) species complex in the Indo-Pacific region

Rubén Vázquez[1], Jose María Gabriel y Galán†[1], Sonia Molino[1], Manuel Pimentel Pereira[2]

1 Universidad Complutense de Madrid, Madrid, Spain. 2 Universidade da Coruña, A Coruña, Spain.

Cranfillia Gasper & V.A.O. Dittrich, a genus in the leptosporangiate fern family Blechnaceae Newman, was described in 2016, based mostly on molecular evidence. *Cranfillia species* grow in the Neotropics and throughout Oceania, and they present high morpho-anatomical variability between them. Consequently, different authors have cast doubt on the taxonomic reliability of the genus. In addition to this, in the last decade many nomenclatural changes have been proposed for the genus. In 2019, a taxonomic assessment of the *Cranfillia vulcanica* species complex from the Indo-Pacific region was completed, and it led to the description of new species, restoration of old combinations and proposals of new ones. Most taxa in the complex are insular, restricted to very small areas and poorly represented in collections. Here, we report on our recent taxonomic review of *Cranfillia*, conducted using molecular and morpho-anatomical characters. This approach has allowed us to clarify some of the unknowns around the systematics of this mostly Pacific group of ferns. Our phylogenetic study is based on three plastid regions (*rps*4, *trn*L-*trn*F and *rbc*L) and we have included many taxa considered in *Cranfillia* for the first time. Our morpho-anatomical assessment was conducted mostly on materials from NY, US and UC herbaria. *Blechnum* sect. *Pilosum* is resolved as monophyletic in *Cranfillia*, and as sister to the type species *C. fluviatilis*. The easternmost representatives of the genus (growing in Samoa, Cook Islands and French Polynesia) and the Australasian specimens are also nested within this group. Some taxa are poorly defined and apparently paraphyletic. This could be due to the use of imprecise taxonomic characters which could vary based on external factors. The Polynesian species group is revealed as not monophyletic. Therefore, it must have reached its current distribution through different dispersal events from Australasia.

S.024. BEYOND PLANT BLINDNESS: BRINGING PLANTS INTO THE FOREGROUND

P.0224 Is the cactus flora valued in the semi-arid high Andean enclaves of Colombia?

Daniela Porras–Flórez[1], Sofía Albesiano[2], Kendry Hernández–Herrera[3], Nubia Gómez–Velázco[4]

1 Area de Biodiversidad, Fundacion Cataruben, Yopal, Casanare, Colombia. 2 Departamento de Biologia, Facultad de Ciencias, Universidad del Tolima, Ibague, Colombia. asalbesianoh@ut.edu.co 3 Grupo de Estudio en Biotecnologia, Universidad de La Guajira, Riohacha, Colombia. 4 Grupo de Estadistica–GAMMA, Universidad Pedagogica y Tecnologica de Colombia, Tunja, Colombia.

Ethnobotany rescues and preserves the understanding of the human-nature relationship, fundamental information for the design of culturally appropriate and sustainable economic promotion and development projects. In the semi-arid high Andean enclaves of Colombia, economic conflicts occur, which lead to poverty and hunger, and where cacti stand out, which, due to their asexual reproduction and few requirements for their establishment, could contribute to the economic development of these ecosystems. The objectives were to identify the most used species, determine the uses attributed to cacti, measure the knowledge index of the informants, recognizing the most important species with the highest use value, and correlate the ethnobotanical indices with socioeconomic factors. For this, 262 semi-structured interviews were applied; eight categories of use were proposed: agricultural, agroecological, food, commercial, medicinal, ornamental, environmental and technological service; and three indices were used, relative importance, use value for each of the species and wealth of knowledge. Nine species were identified, of which eight are used as food and ornamental, with *Opuntia ficus-indica* standing out for its richness of uses, compared to *Cylindropuntia tunicata*, which does not report importance. Variables such as age and residence time showed a significant relationship with the number of plants used. It is expected that the results will contribute to disseminating local knowledge, preserving cactus flora, and promoting its large-scale cultivation, since species such as *Mammillaria columbiana*, *Melocactus andinus* and *Melocactus curvispinus* are being used in an unsustainable manner, which could cause their local extinction.

P.0225 Diversity of edible aroid species and varieties sold as 'tajer' in the Netherlands

Fang Qiong[1], Peter Matthews[2], Eric Schranz[1], Tinde van Andel[1,2]

1 Biosystematics Group, Wageningen University & Research, Wageningen, the Netherlands. 2 National Museum of Ethnology, Osaka, Japan. 3 Naturalis Biodiversity Center, Leiden, the Netherlands.

'Tajer' is a generic Surinamese name for edible plants including taro, Colocasia esculenta (L.) Schott and Xanthosoma spp. from Araceae. They are widely distributed and cultivated, known to have high nutritional value, and rank among the most important root and tuber crops globally. 'Tajer' consumption is limited because of its acridity, which may severely irritate the throat and lips if not cooked properly. However, no in-depth studies have been done on the 'tajer' acridity variation and how to diminish it. In this study, we used ethnobotanical methods to document the diversity of 'tajer' species and varieties and plant parts available on the Dutch market and how 'tajer' consumers in the Netherlands deal with its acridity. Ethnobotanical methods were used to collect samples, specimens, and document information. In total, 60 samples were collected from 27 different locations in six cities, and 55 people were interviewed. We found at least three species, C. esculenta, Xanthosoma sagittifolium (L.) Schott, Xanthosoma violaceum Schott and Caladium bicolor (Aiton) Vent., are sold under the name of 'tajer'. Plant parts sold as 'tajer' include corm, leaf, inflorescence, and young plant, with various processing. 'Tajer' is mostly sold in groceries, markets and supermarkets that mainly serve immigrant communities. People from different countries use different processing methods to avoid and reduce 'tajer' acridity, including peeling, cooking, and addition of specific ingredients such as milk and sour fruits. Further molecular experiments will assist with the identification of these plants at the species and varietal level. We also present the first findings on the cultivation of 'tajer' in western Europe. Our work will contribute to a better awareness of 'tajer' varieties and processing methods in Western Europe and promote a higher diversity in greenhouse crops.

P.0226 Mimicking stink bugs: ecological strategies of defensive traits in the endangered plant Aristolochia delavayi

Jia Ge[1, 2], Yu-Long Yu[1, 2, 3], Wen-Qi Dong[4], Guillaume Chomicki[5], Shi-Long Yang[4], Yupeng Geng[3], Gao Chen[1, 2]

1 CAS Key Laboratory for Plant Biodiversity and Biogeography of East Asia, Kunming Institute of Botany, Kunming, Yunnan, China. 2 Yunnan Key Laboratory for Integrative Conservation of Plant Species with Extremely Small Populations, Kunming Institute of Botany, Kunming, Yunnan, China. 3 Ministry of Education Key Laboratory for Transboundary Ecosecurity of Southwest China and Yunnan Key Laboratory of Plant Reproductive Adaptation and Evolutionary Ecology, Institute of Biodiversity, School of Ecology and Environmental Science, Yunnan University, Kunming, Yunnan, China. 4 College of Wildlife and Protected Area, Northeast Forestry University, Harbin, Heilongjiang, China. 5 Department of Biosciences, Durham University, Durham, United Kingdom.

Mimicry is a phenomenon wherein one species, the mimic, closely imitates another, the model, enhancing its adaptability by misleading a third party into interacting with it as though it were the model. In the plant kingdom, mimicry is predominantly employed to enhance adaptability by either withholding rewards from mutualistic partners or deterring herbivores cost-effectively. In this study, we conducted field experiments, chemical analyses, behavioral assays, and electrophysiological studies to test the hypothesis that *Aristolochia delavayi*, a member of the birthwort family, employs chemical mimicry by emitting leaf scents closely resembling those of stink bugs, thereby repelling vertebrate herbivores. Our findings reveal that the leaf scent of *A. delavayi* shares both chemical composition and functional characteristics with the generalized defensive volatiles emitted by stink bugs. This scent effectively deters vertebrate herbivores, likely through activating TRPA1 channels via (*E*)-2-alkenal compounds. Despite the potent deterrent effect of (*E*)-2-alkenals, a swallowtail species *Byasa daemonius* has evolved to bypass these defenses. This butterfly specializes in feeding on *A. delavayi* and depends on it for its life cycle, with the larvae sequestering aristolochic acids as defense substrates from the plant as they feed. Additionally, *A. delavayi* is a commonly used spice plant along the Jinsha River, and over-harvesting has resulted in a reduction in its population, posing cascading effects and increasing the possibility of extinction for other species.

P.0228 The festival "Botany: Between Science and Art" – an educational activity to raise awareness of plants among children aged 3 to 12

Mercè Rocadembosch[1], Elodie Hidalgo[2], Oriane Hidalgo[3,4]

1 Universitat Oberta de Catalunya, Barcelona, Spain. 2 Ecole de la Placette, Nîmes, France. 3 Institut Botànic de Barcelona, Barcelona, Spain. 4 Royal Botanic Gardens, Kew, Richmond, UK

Plants are one of the main keystones of biodiversity. For that reason, raising consciousness about their importance is a major and urgent educational challenge, especially in the face of ongoing global crisis. The activity presented here, stemming from the collaboration between an artist, a schoolteacher and a botanist, was aimed at children aged 3 to 12, and used both scientific and artistic tools to foster awareness and transform their relationship with plants and nature. As part of the 4th edition of the "Cuenta la Ciencia" program, a botanical festival was organised at the Botanical Institute of Barcelona and the Botanical Garden. The festival's programme offered twelve different activities for children aged 3-6 and nine for those aged 7-12, covering sensory experiences and activities based on manipulation, observation, creation, appropriation of botanical vocabulary and teamwork performances. The whole experience was highly successful, with both children and parents expressing their wish towards having more festivals of this kind organised during the year. We strongly believe that this approach could be further promoted by developing and sharing educational materials to engage children through a playful exploration of the diverse and fascinating aspects of the botanical world.

P.0229 A forgotten botanical language: the phytoiconology in the archaeological collections from the National Roman Museum

Alessandro Lazzara[1], Alma Kumbaric[1], Chiara Giobbe[2], Giulia Caneva[1]

1 Department of Science, University of Roma Tre, Rome, Italy. 2 National Roman Museum, Rome, Italy.

Nature was deeply rooted in ancient cultures, where any natural phenomena were carefully observed and explained within the divine sphere. Humans and Nature's relationship is visible in classical themes such as food or medicine, but also in paintings and monuments, like columns, capitals, festoons, and landscapes. This profound knowledge of nature created an iconographic and symbolic language where the botanical elements, extrapolated from their natural context, were used to transmit messages and abstract ideas, as shown in the Ara Pacis and Villa di Livia's frescoes, at the Augustan time. However, culture and religion led to forgetting this language, and Nature lost its exceptional role. Naturalistic representations became just ornamental motifs, without any symbolic meaning. To strengthen the previous analysis, we further investigated the role of these motifs in the Roman world, looking at their identification and their symbolism according to the context of representation. We analysed a wide typology of artworks (frescoes, sculptures, and architectural elements) from the National Roman Museum, selecting a significant number (191) dated between the VII cent. BC and the III cent. AD, 88.5% of which are sculptures. Until now, about 60 different botanical taxa have been identified through the support of a botanical atlas, online databases and ancient texts. *Acanthus mollis, Laurus nobilis*, *Hedera helix*, *Asphodelus* sp. and fruits such as *Cydonia oblonga*, *Malus sp.*, *Pyrus sp.*, had the highest recurrence. Some of them appear linked to specific typologies of artworks and context, with a more or less complex symbolic aim. This study will provide a better understanding of the role of plants in Roman culture and reconstruct the ancient landscape. The final goal is to bring nature back into museums, as the ancients perceived it, using artefacts as the connection between a forgotten language and modern society.

P.0230 Carbon stocks and sequestration potential of mangroves of Kannur district, Kerala, India

M Swedha Madhavan[1], K T Chandramohanan[2], P Sreeja[3]

1 Government Brennen College, Thalassery, Kannur, India. 2 Krishna Menon Memorial Government Womens College, Kannur, India. 3 Sir Syed College, Taliparamba, Kannur, India.

Mangroves are important sinks of organic carbon (C) and there is significant interest in their use for greenhouse gas emissions mitigation. The preliminary aim of the study includes estimation of biomass and carbon storage potential of mangrove species distributed in the selected study stations of Kannur district, Kerala. The selected stations of Kannur district for the study include Cherukunnu (S_1) and Nadal (S_2). Quadrant study was carried out for the non-destructive estimation of biomass of mangrove species. Existing general allometric equations were applied for computing biomass and carbon content of mangrove species. The total biomass and carbon content of mangrove trees in ten study plots from S_1 was found to be higher in *A. officinalis* (9,274.53 kg and 6,058.64 kg C) and lower in *K. candel* (94.65 kg and 46.8 kg C).

Total biomass and carbon content of *A. officinalis* in ten study plots from S_2 had greater values (6,563.8 kg and 3,562. 51 kg C), whereas *K. candel* had lower values (117.5 kg and 58.3 kg C). The total biomass of all true mangrove trees from the study plots was estimated to be 19,951.42 kg in S_1 and 14,336.79 kg in S_2. The total carbon content (AGC + BGC) of all true mangrove trees from the study plots was estimated to be higher in S_1 (10,584.21 kg C) compared to S_2 (7,231.15 kg C) which is equivalent to the weight of 38844.04 CO_2 and 26538.32 CO_2. Mangrove species distributed in the undisturbed area of the study stations (S_1) exhibit high biomass and carbon content. It signifies the potential of mangrove species in carbon sequestration and thereby plays a vital role in climate change mitigation by reducing atmospheric CO_2 emissions.

P.0231 Cytotoxic activity of different extracts of spotted knapweed (Centaurea stoebe L., Asteraceae) from Serbia

Milica Miletić[1], Jelica Novaković[1], Bogdan Jovanović[1], Pedja Janaćković[1]

1 Chair of Plant Morphology and Systematics, Faculty of Biology - University of Belgrade, Belgrade, Republic of Serbia.

The knapweeds, members of the genus *Centaurea* L., belong to the tribe Cardueae and represent one of the largest genera in the family Asteraceae. According to recent data, the genus comprises about 250 species, which are mainly distributed in Eurasia, especially in the Mediterranean and Irano-Turanian regions, with some species (mostly representatives of the section *Jacea*) extending northwards into temperate areas of Europe. The species of the genus are used in traditional medicine to treat various diseases. Therefore, many species have been pharmacologically characterized. However, the object of this study, a spotted knapweed, *Centaurea stoebe* L. from Circum-Mediterranean Clade, remains largely uncharacterized pharmacologically. The species is a biennial or perennial herbaceous plant widely distributed in Serbia and considered as one of the most aggressive invasive and economically damaging allochthonous plant species in North America. The aim of this study was to investigate the cytotoxicity of different extracts of *C. stoebe*. The plant material was collected during the flowering period in July 2021 near Kruševac, Serbia. The cytotoxic activity of diethyl ether (Et_2O), methanol (MeOH), 70% ethanol (EtOH), ethyl-acetate (EtOAc), 50% acetone (Me_2CO) and dichloromethane:methanol (DCM:MeOH, 1:1) extracts of the aerial parts of *C. stoebe* was investigated for the first time on the HeLa cell line using the MTT assay. The results showed a strong cytotoxic activity of *C. stoebe* extracts. The highest observed cytotoxicity in the HeLa cell line was induced by Et_2O and EtOAc extracts (IC_{50} = 51.21 µg/mL and 56.81 µg/mL, respectively), while the 70% ethanol extract exhibited the lowest cytotoxicity (IC_{50} = 250.5 µg/mL). Further phytochemical studies, as well as tests on non-cancerous cell lines are necessary to determine the relevance of these extracts for potential therapeutic applications.

P.0233 From pandemic to the world: Botânica sempre viva

Maria L. S. de Carvalho[1], Ariane L. Nascimento[1], Carolina S. Pinho[1], Cecília S. Rodrigues[1], Jessica L. B. Tanajura[1], Lana L. B. dos Santos[1]

1 Institute of Biology, Federal University of Bahia, Bahia, Brazil.

Botanical Unawareness has been tentatively tackled with the aim of increasing people's awareness of plants, which are essential for maintaining life on the planet. However, this is not a simple task, requiring a constant investment in didactic, engaging, accessible, and contextualized communication between academic community and society. In this sense, the Botânica Sempre Viva (BSV) university extension project was born at the Federal University of Bahia, which aims to mitigate the effects of Botanical Unawareness in both academic and non-academic audiences. Amid the Covid-19 pandemic in 2020, we started our activities on social media with posts about curiosities, interdisciplinary content, and the appreciation of personalities in the history of botany. However, considering that the main root of botanical unawareness lies in the field of education, three free virtual educational materials were also produced, which, two years later, received a scientific women award (2022). Continuing with educational initiatives, in 2021 we began developing a mobile app game (ADAPTO) that involves plant morphology and anatomy within the context of Brazilian biomes. This work was awarded at the Biology Week of the Institute of Biology at UFBA the following year. In 2022, BSV initiated a partnership with the Botanical Parks project in cataloging and promoting *plants in public parks in the city of Salvador, Bahia. In 2023, botanical art workshops were conducted with children from public schools during the Science and Technology Week. Additionally, the construction of two catalogs (one with an audiobook version for visually impaired individuals) showcasing the flora of Mucugê Municipal Park - the Sempre Viva Project - began. In the future, we hope to continue contributing to the expansion of botanical knowledge and interaction with society through accessible and engaging language, transcending the boundaries of the university and helping to promote empathy and respect for botany.*

P.0234 Ritual plants in an industrialized country: an analysis of blessed herbal bouquets in the Netherlands

Isabela Pombo Geertsma[1,2], Berber Zandstra[3], Marieke Duinhouwer[2,4], Sjors Kleuskens[5], Corné van der Linden[3], Tinde van Andel[2,3]

1 Quantitative Biodiversity Dynamics, Botanical Gardens Utrecht University, Utrecht, the Netherlands. 2 Naturalis Biodiversity Center, Leiden, The Netherlands. 3 Biosystematics Group, Wageningen University & Research, Wageningen, the Netherlands. 4 Leiden University. 5 Quantitative Biodiversity Dynamics, Botanical Gardens Utrecht University, Utrecht, the Netherlands.

Ethnobotanical research is often centred around edible and medicinal plants, as these species are generally considered most important for human society and their study assists knowledge conservation of culturally important plants. The Netherlands is an industrialized country where only 15% of its land area is set-aside for nature conservation and where foraging plants for food and medicine are not generally practised in modern history. Here, conservation efforts focus on the intrinsic value of species and ecosystem services but are unable to shift attitudes to nature-positive thinking. For this to occur, fostering a close connection with species via direct interaction may be a more important, but overlooked driver. A rare example of such a cultural link between society and nature in the Netherlands is found in the Catholic south of the country, where Saint John's Day (June 24th) and Mary's Assumption (August 15th) are important celebrations wherein plants play a prominent role. For these celebrations, people assemble bouquets which are blessed in church, brought home and hung up in the house where they serve to protect the building and its inhabitants. These bouquets are beautiful assemblages of wild species such as *Centaurea cyanus*, *Tanacetum vulgare* and *Hypericum* spp., combined with garden plants such as *Rosa* spp. Interviewees express concern over the ever-growing distance to desirable harvesting locations, the municipality's mowing policy and the shifting of blooming periods due to climate change. But possibly the biggest threat to the survival of this ritual is the sharp decline in churchgoers. Rituals such as these have the potential to influence peoples' attitude towards nature and strengthen people-plant relationships locally. A closer look at -not only religious- seasonal feasts may guide us in understanding how people in industrialized countries can develop a larger appreciation of their surrounding nature and the drive to conserve it.

P.0235 Showcasing Cerrado's representative flora of Chapada dos Veadeiros as an important factor to conservation and restoration

Gabriel R. Vedovello[1], Natashi L. Pilon[1], Rafael S. Oliveira[1]

1 Department of Plant Biology, Institute of Biology, Campinas State University, Campinas, Brazil.

Restoration efforts in the biodiverse Cerrado savanna biome are crucial for ecosystem recovery. However, restoration projects in the Chapada dos Veadeiros region, a key Cerrado area, often face challenges using inappropriate species. This project tackles the issue by creating a comprehensive Field Guide developed through on-site floristic surveys in diverse Chapada dos Veadeiros National Park (CVNP) environments. This guide, focusing on savannas, forests and grasslands, aims to enhance understanding of the region's biodiversity of flora. The Field Guide, encompassing over 150 plant species, bridges the gap in knowledge about the composition of flora in CVNP. Not only does it list species, but it also provides easily understandable descriptions and information on occurrence, endemism, and vulnerability. Surprisingly, 75% of the species found have no vulnerability data, highlighting the need for further studies as these species face potential local extinction due to land conversion, biological invasion, and improper land management. More than a tool for ongoing restoration initiatives, the guide enriches knowledge for future projects and supports seed collectors. Simultaneously, it promotes botanical tourism by introducing the local flora to the public. By increasing awareness of the Chapada's natural wealth, the guide encourages individuals to become advocates for conservation, aiming to reduce plant blindness. Furthermore, the project significantly contributes to the Unicamp Herbarium's collection, providing valuable insights into Cerrado plant diversity. The illustrated Field Guide emerges not only as a support system for restoration but as a catalyst for broader goals, fostering a deeper connection between the public and the unique ecosystems of the Chapada dos Veadeiros.

P.0236 Contribution of the Limbe Botanic Garden to the population awareness raising on plant biodiversity and students education

Serges V. Mtemching Djomo[1], Eric W. Fondzenyuy[2], Christopher Forminyam[3]

1 Limbe Botanic Garden, Limbe, Cameroon. 2 Limbe Botanic Garden Education Unit, Limbe, Cameroon. 3 Wildflower Ecology Foundation, Limbe, Cameroon.

The Limbe Botanic Garden is one of the oldest and richest in situ tropical biodiversity conservation sites in Central Africa founded by German Horticulturists as the Victoria Botanic Garden in 1892. The British took over the management of the Garden in 1920 and established a living plant collection with diverse endemic and exotic species. The living plant collection of the Garden, planted following a thematic pattern is estimated at about 1,500 taxa of different types, families and genus consisting approximately of 1,000 herbaceous and 500 woody plants made up of timbers, non-timbers and ornamentals displayed on 48 hectares of land at the central town of Limbe. The Botanic Garden Herbarium with acronym "SCA" harbors 30,000 herbarium specimen and more than 13,000 ecological specimens of over 32 types, 260 plant families, 700 genera, 1400 species of which 46 are endemic to the Mount Cameroon area. This Herbarium was established since the creation of the Garden and was enriched thanks to the collaboration with the Royal Botanic Garden Kew (UK), where the duplicates of many plant specimens of Limbe are duly conserved. This Herbarium works in close collaboration with the National Herbarium and has played a vital role during the various botanical expeditions to study the flora of Cameroon. The Botanic Garden Limbe receives an average of 40,000 visitors per year who are giving guided tours during which they have the privilege to learn about plants and their importance. About 500 students in Botany and Agriculture from Buea and Bamenda Universities do visit the Limbe Botanic Garden Living plant collection and Herbarium yearly during their field study trip where they receive practical training on plant identification and Herbarium techniques. An average of 15 university students received yearly for academic internship and research for Msc and PhD thesis in plant science.

P.0237 Botanical online courses and Citizen Science increases the number of amateur botanists in the Netherlands

Laurens Sparrius[1], Stef van Walsum[1]

1 FLORON Plant Conservation, Nijmegen, Netherlands.

The domain of botany, particularly in the realms of taxonomy and floristics, is increasingly relying on the expertise of dedicated amateur botanists. The majority of these enthusiasts are self-taught self-taught experts. In The Netherlands, this group has remained relatively modest over the past three decades and has aged significantly. Botanical courses set up throughout the country were simply not effective enough to provide sufficient inflow of younger people. In 2021, halfway the pandemic, FLORON launched an online course to get more people interested in studying wild flora. Comprising 14 weekly online sessions featuring three instructional videos elucidating diverse topics such as species identification within specific plant families, plant ecology, floristics, and botanical uses and knowledge, the course aimed to engage participants. Following completion, students were encouraged through newsletters to actively participate in citizen science projects or join local botanist groups. Between 2021 and 2024, a noteworthy 2800 students undertook the course. By tracking students in the involvement of botanical monitoring and citizen science projects, we were able to estimate the percentage who transitioned into active botanists in subsequent years. Despite a relatively modest percentage (1-2%), the numerical influx of newly emerged botanists proved sufficient to foster growth and rejuvenation within the Dutch botanical community.

S.025. BIOGEOGRAPHIC AND EVOLUTIONARY PATTERNS AND PROCESSES OF THE TROPICAL TEMPERATE BIOME TRANSITION

P.0238 A global blueberry phylogeny: evolution and classification of tribe Vaccinieae (Ericaceae)

Anna L. Becker[1,2], Andrew A. Crowl[a1,3], James L. Luteyn[4,5], Andre S. Chanderbali[1], Walter S. Judd[1], Paul S. Manos[3,4], Pamela S. Soltis[1], Doug E. Soltis[1,2], Stephen A. Smith[6], Deise J. P. Goncalves[6], Christopher W. Dick[6,7], William N. Weaver[6], Nico Cellinese[1], Peter W. Fritsch[8]

1 Florida Museum of Natural History, University of Florida, Gainesville, USA. 2 Department of Biology, University of Florida, Gainesville, USA. 3 Department of Biology, Duke University, Durham, USA. 4 Institute of Systematic Botany, New York Botanical Garden, Bronx, USA. 5 Present address: 32075 East Side Drive, Beaver Island, USA. 6 Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, USA. 7 Smithsonian Tropical Research Institute, Panama City, Republic of Panama. 8 Botanical Research Institute of Texas, Fort Worth Botanic Garden, Fort Worth, USA.

Vaccinieae is a morphologically diverse and species-rich tribe in the Ericaceae. Although the majority of its diversity is tropical, Vaccinieae is best known for temperate crops (i.e., blueberries, cranberries, huckleberries) of the genus *Vaccinium*. *Vaccinium* itself has been previously suggested to be highly polyphyletic, and taxonomic boundaries of most other genera remain uncertain. To better understand the extent of polyphyly of *Vaccinium* in the context of closely related genera, and gain insights into the evolutionary history of Vaccinieae as a whole, we assembled an Angiosperms353 nuclear dataset of over 200 taxa representing 30 of the 34 genera in the tribe and 25 of the 30 sections of *Vaccinium*. We additionally constructed a plastome dataset for a subset of these taxa. We conducted phylogenetic and time-calibrated biogeographic analyses to address the following questions: 1–What are the phylogenetic patterns within Vaccinieae? 2–How do the clades compare with current generic and sectional? 3–Where and when did major dispersal and diversification events take place? Clades recovered generally align with geography, not current classification. Biogeographic reconstruction suggests that tropical diversity of Vaccinieae results from multiple independent movements into tropical habitats from temperate ancestral areas, mostly North American. Dispersal events were found to align with major geographic changes such as the uplift of the Andes, and some of these events coincide with increased diversification rate. The pseudo-10-locular ovary, which appears to have evolved from a 5-locular ovary a single time, was found to group many sections of *Vaccinium* into a single clade. Options for reclassification range from the recognition of a single species of *Vaccinium* and many more genera, to the recognition of the single genus *Vaccinium* with many more sections. We consider an infratribal reclassification premature pending more taxonomic and phylogenetic study of the many problematic generic and sectional boundaries needing resolution.

P.0239 Areas of endemism and conservation implications of the Mexican carnivorous plants of the genus Pinguicula (Lentibulariaceae)

Claudia Reaño Jiménez[1*], Raúl E. Alcalá[1], Tania Escalante[2]

1 Centro de Investigación en Biodiversidad y Conservación, Universidad Autónoma del Estado de Morelos, Cuernavaca, Mexico. 2 Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad de México, Mexico.

The study of endemism patterns is crucial for understanding biodiversity and proposing conservation actions. Carnivorous plants of the genus *Pinguicula* L. (Lentibulariaceae) have the main center of diversification in Mexico, where 90% of the species are endemic and have restricted distribution. The loss of this group would represent the extinction not only of some species but of unique adaptation modes to nutrient scarcity. This study evaluates for the first time the identification of areas of endemism for this gender in Mexico, a necessary precursor to the implementation of conservation strategies and actions. *Pinguicula*´s evolutionary history allows us to hypothesize the existence of congruence in the geographical distribution of species present in mountainous areas such as the Sierra Madre Oriental (SMOr) or the Faja Volcánica Transmexicana (FVT). Employing climate and topographic variables from ENVIREM, potential geographical distribution models were generated using the kuenm tool in R, quantifying the distribution of 51 species. The identification of the areas of endemism was carried out using an Endemicity Analysis (AE). We identified two areas of endemism. The first includes the southern region of the SMOr and part of the FVT, but also small portions of Desierto Chihuahuense (DeCh) and Veracruzana (Vzna). The second comprises the north of the SMOr, and areas of the provinces DeCh, Tamaulipas (Tpas), and Vzna. Most of the Mexican species exhibit a highly restricted distribution ranging from one to some unique localities. Extinction risk was statistically higher in species with restricted geographic distribution areas, and those that are distributed at high altitudes (around 1700 m). Although the highly restricted and allopatric distribution of most species made it complicated to find patterns in geographical distributions, the results of this study provide key elements to take into account to establish priority areas for the conservation of *Pinguicula*.

P.0240 Spigelia (Loganiaceae) with mariachi and samba. Distribution and diversity of the genus in the Americas

Carla Sofía Islas-Hernández[1], Leonardo Osvaldo Alvarado-Cárdenas[1], Daniela Quintos Baez[1]

1 Departamento de Biología Comparada, Laboratorio de Plantas Vasculares, Facultad de Ciencias, Universidad Nacional Autónoma de México, Ciudad de México, Mexico.

Spigelia L. is a genus from the Loganiaceae family, endemic to the American continent with an estimated 65 to 80 species distributed from the southeastern United States to northern Argentina, with no records in Canada and Chile. There are several regional works that address the diversity of the group by country, but little has been studied about its distribution and there is no work that integrates the number of *Spigelia* species on the continent and in each country. Our work aims to provide a general overview of the diversity and distribution that the genus presents in America. In order to know the number of total species accepted and by country as well as the areas of greatest diversity in each region, a bibliographic review, herbaria and virtual databases was carried out. A map was generated to know the distribution of diversity and endemism, as well as their ecological affinities. The total number of accepted species is 81, recorded in 34 countries in America, with Brazil (47 spp.) and Mexico (23 spp.) being the countries with the most taxa. Regarding endemism, it was found that only seven countries have endemic species, highlighting Brazil and Mexico with 33 and 14 species. The greatest diversity of the group is concentrated in two opposite extremes: in the north (southeast of Mexico) on the Pacific side and in the south (southwest of Brazil) on the Atlantic, both areas share similar environmental and vegetation conditions that could play an equivalent role in the group speciation. Likewise, the tropical and subtropical affinity reported in previous works for the genus is highlighted. This approach allows establishing an updated number of *Spigelia* and a better idea of its chorology. Biogeographic and phylogenetic studies could provide better ideas about the causes of the current distribution and diversity of the group.

P.0241 Exchanging vanilla genetics resources between Mexico and Cuba

Edgar López Herrerea[1], Miguel Esquivel[2]

1 Universidad Autónoma Chapingo, Texcoco, México. 2 Centro Nacional de Animales de Laboratorio, Havana, Cuba

Vanilla (*Vanilla planifolia* Andr.), is a native species from the Totonac region of the current Mexican states of Puebla and Veracruz, where this orchid evolved along with its natural pollinators. The afore mentioned is a more sophisticated species in terms of its domestication, however there are others with different degrees of evolution and management. As has been recorded, it was the Spaniards, once they made incursions into continental America, who on their return trips to the kingdom of Castile at their obligatory stopover on the largest island of the Antilles, that is, Cuba, could have dispersed it, without prejudice to the fact that native species of these orchids already existed in Cuba. According to current records, where a little more than 10 species are documented and in this the Baron Alexander von Humboldt also contributed decisively three centuries later in his expeditions throughout America and the world. Efforts were made in the past to promote the cultivation of vanilla in Cuba without success, even 100 years ago, surely the flowering of sugar cane and tobacco occupied the agricultural spectrum and this crop went unnoticed due to its complexity. A preliminary review of how Mexico and Cuba have had encounters in the past and currently around the cultivation of vanilla is carried out.

P.0242 Middle Asian mountains as the cradle of Eurasian steppe flora—why here?

Gábor Sramkó[1,2]

1 Department of Botany, University of Debrecen, Debrecen, Hungary. 2 HUN-REN–UD Conservation Biology Research Group, Debrecen, Hungary.

The Eurasian Steppe biome is one of the largest biomes in Eurasia stretching from Central-Eastern Europe through Middle to Central Asia. It can be characterised by a specialised steppe flora that has adapted to low precipitation and extreme temperatures spanning winter cold to summer heat. If we examine the phylogenetic relationships of characteristic genera of this steppe flora two noticeable shared patterns emerge: (i) the basal species often lives in Middle Asian mountains (i.e., Pamir-Alay, Tian Shan, Altai) usually above the treeline and close sister lineages also live either in high mountain or tundra environment; (ii) widely distributed steppe species, found throughout the Eurasian steppe zone, usually form crown groups and their sister species also live in Middle Asian mountains. The genera *Adonis* and *Pulsatilla* are excellent examples of this pattern, which can be seen in several other genera published in the literature (e.g., *Atraphaxis*, *Lagochilus*, *Calophaca*, *Caragana*, *Dontostemon*). Moreover, a similar biogeographic pattern manifests in steppe animal genera (e.g., *Sicista*, *Vipera*). Given the apparent universality of these patterns, we may suspect a major environmental (i.e., geo-climatological) driving force behind them. The timing of separation of the basal species in these genera dates back to around 12–8 million years ago (mya) when global cooling and large-scale aridification started in Eurasia, and the first grasslands started to spread from Central Asia (i.e., today Mongolia). We believe the basal species are the relicts of these first grasslands that were forced up to their current habitats which might be relict habitats resembling these early grasslands. As for the second group of species, these are usually relatively recent isolations and might relate to the pre-adaptive arid environment Middle Asian mountains provided at the end of the Pliocene for the current wave of grassland development from Central Asia.

S.026. BIOGEOGRAPHIC HISTORY AND ECOLOGICAL PROCESSES OF THE ASIAAUSTRALASIA FLORISTIC EXCHANGE

P.0243 Phylogenetic relationships and geographic genetic structure of Cerasus jamasakura var. chikusiensis

Yoshinobu Fukushima[1], Toshio Katsuki[2], Akiko Soejima[3]

1 Graduate School of Science and Technology, Kumamoto University, Kumamoto, Japan. 2 Kyushu Research Center, Forestry and Forest Products Research Institute, Kumamoto, Japan. 3 Department of Biological Science, Faculty of Advanced Science and Technology, Kumamoto University, Kumamoto, Japan.

Cerasus jamasakura (Rosaceae) is endemic to Japan and consists of two varieties. One of the varieties, var. *jamasakura,* is widely distributed on Honshu (Miyagi and Niigata prefectures and southwards) to Shikoku and Kyushu islands, while another varieties, var. *chikusiensis*, is distributed from southwestern Kyushu to the Tokara islands. They are distinguished by morphological characteristics such as the color of young leaves, serrations on sepals, and width of bracts of flower. A previous study based on nuclear SSR analysis did not find clear genetic differentiation between the two varieties. In this study, SNP analysis using MIG-seq (Multiplexed ISSR genotyping by sequencing) was conducted to elucidate the genetic differentiation between var. *jamasakura* and var. *chikusiensis*, and the phylogenetic relationship between them. In the phylogenetic trees, individuals from southwestern Kyushu and Satsunan Islands formed a clade (BS=96), and within that clade, individuals from the Satsunan Islands formed a subclade (BS=91). The subclade consisting of individuals from the Satsunan Islands is considered to be var. *chikusiensis*. On the other hand, genetic structure analysis showed two genetically differentiated groups in *C. jamasakura* s.l. One includes the individuals from the islands, and the another include the individuals from the mainland Kyusyu and Honsyu. It suggests that var. *chikusiensis* is derived from var. *jamasakura*. However, individuals from southwestern Kyusyu possessed mixed genetic structure of the two groups. Because the individuals located in the boundary between the two groups, it is likely that genetic exchange occurs between var. *jamasakura* and var. *chikusiensis*.

P.0244 An attempt to compare the vegetation map of Mt. Hakkoda made in the 1930s with the existing vegetation map

Tetsuya Matsui[1], Takuto Shitara[2], Hiroko Kurokawa[3], Michio Oguro3, Takehiro Sasaki[4], Haruka Ohashi[5], Kaoru Niiyama[3], Mitsue Shibata[3]

1 Center for Biodiversity and Climate Change, Forestry and Forest Products Research Institute, Forest Research and Management Organization, Tsukuba, Ibaraki, Japan. 2 Tama Science Forest Garden, Forestry and Forest Products Research Institute, Forest Research and Management Organization, Hachioji, Tokyo, Japan. 3 Department of Forest Vegetation, Forestry and Forest Products Research Institute, Forest Research and Management Organization, Tsukuba, Ibaraki, Japan. 4 Graduate School of Environment and Information Sciences, Yokohama National University, Yokohama, Japan. 5 Department of Wildlife Management, Forestry and Forest Products Research Institute, Forest Research and Management Organization, Tsukuba, Ibaraki, Japan.

A set of vegetation survey data from the early 1930s in the Towada-Hakkoda region of Aomori Prefecture, northern Japan, was discovered in a warehouse of the Forestry and Forest Products Research Institute. By digitizing these documents and comparing them with the current situation, the authors attempt to determine how the vegetation in the area has changed over the past 90 years, and what the characteristics and factors has changed. In this presentation, the authors focus on the vegetation map and compare it with the vegetation maps (1/50,000 and 1/25,000) of the Ministry of Environment in GIS. The vegetation maps were georeferenced and converted to polygon format for GIS analysis. As a result, the *Abies mariesii* community decreased by about 50 % and was replaced either by *Fagus crenata* community and pseudo-alpine vegetation. The *Fagus* community increased by about 1.5 times and the *Quercus crispula* community decreased by about 60%. In the valley near the village, in the vicinity of the coppice forests and the forest roads, the *Fagus*, *Quercus* and *Betula* communities have been replaced by *Cryptomeria japonica* plantations. The factors that may have caused these vegetation changes include vegetation succession due to the cessation of coppice forest use and afforestation during the post-war afforestation expansion period.

P.0245 Taxonomy, biogeography, and sectional boundaries of the tropical blueberries (Vaccinieae, Ericaceae) of Malesia

Maverick N. Tamayo[1], Wendy A. Mustaqim[2], John D. Horner[1], Matthew C. Hale[1], Peter W. Fritsch[3]

1 Department of Biology, College of Science and Engineering, Texas Christian University, Fort Worth, USA. 2 Program Studi Biologi, Fakultas Teknik, Universitas Samudra, Langsa, Indonesia. 3 Botanical Research Institute of Texas, Fort Worth, USA.

The tribe Vaccinieae (Ericaceae) is a large group of more than 1000 species mostly found in the tropics, and a third of which are found in Malesia. *Vaccinium* is the largest genus of Vaccinieae in Malesia, comprising ca. 250 species, more than half of which are endemic to the island of New Guinea. Malesian species of *Vaccinium* are mainly adapted to high-elevation zones, exposed mountain ridges and peaks, montane mossy rain forests, nutrient poor habitats, and rarely littoral areas. They are often rare in the wild; hence, few studies on its taxonomy have been conducted in Malesia. A revision was included in the account for Ericaceae in the *Flora Malesiana*. However, limited specimen availability and utilization of ambiguous and poorly defined morphological characters hindered resolution of many species complexes. Moreover, sectional boundaries of Malesian *Vaccinium* are poorly defined, and the morphological characters overlap with those of other sections, thus limiting their utility. Furthermore, a comprehensive phylogeny for the Malesian *Vaccinium* is lacking. A preliminary phylogenetic analysis of Ericaceae reveals that *Vaccinium* is non-monophyletic, with the genera *Agapetes*and *Rigiolepis* nested within it. We present recent findings from field and herbarium work helping to clarify the systematics and evolution of Malesian Vaccinieae. A taxonomic revision of Philippine *Vaccinium* has resulted in the discovery of 11 new species, three new island records, rediscoveries, and clarification of species complexes. In Indonesia, we have discovered a new species and a variety of *Vaccinium*, including three new species of *Rigiolepis*. We provide assessment of the morphological basis for the sectional boundaries of Malesian *Vaccinium* in the context of ongoing molecular analysis. The biogeography, distribution, and morphological distinctions among *Agapetes*, *Rigiolepis*, and *Vaccinium* will be discussed.

P.0246 Geographical distribution and conservation strategy of national key protected wild plants of China

Chao Ye [1,2,3], Huiyuan Liu [1,3], Haining Qin [1,3], Jiangping Shu [4 5], Zhihua Zhou [4,] Xiaohua Jin[1,3]

1 State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing, China. 2 University of Chinese Academy of Sciences, Beijing, China. 3 China National Botanical Garden, Beijing. China 4 National Forestry and Grassland Administration, No. 18, Hepingli Dongjie, Beijing, China. 5 Key Laboratory of National Forestry and Grassland Administration for Orchid Conservation and Utilization, The Orchid Conservation and Research Centre of Shenzhen, Shenzhen, China.

National key protected wild plants (NKPWPs) are considered flagship species for plant diversity conservation in China. Using data for 1,101 species, we characterized NKPWPs distribution patterns in China and assessed conservation effectiveness and conservation gaps. In total, 4,880 grid cells at a 20 × 20 km resolution were filled with occurrence records for NKPWPs. We identified 444 hotspot grid cells and 27 diversity hotspot regions, containing 92.37% of NKPWPs. However, 43.24% of these hotspot grid cells were fully or partially covered by national nature reserves (NNRs), where 70.21% of species were distributed. Approximately 61.49% of the NKPWPs species were protected by NNRs, but the populations or habitats of 963 species were partially or fully outside of NNRs. With global warming, the overall change in the extent of suitable habitats for NKPWPs is expected to be smaller, however, habitat quality in some areas with a high habitat suitability index will decrease.

S.027. BIOGEOGRAPHY AND DIVERSIFICATION OF INTERCONTINENTAL TROPICAL PLANT DIVERSITY.

P.0247 The evolutionary significance of plant architecture: adapting the structure to overcome environmental constraints

Artémis Anest1

1 AMAP, Univ Montpellier, CIRAD, CNRS, INRAE, IRD, Montpellier, France.

Environmental factors vary across biomes worldwide, shaping different vegetation types. In response to the varied effects of these factors, plants have evolved contrasted architectures adapted to the most constraining factors for growth and survival. While the influence of plant structure on ecological performance is recognised, its role in plant evolution remains relatively unexplored. Plant architecture, an integrative approach to describing plant structure, contains valuable information for understanding the evolution of plant forms shaped by main environmental factors over time. My research aims to enhance our understanding of the relationship between plant form and environmental factors throughout the plant evolutionary history by investigating the evolution of plant architecture under diverse climatic constraints and disturbances. Here, I will present a framework that categorises plant traits into distinct evolutionary groups. These groups include: 1) developmental constraints, comprising traits that are useful for taxonomy; 2) convergences, focusing on traits related to ecology; and 3) key confluences, which involve traits that are valuable for studying evolutionary ecology. Using this framework through two examples, I will illustrate how plants have developed contrasted architectures in response to different environmental constraints: Climatic constraints, particularly drought and frost, have selected for specific morphologies in the large genus Euphorbia. Conversely, in stable tropical climates, the ecologically dominant family Combretaceae exemplifies how specific structural traits have evolved to defend against large mammal herbivores.

P.0248 Drift in the tropics: Phylogenetics and biogeographical patterns in Combretaceae

Olivier Maurin[1], Artémis Anest[2,3,4], Félix Forest[1], Ian Turner[5,6], Russell L. Barrett[7], Robyn C. Cowan[1], Lijia Wang[8], Kyle W. Tomlinson[2,9], Tristan Charles-Dominique[4,10]

1 Royal Botanic Gardens, Kew, Richmond, UK. 2 Center for Integrative Conservation, Yunnan Key Laboratory for Conservation of Tropical Rainforests and Asian Elephants, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Menglun, Yunnan, China. 3 University of Chinese Academy of Sciences, Beijing, China. 4 AMAP, Univ Montpellier, Montpellier, France. 5 Singapore Botanic Gardens, National Parks Board, Singapore, Singapore. 6 Singapore Botanical Liaison Officer, Royal Botanic Gardens, Kew, Richmond, UK. 7 National Herbarium of New South Wales, Australian Botanic Garden, Mount Annan, New South Wales, Australia. 8 University of Michigan School of Public Health, Ann Arbor, USA. 9 Center of Conservation Biology, Core Botanical Gardens, Mengla, Menglun, Yunnan, China. 10 Centre National de la Recherche Scientifique (CNRS), Sorbonne University, Paris, France.

Certain plant clades are distributed across every continent, occupying various contrasting biomes. Within these globally distributed clades, the ecologically dominant Combretaceae family shows intercontinental disjunctions. Fruit morphology in Combretaceae suggests various seed dispersal modes, potentially explaining the observed geographical patterns. To enhance our understanding of the mechanisms that have facilitated such distribution, this study explores the dispersal strategies of the Combretaceae family, the acquisition of new modes throughout their evolutionary history, and their impact on present and past plant biogeography. The study integrates data on natural distribution, biomes, and dispersal types into comparative phylogenetic analyses.Estimates of the ancestral distribution of Combretaceae suggest a Gondwanan origin for this family, with minimal transitions between different biomes. Our findings indicate that drift fruits, dispersing seeds by water, played a critical role in colonising new continental lands. Conversely, biome shifts appear unaffected by dispersal strategies. The study highlights a dispersal mode paradox, wherein specialised modes of seed dispersal can facilitate intercontinental dispersal but limit colonisation of new biomes and strengthen biome conservatism. Our study emphasises the implications for species preservation in changing environments and the importance of understanding the relationship between plant distribution and dispersal modes for effective conservation efforts.

P.0249 Development of KASP markers for identification of Pueraria candollei var. mirifica

Sun Hee Lee[1], Boreum Park[1], Hyung-il Kim[1], Kyung-Hun Son[1]

1 Center for Advanced Analysis, National Institute of Food and Drug Safety Evaluation, Ministry of Food and Drug Safety, Cheongju, Korea.

Pueraria candollei var. mirifica has been used in Thailand conventional medicine for rejuvenation. P. mirifica products are growing worldwide for breast enlargement, menopausal symptoms and functional foods for woman. It is important to use pure phytoestrogen herbs to derive the safety and efficacy of herbal medicine. However, the identification of these herbs by conventional taxonomic methods is difficult. Recently, many studies have applied these DNA barcoding for the identification of herbal medicinal species using standard DNA markers. In this study, we developed three KASP markers to determine whether P. mirifica contain in the P. mirifica products. KASP genotyping assays are based on the reading of the terminal fluorescence signal, and genotypes can be identified by universal fluorescence primer amplification. To develop KASP-SNP markers, we selected three SNPs specific to P. mirifica on ITS2 and psbA-trnH intergenic space region. In the result, the targeted plants and products were clustered into FAM-positive section, non-targeted plants were clustered either HEX-positive or negative section. Analysis using three KASP markers on eight foods advertising the effect of enlarging the breast confirmed that six products showed FAM fluorescence and contained P. mirifica. Therefore, we have developed KASP assay that allow rapid and easy P. mirifica identification using three KASP markers. And it was possible to confirm the content of P. mirifica in the food, and it will be possible to manage the illegal distribution of prohibited food materials.

P.0250 Taxonomic diversity, phylogeny, and ecological evolution of neotropical Prunus (Rosaceae)

Jorge Andrés Pérez Zabala[1]

1 Facultad de Ciencias, Universidad Nacional de Colombia, sede Medellín. Medellín, Colombia.

Prunus L., is a well-known genus including several economic important fruit crops (e.g. cherries), that extends across a wide ecological spectrum with many species tolerant to seasonality of water availability (by dryness or freeze) or adapted to extreme conditions as deserts or high elevation mountains.The occurrence and diversity of *Prunus* outside of North America and Eurasia is generally underestimated and the Neotropics is the region with the most outdated taxonomic knowledge (Koehne, 1915) and less represented in phylogenetic studies. In this work, the diversity of Neotropical *Prunus* was extensively revised, molecular phylogenetic analyses with improved sampling of tropical members were performed and ecological (climate niche) evolution examined. The study of around 5000 collections of the Neotropics resulted in the recognition of 257 evergreen racemose taxa (238 species), 97 of which were accepted from legitimate published basionyms and 160 (including 14 infraspecific taxa) were identified as novelties. Consequently, the once considered typical temperate taxon, now accounts its highest diversity in the tropics and particularly in the New World side. Phylogenetic Bayesian analysis of the genus (126 species including 41 neotropical) suggests its splitting in two main clades similarly to previous studies: one with mostly deciduous species with solitary flower, corymbs, or racemes, and some evergreen racemose but pubescent; and the other with evergreen species, glabrous and racemose (and mostly tropical). Neotropical species were recovered as polyphyletic with two small groups in the first deciduous main clade and most of them into a single clade within the evergreen racemose main clade. Ecological evolution of hydraulic niche (in terms of aridity index) was significantly correlated with the phylogeny and main monophyletic groups have an identifiable range of hydraulic tolerance. Finally, some of the current geographic wide spread of the genus seems to be favored by retention of tolerance to water stress.

P.0251 Diversity of terrestrial Chlorophyta in the Universitas Gadjah Mada Campus, Karanggayam, and Sawitsari Research Stations

Dita Rahmadani[1], Faiq Iqbal Majid[1], Juntria Ramadhani Khasanah[1], Nouva Yudha Perdana Yasir[1], Ludmilla Fitri Untari[1]

1 Laboratory of Plant Systematics, Faculty of Biologi, Universitas Gadjah Mada, Teknika Selatan Street, Sinduadi, Mlati, Sleman, Yogyakarta, Indonesia.

Algae can be found in various habitats, including terrestrial ones. Chlorophyta are algae often found as the main constituents of terrestrial algae populations. Molecular data also explains that the diversity of terrestrial algae is much higher than the others. However, several problems in the study of terrestrial algae make research on terrestrial green algae challenging to carry out. As a result, data regarding terrestrial green algae and its species diversity is challenging to find, especially in Indonesia. In Indonesia, more research on the diversity of terrestrial Chlorophyta species still needs to be done. Therefore, this research was conducted to determine the diversity of terrestrial Chlorophyta species in Indonesia, especially in the Universitas Gadjah Mada Campus Environment, Sawitsari, and Karanggayam Research Stations. This research was conducted in January-July for sampling at several locations and data analysis. At the time of sampling, measurements of the physicochemical parameters of the growth environment were also carried out. The algae samples were analyzed under a microscope, and then their morphology was compared with several related books and journals. Diversity and Evenness Index and Importance Values were calculated using Microsoft Excel software and presented in tabular form. Twenty-one species grouped into eleven families were reported here and the environmental factors such as temperature, humidity, wind velocity, and light intensity affect the growth and density of terrestrial algae. However, each type of terrestrial algae has different tolerances to these environmental factors.

S.028. BIOLOGICAL DIVERSITY HIDDEN IN EARLY TERRESTRIAL SITES OF EXCEPTIONAL PRESERVATION

P.0252 The Late Holocene subfossil forest in Altos de la Morcuera (Madrid, Spain)

Mar Génova[1], Jose Mª Postigo-Mijarra[2], Salvia García-Álvarez[1], Ignacio García-Amorena[1]

1 Department of Natural Resources and Systems, Technical University of Madrid, Madrid, Spain. 2 Department of Biodiversity, Ecology and Evolution, Faculty of Biological Sciences, Complutense University of Madrid, Spain.

The discovery of a large number of macrofossils in the Altos de La Morcuera (Madrid, Spain), located between 1660 and 1760 m a.s.l., represents to date one of the largest local assemblages of Holocene woody remains in the Iberian Central System and the Iberian Peninsula as a whole. In this area, three nearby sites were sampled: Raso de los Toros (the most extensive and richest in remains), Peña Morcuera (peat bog), and Los Tres Mojones. At these sites, samples of almost 60 woody remains were recovered and identified, mainly trunks of different sizes and stumps in a living position. In total, nineteen samples from different types of remains were radiocarbon-dated, yielding a range of ages between 3960 and 2350 cal yr BP. The information obtained from the identification and dating of the remains proves the local presence of an extensive natural pine forest of *Pinus* gr. *sylvestris* in the area, being the first time that the Late Holocene presence of this taxon has been confirmed in the Sierra de Guadarrama through the study of macrofossils. Indeed, the high spatial and temporal concentration of trunks and stumps provided an exceptional opportunity to obtain new data about the environmental conditions occurring during the living period of these trees. Dendrochronological studies were therefore carried out to complete the palaeoecological information of the area studied.

P.0253 Studies of macroremains in the Iberian Central System

Mar Génova[1], Jose Mª Postigo-Mijarra[2], Salvia García-Álvarez[1], Ignacio García-Amorena[1], Carlos Morla[1]

1 Department of Natural Resources and Systems, Technical University of Madrid, Madrid, Spain. 2 Department of Biodiversity, Ecology and Evolution, Faculty of Biological Sciences, Complutense University of Madrid, Madrid, Spain.

The Iberian Central System presents high interest from the point of view of vegetation dynamics, being an area in which numerous palaeobotanical and archaeological studies have been carried out. Palaeoecological studies based on macroremains take on special relevance due to their high degree of taphonomic autochthony, they can provide very precise information on the taxa and plant communities at a regional and local scale. The potentiality of macroremains to detail the taxonomic range, besides establishing a more precise location of the different types of vegetation, has allowed partially to resolve important doubts about the persistence, extension, and composition of some of the forests and other plant communities that were distributed throughout the Central System during the Holocene. We compile all the knowing studies with spatial and temporal information that analyse the macroremains in this territory. We also present graphic information and provide specific data on the location and characteristics of the macroremains sites, from those located in the Serra da Estrela (the westernmost area of the Central System range) to those located in the Sierra de Ayllón, in the most northeastern area. In each site, we have placed special emphasis on collecting and contrasting taxonomic and chronological information. In this way, we try to help to understand the characteristics and changes of the vegetation that have occurred during the Holocene, outlined with the greatest possible chronological precision, which has led to the current landscape of the Central System range. We also try to help in the process of identifying what issues are more crucial to take the most appropriate measures for the management of the territory.

P.0254 Multidisciplinary research of the cryptogamic diversity in Chile's southernmost natural laboratory

Sánchez-Jardón L.[1,2], Mackenzie R.[1,2,3], Oyarzún Contreras L.[4], Zambrano S.[1,2], Ojeda Vásquez F.[1], McCool M[5], Lemas M.[6]

1 Universidad de Magallanes, Punta Arenas, Chile. 2 Cape Horn International Center, Puerto Williams, Chile. 3 Millenium Institute Biodiversity of Antarctic and Sub-Antarctic Ecosystems, Santiago, Chile. 4 Universidad Austral de Chile, Valdivia, Chile. 5 Life Sciences Building, University of Louisville. Louisville, Kentucky, USA. 6 Tenencia Caleta 2 de mayo, Carabineros de Chile, Chile.

The Magallanes sub-Antarctic ecoregion has a unique biodiversity, with ecological singularities, among which the cryptogamic diversity of its forests and peatlands stands out. Sub-Antarctic bryophytes, lichens and fungi form a fundamental part of these terrestrial ecosystems, yet they are still poorly known. This affects the ability to make decisions for the management and conservation of protected wild areas, which is highly relevant in a remote region like Magallanes, with more than half of its territory under some category of conservation. With the general objective of contributing to the knowledge of the diversity of sub-Antarctic bryophytes, lichens and fungi, a study will begin to strengthen previous initiatives, such as the "Herbarium of Subantarctic Cryptogams" of the Cape Horn International Center in collaboration with researchers from the Universidad de Magallanes. So far, this herbarium houses collections of macroalgae, bryophytes, lichens and fungi and allows maintaining scientific information about the biodiversity of these organisms in the sub-Antarctic ecoregion of Chile, to support the generation of knowledge on biodiversity and the understanding of global climate change. To this end, field exploration of the diversity of bryophytes, lichens and fungi will be carried out through systematic sampling to record observations and biological collections. The study is framed within the framework of the Cape Horn International Center and will be developed in different locations, including Cape Horn National Park and Yendegaia National Park from January 2024 to January 2025 and is supported by the National Forest Service (CONAF).

S.030. BOTANICAL CONTRIBUTIONS FROM THE BIODIVERSITY HERITAGE LIBRARY

P.0255 Notes on Indian Purslane (Portulaca L., Portulacaceae)

Jagdish Dalavi[1], Varsha Jadhav[2*], Shrirang R. Yadav[2]

1 Botanical Survey of India, Western Regional Centre, Pune, India. 2 Department of Botany, Shivaji University, Kolhapur, India.

Portulacaceae Juss. or Purslane family is monogeneric family with only genus *Portulaca* L. having 152 species worldwide. In India it is represented by 11 taxa (10 species and 1 variety) of which two are endemic. Morphologically two species are opposite leaved *i.e., Portulaca quadrifida* L. and *P. wightiana,* eight taxa are having linear, terete and whorled leaves *i.e. P. badamica, P. grandiflora, P. lakshminarasimhaniana, P. pilosa, P. suffruticosa* and *P. tuberosa* and third group is having obovate to ovate flat leaves *P. oleracea, P. oleracea* var. *linearifolia* and *P. umbraticola. P. oleracea, P. Pilosa* and *P. tuberosa* are highly polymorphic in India. Most of the species are annual and adapted for the arid ecosystem, whereas *P. oleracea* and *P. pilosa* are growing as weed in open fields and farms of variable environments. *P. suffruticosa* and *P. pilosa* are perennial species due to presence of tuberous or fascicled roots, rarely *P. wightiana* also shows such type of roots. *P. grandiflora* and *P. umbraticola* are cultivated species and are rarely escaped in forest areas. Roots, Leaves, Flower, Stigma and Seeds are the characters of taxonomic importance to delimit the species. The micromorphology of Portulaca seeds is also useful for taxonomic classification. The accounting of Indian Portulaca species for their taxonomy, distribution, and phenology, as well as comprehension the relationships between the taxa through molecular taxonomy and seed micromorphology, are the topics of this communication. The variety, variance, and relationships among Indian Purslane will be made clear by this work.

P.0257 Essential oils composition of Calocedrus decurrens (Torr.) Florin according to its growth and development state in Madrid (Spain)

Jesús Palá-Paúl[1], Diego Martín-Resco[1], Manuela Bravo-Castaño[1], Rubén Abad-Calderón[2,*]

*1 Dpto. Biodiversidad Ecología y Evolución, Facultad de Ciencias Biológicas, Universidad Complutense de Madrid, Madrid, Spain. Quibey@bio.ucm.es 2 Dpto. de Química en Ciencias Farmacéuticas. Unidad Docente de Edafología, Facultad de Farmacia, Universidad Complutense de Madrid, Madrid, Spain, *rubabad@ucm.es.*

Calocedrus decurrens (=*Libocedrus decurrens* Torr.), also known as bastard cedar, California incense cedar, California post cedar, incense cedar, or white cedar, belongs to the *Cupressaceae* family that comprise trees to 57 m, trunk to 3.6 m diameter, bark cinnamon brown, fibrous, furrowed and ridged. It is native from North America whose distribution is limited to the American mountain ranges, from northern Oregon to Baja California. Although it is widely used as an ornamental in parks and gardens in temperate zones around the world, it is considered as an inventory of alien invasive species in Europe. The “Parque del Oeste” one of the numerous parks of Madrid, present 32 plants of this species. The height and diameter of each were measured and arranged into three categories: big, medium and small. The young stems and leaves (<3mm) of two samples of each one were gathered. All the samples were air-dried before the oil extraction by hydro-distillation. The essential oils were analysed by gas chromatography (GC) and gas chromatography coupled with mass spectrometry (GC-MS). The oil yield of the samples varied from 0.28% to 0.77%. It is worth nothing that a significant correlation was detected between the oil yield with the height and diameter of the plant studied (p=P.094 y p=P.038 respectively) at 95% confidence level. The essential oils analysed showed qualitative and quantitative differences between the samples studied. The monoterpene was the predominant fraction of the oil. The main compound was identified as delta-3-carene, limonene and alpha-pinene. According to our results, the youngest plants (with low height and diameter) seem to produce higher amount of essential oil. This could be because they are metabolically more active or because the oils play an important role as repellent or biocides compounds in this growth and development state.

P.0258 Interactions of people and plants in Dominican Republic

Omar P. Perdomo[1]

[1] Escuela de Biología Facultad de Ciencias Universidad Autónoma de Santo Domingo, Santo Domingo, Dominican Republic.

Ethnobotany as a discipline oriented to understand what people know about plants, how plants are part of their belief structures, use, management and the influence of plants in social and cultural life. In the Caribbean region it has received a remarkable development in recent years. The objective of this research is to provide an overview of the historical use of ethnobotany in the Dominican Republic from pre-Columbian times to the modern emergence of ethnobotany as a field of research and to link the discipline with other disciplines such as anthropology, archaeology, ecology and evolutionary biology. We have relied on a literature review, participant observation, interviews and information from years of field trips by the author. The main species used as forest products, utensils, dyes obtained from plants, genetic improvement, plants used in food, endangered species, pharmacopoeia, urban botany, and religiosity are identified. Ecological information is offered on important problems such as human influence on the distribution and abundance of flora in the country and the importance of plants for the Dominican people is discussed in order to establish socioecological visions through transdisciplinary approaches and analyze practical problems in the context of the associated insular environmental crisis.

S.031. BRYOPHYTE DIVERSITY, ENVIRONMENT AND CONSERVATION IN MEDITERRANEAN CLIMATE AREAS

P.0259 List of Bryophytes located in Badajoz: new identified taxes and mechanism for surviving in Mediterranean environments

Naomi Campos-Palacios[1], Josefa López Martínez[1], Francisco J. Valtueña Sánchez[1]

[1] Botany Area - Department of Plant Biology, Ecology and Earth Sciences, Faculty of Science, University of Extremadura, Badajoz, Spain.

Bryophytes were the first organisms to colonize the terrestrial environment, for this reason they developed mechanisms that favored their adaptation to land and as a result, they are now found in practically all existing terrestrial environments. Bryophytes are divided into large groups; hornworts, liverworts and mosses all sharing similarities in terms of life cycle, which is digenetic and gametophyte dominant. The presence of these organisms in their niches is of the utmost importance, since their qualities allow the growth of the rest of the flora and help maintain optimum levels of humidity, among other functions. The main aim of this work was to inventory the biodiversity of bryophytes in Badajoz, where only one previous study by Benitez & Alvarez considering only the urban center. Different areas urban center and the peri-urban were sampled, and the individuals collected were identified with its correspondence identification card. As a result, the obtained list includes three taxa in *Atlas y Libro Rojo de los Briófitos Amenazados de España*, and another two taxa were identified in Badajoz for the first time. The number of species collected in the same area that the previous study was lower, probably due to changes in green areas and/or an increase in air pollution. All genera found in the urban center presented similarities in terms of adaptative mechanisms for living in anthropogenic environments and for surviving in Mediterranean environments. Nevertheless, the lack of previous information regarding the study area does not allow knowing if there has been alteration over time in the bryophytes present in Badajoz consequence of the city development, therefore, further study is required to complete the current investigation and adequately inventory the bryoflora.

P.0260 Effect of canopy damage in Quercus ilex due to the storm Juliette on three epiphytic mosses

Pere M. Mir-Rosselló[1], Antoni J. Far[1], Marcello Dante Cerrato[1], Lluís Salom-Vicens[1], Carles Cardona[1,2], Marc Carriquí[1], Maria José Clemente-Moreno[1], Jaume Flexas[1], Llorenç Sáez[3], Llorenç Gil[1]

1 Universitat de les Illes Balears, Palma, Spain. 2 Centre Forestal de les Illes Balears, Escorca, Spain. 3 Universitat Autònoma de Barcelona, Barcelona, Spain.

Epiphytes depend on the microclimatic conditions generated by their phorophytes (illumination, temperature, humidity, etc.). Climate change is expected to increase extreme climatic events in the Mediterranean Basin, such as drought, heat waves or intense storms and hurricanes. Intense storms can physically damage trees, affecting their canopy or even killing them. This can affect epiphytes due to their sudden exposure to harsher conditions. During February 2023, the squall Juliette heavily affected many *Quercus ilex* forests in Mallorca. In this study, we aimed to evaluate the effect of *Q. ilex* canopy damage due to Juliette on three epiphytic mosses (*Leucodon sciuroides*, *Leptodon smithii* and *Homalothecium sericeum*). Treatments consisted in 1) plants still covered from unaffected trees, 2) plants previously uncovered from unaffected trees, and 3) plants exposed after their phorophyte was affected (canopy damage) by Juliette. Light availability in all three treatments was first characterized with a PAR sensor. Chlorophyll fluorescence (Fv/Fm), oxidative stress biomarkers and mortality rates were monitored in each species during April and December 2023. Fv/Fm decreased in newly exposed plants of *L. sciuroides* and *H. sericeum*, and did not significantly change in *L. smithii*. Surprisingly, mortality rates remained relatively low in all three species, and remaining zero in many samples. Our results suggest that, although being physiologically affected, the three selected species showed a certain degree of resistance to sudden environmental exposure due to canopy damage in their phorophyte. Although these mosses have shown a notorious survival capacity, further studies should be conducted to better assess the presented problem in other epiphytes such as liverworts or lichens, and how epiphytic communities will change after canopy damage.

P.0261 Study of the altitudinal variation of the chlorophyll fluorescence in some common moss species in central Iberian Peninsula

Sofía Carmona Bellón[1], Belén Estébanez Pérez[1], Patricia Haro González[1]

1 Universidad Autónoma de Madrid, Madrid, Spain.

Nowadays, our climate is changing rapidly, affecting to all ecosystem levels, boosting the study of organism responses to these environmental factors. Mosses, especially vulnerable to these changes, have different mechanisms of adaptation to the environmental conditions and the studies of these mechanisms are increasing. In this research, we delve into the impacts of altitudinal gradient of the mountain slope, as a proxy of variations in diverse temperature, irradiation, and humidity on the health status of mosses. We gathered samples of Hypnum cupressiforme, Syntrichia ruralis, Grimmia pulvinata, and Homalothecium aureum at various altitudes along Sierra de Guadarrama. Our preliminary investigation examined the effects of seasonality and orientation on the photosynthetic efficiency of the mosses. The mosses' condition was evaluated through both macroscopic and microscopic analyses and by measuring the chlorophyll fluorescence of fresh samples almost immediately, leaving them some hours to acclimatize them to laboratory conditions, and dark-adapting them for at least 30 minutes before fluorometric measurements. We found the measurement of chlorophyll fluorescence as the most reliable method for studying the health status of these mosses. This method revealed 1) the influence of different orientations, and 2) a clear effect of seasonality: even considering interspecific variations: in spring the status of the mosses is better at higher altitudes, probably due to higher humidity. Irradiation emerged as a positive factor for the moss health, with temperature maintaining opti-

mal conditions and avoiding extremes. However, during winter conditions, we observed a contrary trend, possibly due to cryptobiosis triggered by low temperatures. The use of chlorophyl fluorescence proves to be a simple, economic, and reliable method to study the effects of different environmental factors on mosses.

P.0262 Effects of radon radioactivity on bryophyte communities: a case study of a natural spring in Valdemorillo, Madrid.

Belén Estébanez Pérez[1], Sofía Carmona Bellón[1]

1 Universidad Autónoma de Madrid, Madrid, Spain.

Exposure to radioactivity poses significant health risks, with radon, a radioactive decay product of uranium naturally present in rocks and soils, serving as the primary pathway for human exposure to ionizing radiation. There are few studies on the effects of radon on wild species in their natural habitats, especially of bryophytes, despite their wide usage in biomonitoring many different pollutants, as they often respond quickly and distinctly to environmental changes. In Spain, there are several regions heavily affected by radon, due to their richness in granite, schists, and slate stone, often associated to radon emissions. These regions include some areas in the Sierra de Guadarrama, particularly Valdemorillo, a municipality in the mid-slope zone of the mountain range. One notable location there is Manantial de los Barrancos, a natural spring classified as mineral-medicinal water due to its exceptionally high radon content (3,000 Bq/m³). We have studied the effects of these high radon emissions on the communities of bryophytes: coverage, species composition, development, and reproductive ability, based on their distance to the spring and on-site radioactivity measurements. We have found that in the first 50 cm close to the source of the spring, with highest levels of radioactivity, there are hardly any bryophytes, and, when present, their level of development is suboptimal, since the majority of the specimens are sterile or undersized. However, even in close proximity to the affected area, the measured radioactivity drops significantly, and the bryophyte communities exhibit greater diversity, higher coverage, and appear healthy and normal, suggesting that the radon effects are localized to a very small area next to the emission focus. We conducted direct irrigation experiments to assess the effects of radiation on different local species. Nonetheless, we did not observe any significant short-term effects, indicating that radiation may induce chronic damage to bryophytes

P.0263 Functional landscape genomics: insights into moss heat stress adaptation and ecological distribution

Mahmoud Magdy[1,2], Olaf Werner[1], Rosa M. Ros[1]

1 Department of Plant Biology, Faculty of Biology, Murcia University, Murcia, Spain. 2 Department of Genetics, Faculty of Agriculture, Ain Shams University, Cairo, Egypt.

Functional landscape genomics in plants investigates the genetic basis of ecological adaptations by integrating high-throughput genomic data with environmental information. This interdisciplinary approach sheds light on how organisms respond and adapt to diverse habitats. Despite extensive studies in various animal and plant species, in bryophytes, the functional characterization of BTB/POZ transcriptional gene regulators during heat stress has remained unexplored. This study conducted a comprehensive genome-wide analysis to characterize BTB/POZ genes in Funaria hygrometrica moss, a representative bryophyte. The research comprised two phases. In the first phase, dry-lab analyses were employed to assemble and identify BTB/POZ genes de novo from DNAseq data. This analysis unveiled a repertoire of five BTB/POZ genes in the F. hygrometrica genome and shed light on their evolutionary relationships with BTB/POZ genes from various plant lineages. Furthermore, examining gene structures, conserved motifs, and predicted protein properties provided valuable insights into their molecular attributes. Subsequently, in phase two, the study delved into the landscape distribution of F. hygrometrica populations in the Sierra Nevada Mountains of Spain. RNAseq expression patterns and rnaSNPs of the identified BTB/POZ genes were scrutinized in correlation with the population's geographic distribution. Notably, variable rnaSNPs exhibited a consistent presence among genotypes found in warmer zones, contrasting with those from colder ones. This integrative approach enhances our understanding of the adaptive molecular mechanisms in plants, particularly, the heat stress adaptation in bryophytes. Understanding moss molecular adaptive mechanisms to climate change and landscape distribution through the role of BTB/POZ genes as a biomarker to heat stress, is crucial for predicting moss distribution shifts and informing conservation strategies amid ongoing environmental changes. Notably, this study reports for the first time, the characterization and functional regulation of the BTB/POZ gene family expression under heat stress, at least in bryophytes, and has never been associated with geographic distribution.

P.0264 Petalophyllum ralfsii in the Balearic Islands: An example of why we should consider islands separately for conservation purposes

Pere M. Mir-Rosselló[1], Iván Cortés-Fernández[1], Llorenç Sáez[2], Marcello Dante Cerrato[1], Arnau Ribas-Serra[1], Carles V. Cardona[1,3], Maria Roselló-Salvadó[1], Toni J. Far[1], Lluís Salom-Vicens[1], Llorenç Gil[1]

1 Universitat de les Illes Balears, Palma de Mallorca, Spain. 2 Universitat Autònoma de Barcelona, Barcelona, Spain. 3 Centre Forestal de les Illes Balears, Escorca, Spain.

Petalophyllum ralfsii is a thalloid liverwort considered to be declining throughout Europe, leading to its inclusion in numerous Red Lists. for which it is included in many Red Lists. In mainland Spain, its occurrences are limited to very few localities. Conversely, within the Balearic Islands its presence is known from 19 localities, for which it is classified as a Nearly Threatened species. After three years of survey, we present 17 new localities in the Balearic Islands. We contrasted the chorological data with topographical, geological and soil use data to make an approach to the ecology of the species. The currently known distribution of *P. ralfsii* extends to 26 % of the 10 km x 10 km UTM squares of the Islands. It shows preference for flat, low soils near the coast, but some populations can be found in inner areas, kilometres away from the coast. It mainly inhabits calcareous and sandy soils, yet it demonstrates adaptability across various other soil types. Regarding soil use, it shows preference for open meadows, but can also be found in woodlands and coastal areas. A remarkable result is the fact that all the localities are in or near some kind of anthropogenic infrastructure (urban areas, roadsides, gardens, etc.) or crop. These data suggest that *P. ralfsii* shows a certain degree of ruderal behaviour in the Balearic Islands, where it would be in optimal conditions. Overall, our data support *P. ralfsii* being a mainly insular and coastal species, as reported in other regions in Europe. This study also supports that 1) bryophytes on the Balearic Islands are still understudied, 2) accurate chorological and ecological work is needed to correctly assess the conservation status of bryophytes, and 3) conservation status for bryophyte species requires distinct considerations between island and mainland environments.

P.0265 Characterization of cryptogamic communities of the coastal dune systems of the Balearic Islands

Pere M. Mir-Rosselló[1], Iván Cortés-Fernández[1], Marcello Dante Cerrato[1], Carles Cardona[1,2], Dessiré Sicilia[1], Llorenç Sáez[3], Lluís Salom-Vicens[1], Llorenç Gil[1]

1 Universitat de les Illes Balears, Palma, Spain. 2 Centre Forestal de les Illes Balears, Escorca, Spain. 3 Universitat Autònoma de Barcelona, Barcelona, Spain.

Plants in coastal dune systems are affected by many abiotic factors, such as salt spray, wind and soil mobility. As a result, dune vegetation develops in bands parallel to the sea. Although being ecologically relevant in these ecosystems, cryptogams (bryophytes and lichens) have been poorly studied in Mediterranean coastal dunes. In this study, we aim to characterize the cryptogamic communities of the dune systems of the Balearic Islands and the ecological factors determining them. Four dune systems were surveyed in Mallorca (2) and Menorca (2). In each location, at least three random plots per vegetation band were conducted; species richness and coverage, soil conductivity, soil organic matter, distance to the sea and to the nearest pathway, and the corresponding vegetation band were analysed. We catalogued 33 species of cryptogams (21 bryophytes and 12 lichens), being the moss *Tortella flavovirens* the most common species at all locations. Species richness and coverage increased with distance to sea and decreased with soil conductivity. Bryophytes and lichens distributed zonally, similarly to tracheophytes, being acrocarpous mosses the only ones inhabiting mobile dunes, followed by crustose lichens. Pleurocarpous mosses, liverworts, foliose and fruticulose lichens were exclusive of very stabilized dunes. A rare case of pleurocarpous mosses in mobile dunes is reported in Menorca. *Petalophyllum ralfsii*, a Nearly Threatened liverwort, was found during the survey. Moreover, at least 6 moss species are cited in dunes for the first time in the Balearic Islands. Our data suggests that cryptogams form an important part of dune ecosystems, where their ecology resembles that from tracheophytes. Moreover, dune systems may be key for cryptogam conservation in the Mediterranean Basin. This experiment will be extended to 10 dune systems from the four main Islands to complete our understanding of cryptogam ecology in Mediterranean dunes.

P.0266 Aquatic and semi-aquatic bryophytes of Spanish Mediterranean streams: diversity, environmental ranges and use as bioindicators

Manuela Ramírez-Valle[1], Rosa M. Ros[2], Laura Monteagudo[1], Joaquín Téllez[1], Jose Luis Moreno[1]

1 University of Castilla-La Mancha, Albacete, Spain. 2 University of Murcia, Murcia, Spain.

Aquatic and semiaquatic bryophytes are a group of river plants included in the broader group of macrophytes, which are a biological element to be monitored for the assessment of the ecological state of streams and rivers under the European Water Framework Directive. As a result of this use as biological indicators, extensive surveys of river macrophytes are being carried out in the last decades as a part of the characterisation of river macrophyte community. In this study we gather bryophyte data (mosses and liverworts) from Spanish Mediterranean rivers obtained during the years 2001-2013. The study area included three geographic zones that covered 9 river basins: south-central Spain (region of Castilla-La Mancha, including part of the Tajo, Júcar, Segura, Guadiana and Guadalquivir river basins); the whole Ebro River basin, located in north-east Spain; and three smaller Catalonian river basins (Foix, Besòs and Llobregat), also in north-east. A total of 221 sites were monitored, belonging to 10 national river types. One-hundred-meter stream reaches were waded in an upstream zigzag pattern, collecting all bryophytes found submerged and in the immediately emerged zone above the water line. We recorded 61 bryophyte species, of which 50 were mosses and 11 were liverworts. The most frequent species were *Apopellia endiviifolia*, *Didymodon tophaceus*, *Leptodictyum riparium*, *Hydrogonium bolleanum* and *Rhynchostegium riparoides*. The objectives of the study included: 1) to analyse species richness by sites, river basins and river types; 2) to define environmental ranges of species; 3) to make a proposal of water quality indicator species; 4) to identify river type-specific bryophyte communities for the 10 river types studied. Finally, we discuss the usefulness of bryophytes as tools to evaluate the ecological status of river ecosystems.

P.0267 Defining bryophyte communities in the national reference network of Spanish rivers

Manuela Ramírez-Valle[1], Andrés Mellado[2], Sara Calero[2], David Martín[2], Alfredo Corrochano[2], Juan Alández[3], Juan Guerra[4], María Jesús Cano[4], Jose Luis Moreno[1]

1 University of Castilla-La Mancha, Albacete, Spain. 2 Tragsatec, Madrid, Spain. 3 Ministerio para la Transición Ecológica y Reto Demográfico, Madrid, Spain. 4 University of Murcia, Murcia, Spain.

The application of European Water Framework Directive (WFD), and more specifically the ecological status assessment of rivers and streams, implies the need of define the reference communities that correspond totally or near totally to undisturbed environmental conditions. The composition and abundance of aquatic flora, and specifically macrophytes, is one of the biological quality elements to be monitored for the classification of ecological status of rivers. Since the year 2019, macrophytes, which include aquatic and semiaquatic bryophytes, are being monitored along with other quality elements to stablish the reference conditions of Spanish rivers. A national network of sites without significant anthropic pressures were defined based on stressors' thresholds. The reference river network used in this study included a total of 306 sites covering the whole Iberian Peninsula and 32 national river types (previously defined based on geographical, geological, hydrological, and climatic variables). The study period covered the years 2019 to 2022, with a survey per year. Stream reaches of 100 meters long were waded in an upstream zigzag pattern, collecting all bryophytes found submerged and in the immediately emerged zone above the water line. A total of 262 bryophyte species were recorded, of which 203 were mosses, 58 liverworts and 1 hornwort. The most frequent species recorded in more than 45% of the sites were: *Rhynchostegium riparoides*, *Apopellia endiviifolia* and *Fissidens crassipes*. The main objective was to define river type-specific bryophyte communities under reference conditions. Multivariate analyses were performed to test significant differences in community structure between river types and to define indicator species for them. Multivariate classification of river types based on bryophyte communities showed no correspondence with present river typology, suggesting the merging of some river types. Finally, we discuss some aspects about the use of bryophytes as bioindicators to evaluate the ecological quality of river ecosystems.

P.0268 Orthotrichum camanchacanum, a new species of epiphytic moss from Chile

Vítězslav Plášek[1,2], Jakub Sawicki[3], Felipe Osorio[4,5,6], Monika Szczecińska[3], Hana Režnarová[1]

1 Department of Biology and Ecology, University of Ostrava, Ostrava, Czech Republic. 2 Institute of Biology, University of Opole, Opole, Poland. 3 Department of Botany and Nature Protection, University of Warmia and Mazury in Olsztyn, Poland. 4 Universidad Austral de Chile, Instituto de Conservación, Biodiversidad y Territorio, Facultad de Ciencias Forestales y Recursos Naturales, Valdivia, Chile. 5 Museo de la Exploración Rudolph Amandus Philippi, Isla Teja Campus de Los Museos, Valdivia, Chile. 6 Laboratorio de Biodiversidad y Ecología del Dosel, Universidad Austral de Chile, Instituto de Conservación, Biodiversidad y Territorio, Valdivia, Chile.

During a bryofloristic survey in the Coquimbo region (Chile) in 2021, a remarkable epiphytic moss from the genus *Orthotrichum* was collected. The moss grew epiphytically on the bark of shrubs within vegetation predominantly composed of shrubs such as *Adesmia argyrophylla* and *Echinopsis chiloensis* subsp. *chiloensis*. Upon closer examination it was proved to represent a species new to science. *Orthotrichum camanchacanum* is primarily distinguished by its emergent capsule with cryptoporous stomata, a double peristome, linear-lanceolate stem leaves with a long hyaline aristae in apex, conspicuously differentiated perichaetial leaves, and a densely hairy vaginula. The territory where the new species was collected possesses distinctive geographical and climatic conditions. On the coast, especially in the coastal mountains, it is affected by the amount of clouds and coastal fog generated in the ocean, known as *camanchaca*. The moss *O. camanchacanum* exhibits morphological characters that distinguish it from related species. It seems to be endemic to this region of Chile.

P.0269 From streams to lakes: gradient of aquatic vegetation in karstic environment (Plitvice Lakes National Park, Croatia, SE Europe)

Anja Rimac[1], Vedran Šegota[1], Marija Bučar[1], Antun Alegro[1]

1 Department of Biology, Faculty of Science, University of Zagreb, Croatia.

The main phenomenon of the Plitvice Lakes National Park is a series of 16 barrage lakes created by the growth of tufa barriers. However, of equal importance are streams that provide the lakes with a constant water supply. From 2021 to 2023 the aquatic vegetation of eleven watercourses was studied. In total 96 river sections were surveyed using standard Central European phytocoenological methodology. Furthermore, basic physio-chemical water parameters were measured and information on water velocity, substrate type and canopy cover was collected. The dominant vegetation of the upper and middle reaches was species-rich bryophyte vegetation of the class *Platyhypnidio-Fontinalietea antipyreticae* Philippi 1956, associated with larger substrates, faster flow and canopy cover. By contrast, the bryophyte vegetation of *Cratoneurion commutati* Koch 1928 alliance was developed on tufa waterfalls in turbulent water and low canopy cover. In the lower reaches of the investigated rivers the herb vegetation with rare NATURA 2000 species *Apium repens* (Jacq.) Lag. occurred. The NATURA 2000 habitat type 3260 – watercourses with *Ranunculion fluitantis* i *Callitricho-Batrachion* vegetation occurred mainly on finer sediment, in deeper water with higher pH, alkalinity and electrical conductivity. Finally, several river lagoons and slow-flowing sections were characterized by stoneworts vegetation belonging to the class *Charetea fragilis* F. Fukarek ex Krausch 1964.

P.0270 The Cryptogams of the Balearic Islands dataset: the first extensive survey of cryptogamic biodiversity in the archipelago

Lluís Salom-Vicens[1], Pere M. Mir-Rosselló[1], Marcello Dante Cerrato[1], Laura López-Vich[1], Llorenç Sáez[4], Arnau Ribas-Serra[1], Antoni Josep Far[1], Maria Roselló-Salvadó[1], Dessiré Sicilia[1,3], Iván Cortés-Fernández[1], Carles Cardona[1,3], Llorenç Gil[1]

1 Interdisciplinary Ecology Group, Department of Biology, University of the Balearic Islands, Palma, Spain. 2 Centre Forestal de les Illes Balears, Institut Balear de la Natura, Palma, Spain. 3 Research Group On Plant Biology Under Mediterranean Conditions, Departament de Biologia, Universitat de les Illes Balears-Agro-Environmental and Water Economics Institute, Palma, Spain. 4 Systematics and Evolution of Vascular Plants (UAB)-Associated Unit to CSIC, Bellaterra, Spain.

Cryptogams refer to a broad group plants that reproduce by spores rather than seeds. Complex taxonomy and, generally, small size are descriptive traits of this heterogenous group (formed by various kingdoms), rendering their identification as difficult, and thus limiting the knowledge on their distribution and ecology. The Balearic Islands is an archipelago located in the western Mediterranean where cryptogams have been partially studied with scattered information and uneven knowledge on the taxonomical composition or distribution of this organisms. While some groups (fungi and ferns and allies) are well documented, there is a lack or uneven assessment for distributional data in algae, lichens, and bryophytes. Taxonomical revision add complexity to this matter proving the ongoing need for updated information and highlights the necessity to form a solid basis of knowledge for future cryptogamic studies in the Balearic Islands. Here, we present the Cryptogams of the Balearic Islands (CBI) GBIF dataset. This dataset is the result of the extensive survey conducted by a work team on all the cryptogamic groups throughout the archipelago. The CBI dataset is an ongoing project aiming to unify distributional data by conducting field trips to poorly sampled or with a lack of records on cryptogams areas. The CBI dataset currently contains more than 1200 records, mainly obtained between 2021 and 2023, and is expected to reach 2000 observations during 2024. Most of the observations are bryophytes (50,65%) and algae (31,70%) result of the work of PMMR (PhD student) and LSV (undergraduate student). Moreover, data from studies regarding bryophyte, lichen and algae ecology are being incorporated to the CBI on an effort to unify knowledge on cryptogamic species. The CBI dataset is expected to become the basis for many studies on Balearic cryptogams in the near future.

S.032. CAREX: THE EVOLUTION OF A MEGADIVERSE GENUS TACKLED FROM MULTIPLE APPROACHES

P.0271 Two-dimensional morpho-geometric variability of the utricles in the Neotropical Carex sect. Fecundae (Cyperaceae)

Angie Paola Mosquera[1], Raúl Lois[1], Ana Morales Alonso[2], Pedro Jiménez-Mejías[3], Carmen Acedo[1]

1 Dpt. Biodiversidad y Gestión Ambiental. Universidad de León. León, Spain. 2 Dpt. Biología y Geología, Física y Química Inorgánica. Universidad Rey Juan Carlos, Madrid, Spain. 3 Dpt. Biología Molecular y Ingeniería Bioquímica, Universidad Pablo Olavide, Sevilla, Spain.

Within the Monocots, the genus *Carex* L. is one of the biggest genera, composed of more than 2000 species. Being such a large group it shows taxonomic difficulties. This research focuses on samples belonging to 31 *Carex* species from the section *Fecundae* Kük. This section is the only one in the genera completely restricted to the Neotropics. The materials collected from

Central Mexico to northern Argentina represented the complete geographical range in the section. The lack of studies, the presence of untyped names, and the absence of sufficient material for some taxa expose some taxonomic problems that can be addressed using morphometric geometry. To carry out this study, the two-dimensional morpho-geometry of 31 species was analyzed. The protocol for obtaining data begins with taking photographs of the utricles using a zoomed-in stereo microscope with the Toup View software. We used nine morpho-geometric points (landmarks) in each utricle that serve to define their shape. The photographs are then treated with the TPSdig2 program and subsequently analyzed with the MorphoJ software to statistically compare the resulting shapes. This study is useful as it facilitates obtaining new taxonomic information on the geometry of the utricles, which is one of the most useful taxonomic characters in the section, as well as distinguishing between closely related species of the *Carex* sect. *Fecundae*. With these shape patterns, it is easier to define precisely the differences in utricles' general shape (elliptical, ovate, obovate, suborbicular), the beak (truncate, bidentate, bifid), and also their respective sizes.

P.0272 An updated inventory of Carex (Cyperaceae) in Kosovo

Naim Berisha[1], Bujar Kadriaj[1], Elez Krasniqi[1], Renata Custerevska[2], Fadil Millaku[1]

1 Faculty of Mathematics and Natural Sciences, University of Prishtina, Prishtina, Kosovo. 2 Faculty of Mathematics and Natural Sciences, Ss Cyril and Methodius University in Skopje, Skopje, North Macedonia.

The Balkan Peninsula, one of the three major peninsulas extending into the Mediterranean Sea in southern Europe, has a remarkable diversity of plant species and endemism compared to the broader Europe. Similar to other Balkan countries, Kosovo has the impact of different floristic regions and is therefore known for its great plant diversity. Moreover, it has acted as a climatic refuge for plants during historical climatic fluctuations and thus deserves a high priority for conservation. *Carex* L. is a vast and extremely diverse genus with a worldwide distribution. With around 2,000 species, it is one of the three largest genera of flowering plants in the world. One of the least researched plant genera in Kosovo is *Carex*, despite its importance. Although species of this genus are listed and reported in the records of neighbouring countries for Kosovo, no specific study of *Carex* flora in Kosovo has been conducted so far. In the first year, from May to August 2023, field work was carried out. This work was complemented by a thorough review of herbarium specimens deposited in the herbarium of the University of Pristina. The results of our first year's fieldwork in conjunction with the review of *Carex* herbarium specimens available in the herbarium have led to a verified inventory of 61 *Carex* taxa for Kosovo (including 42 species, 15 subspecies and 4 varieties). These results are of particular importance for the flora of Kosovo and the wider Balkan region. In particular, we have come across numerous cases where the presence of certain *Carex* taxa in Kosovo, such as *Carex pilulifera* L., was previously uncertain but has now been confirmed. Considering that more extensive research expeditions are planned for 2024, we expect the data on the genus to become even more comprehensive, with a particular focus on hybrid taxa.

P.0273 Development of a web-based interactive identification system for the Korean Carex, the largest genus in Northeast Asia

Minkyung Jung[1], Yanghoon Cho[2], Sangtae Kim[1]

1 Sungshin Women's University, Seoul, Rep. of Korea. 2 Uri Plant Research Institute, Gwangju, Rep. of Korea.

Carex L. (Cyperaceae) is the largest genus in Northeast Asia, with approximately 220 taxa reported in Korea. Species of this genus display remarkable adaptability, thriving in diverse habitats ranging from wetlands to arid zones. They play crucial roles in ecosystems, contributing to soil stabilization, providing habitats and sustenance for wildlife, and serving as resources in medicine and gardening. The species of *Carex* are challenging to identify due to the high degree of morphological similarity between the taxa and the inconspicuous structures of the flowers. Therefore, accurate identification requires a combination of characters, including those observed with a loupe. However, traditional dichotomous keys, which sequentially select diagnostic character states, cannot be used for identification if the characters described in the key are not observed. Such difficulties in identification have constrained the utilization of *Carex*. Instead of traditional keys, an interactive identification method is now actively being introduced to make a taxon-specific identification system or applied to the floral work. We developed a web-based interactive identification system for Korean *Carex* using the Lucid 4.0 program. We provided 31 standard morphological characters with 64 character states based on the literature survey and the observation of herbarium sheets. The system includes illustrations or photographs of the character states of each character to facilitate the identification. The system developed was made available to the public on a website, allowing users to identify species quickly and accurately. This study aims to make *Carex* widely available as a valuable resource for future studies and species utilization.

P.0274 Revisiting the Pacific Southwest-South America disjunction in Carex sect. Junciformes (Cyperaceae): phylogenomic evidence reveals

Mónica Míguez[1], Pablo García-Moro[1], Ana Morales Alonso[2], Karen Wilson[3], Lisa Pokorny[4], Kerry Ford[5], Pedro Jiménez-Mejías[1], Santiago Martín Bravo[1]

1 Universidad Pablo de Olavide, Seville, Spain. 2 Universidad Rey Juan Carlos, Mostoles, Spain. 3 National Herbarium of New South Wales, Mount Annan, Australia. 4 Real Jardín Botánico (CSIC), Madrid, Spain. 5 Allan Herbarium, Manaaki Whenua, Lincoln, New Zealand.

Carex sect. *Junciformes* is a cold-adapted group of *Carex* subg. *Psyllophorae* with its center of diversity in South America. In the SW Pacific it is represented by three accepted species, endemic to the mountains of New Zealand (*C. acicularis*, *C. allanii*, and *C. enysii*), and by one from SE Australia-Tasmania (*C. archeri*). Previous molecular studies suggest that the SW Pacific species result from a single long-distance dispersal event that took place in the Late Miocene-Pliocene. We used both Sanger (ITS, ETS, *matK* & *rps*16 markers) and high-throughput sequencing (Hyb-Seq with Angiosperm-353 probe set) approaches, to shed light on the systematics and historical biogeography of this group of sedges. Both the Sanger and Hyb-Seq phylogenies reaffirmed the monophyly of the SW Pacific group of sect. *Junciformes*, but did not recover the New Zealand taxa as monophyletic. This suggests that cryptic species may be occurring in this archipelago. Previous morphological and field observations have revealed broad morphological and ecological variation across populations regarded as either *C. acicularis* or *C. enysii*, which would also agree with the possibility of unaccounted species. Biogeographic reconstructions consistently point to New Zealand as the ancestral area of the entire SW Pacific sect. *Junciformes* group, with subsequent migration to Australia.Thus, New Zealand could have acted as a stepping-stone in a westward colonization route between the source area in South America and Australia. The lack of diversification of the group in Australia compared to that of New Zealand could be explained in terms of low availability and variability of appropriate habitats for sect. *Junciformes* in the old and low Australian mountains. Conversely, the younger and higher mountains of New Zealand may have provided an ideal setting for the diversification of sect. *Junciformes* through increased ecological availability and heterogeneity.

P.0275 Morphological and ecological diversification at its extreme: phylogeny of the amazing radiation of Carex section Echinochlaenae (Cyperaceae) in New Zealand

Mónica Míguez[1], Ana Morales Alonso[2], María Sanz-Arnal[1], Pedro Jiménez-Mejías[1], Kerry Ford[3], Santiago Martín Bravo[1]

1 Universidad Pablo de Olavide, Seville, Spain. 2 Universidad Rey Juan Carlos, Mostoles, Spain. 3 Allan Herbarium, Manaaki Whenua, Lincoln, New Zealand.

Carex section *Echinochlaenae* (subgen. *Carex*) contains 49 species, 38 endemic to New Zealand, four to satellite archipelagos (Chatham, Kermadec and Norfolk), two to Australia/Tasmania, four to South America, and only one shared between New Zealand, South America, and a few subantarctic archipelagos. Previous studies have detected a significant increase in diversification rates for this lineage. In New Zealand, where it gathers about 40% of the total species diversity, the different species bear a wide arrangement of morphological characters, many of them unusual in *Carex*. Plant height may range from 1-2 cm stems to >1 m among the different species. Leave width varies from capillary <1mm leaves to several centimeters wide. Similarly, spikes vary from millimeters to centimeters long. Among the rarest morphological features are acaulescence, extremely elongated ground-lying stems articulated at the base, or red-colored to bronze foliage, the latter unique among the 2,000 species of the genus. Many species occur in habitats typically regarded as frequent in *Carex* (forests, wet meadows, bogs) but others occupy unusual ones (coastal banks, rock crevices, saltmarshes, temporal pools). These extremely diverse habitat preferences make *Echinochlaenae* the most remarkable ecological radiation in the genus. We reconstructed a Sanger-based (ITS, ETS, *mat*K) phylogeny of the group, in order to set ground for the detailed study of differentiation processes. The phylogeny confirms the monophyly of the lineage, provides support for early cladogenesis events and retrieves some species groups and species sister relationships. The topology points to New Zealand as the diversification hub for the group as well as the ancestral area for the colonization of Australia/Tasmania, the satellite archipelagos, and South America. Overall, phylogenetic evidence together with wide morphological and ecological diversity supports evolutionary radiation processes during sect. *Echinochlaenae* differentiation in New Zealand.

P.0276 The pantropical tribe Spermacoceae (Rubiaceae): Resolving phylogeny and assessing congruence using whole plastome data

Suman Neupane[1], Peter Schafran[2], Mariela Nuñez Florentin[3]

1 Department of Biological Sciences, Ball State University, Muncie, USA. 2 Boyce Thompson Institute, Ithaca, USA. 3 IBONE (UNNE-CONICET), Corrientes, Argentina.

The pantropical tribe Spermacoceae comprises approximately 1,000 species and belongs to the largest subfamily, Rubioideae, within the Rubiaceae family. The genera within the Spermacoceae tribe have a long history of taxonomic confusion and disagreement due to the utilization of inconsistent and overlapping morphological traits in their generic delimitations. Previous molecular phylogenetic studies have made significant contributions to resolving many taxonomic inconsistencies, primarily focusing on taxa from Asia-Pacific and Australia. However, challenges persist in understanding the phylogenetic relationships and taxonomy of Spermacoceae members from the Americas and Africa. In this study, we employ whole-genome plastid data of Spermacoceae members to address these challenges. Our presentation will primarily focus on two objectives: (1) presenting the first plastome phylogeny of Spermacoceae, primarily representing members from Africa and the Americas, and (2) investigating phylogenetic congruence among genes and phylogenetic signals within genes using Bayesian and other methods. By shedding light on the phylogenetic relationships and resolving taxonomic inconsistencies, our research contributes to a better understanding of the evolutionary history and taxonomy of the Spermacoceae tribe. This work is part of an ongoing effort to construct a global genome-wide phylogeny of the Spermacoceae tribe through the utilization of high-throughput DNA data.

P.0277 Genomic islands of differentiation and speciation in a mega-diverse genus (Carex, Cyperaceae) with rapid chromosomal evolution

Rogelio Sánchez Villegas[1], Inés Gómez Ramos[2], M. Luceño[1], M. Míguez[1], J.I. Márquez-Corro[1,3], E. Maguilla[1], Marcial Escudero[2], Santiago Martín Bravo[1]

1 Pablo de Olavide University, Seville, Spain. 2 University of Seville, Seville, Spain. 3 Royal Botanical Gardens, Kew, Richmond, UK.

Holocentric chromosomes have centromeres that are distributed along the entire length of the chromosomes. Almost 20 independent linages of eukaryotes have this kind of chromosomes. Very often they display a large variation in chromosome numbers. While chromosome fragments from fission might be lost in monocentric chromosomes, they are fixed and properly segregated in holocentric chromosomes. Although holocentricity appears to play a crucial role in generating biodiversity, no experimental studies have conclusively demonstrated the crucial role of chromosomal speciation in holocentric organisms. Suppression of recombination due to chromosome fusion and fission may contribute to chromosomal speciation in certain holocentric groups, leading to population differentiation within a species despite ongoing gene flow (supergenes speciation theory). To test this hypothesis, two species from the megadiverse and holocentric genus *Carex* were chosen as a study group: *C. laevigata* and *C. helodes*, as they display wide inter- and even intrapopulation variation in chromosome number. Individuals from different populations of both species with varying chromosome numbers were collected and kept at greenhouse and used for conspecific experimental crosses, generating self-fertilized progeny, F1 (through parental crosses) and F2 (through F1 self-fertilization). Our aim is to assess the fitness of chromosomal rearrangements in F1 and F2. Subsequently, genome comparison between physical genomes and genetic linkage maps of F2 individuals will directly test if recombination is suppressed in structural heterozygotes due to chromosomal rearrangements. Lastly, the role of chromosomal rearrangements in F1 and F2 populations will be evaluated using measures of fitness and reproductive performance, and quantitative trait loci (QTLs) associated with these fitness-related traits in F2 populations will be mapped.

P.0278 Plastome phylogeny and early diversification of the basal lineages of Carex subg. Carex (Cyperaceae)

Kotaro T. Takahashi[1], Shizuka Fuse[1], Hiroshi Noda[1], Okihito Yano[2], Hiroshi Ikeda[3], Sawita Yooprasert[4], Manop Poopath[4], Keshab RajRajbhandari[5], Yong-Ping Yang[6], Minoru N. Tamura[1]

1 Department of Botany, Graduate School of Science, Kyoto University, Kyoto, Japan. 2 Department of Biosphere-Geosphere Science, Faculty of Biosphere-Geosphere Science, Okayama University of Science, Okayama, Japan. 3 The University Museum, The University of Tokyo, Tokyo, Japan. 4 The Forest Herbarium, Department of National Parks, Wildlife and Plant Conservation, Thailand. 5 Department of Plant Resources, Ministry of Forests and Environment, Nepal; 6 Kunming Institute of Botany, China.

The genus *Carex* (Caricoideae-Cyperaceae) is one of the largest genera in the angiosperms, comprising about 2,000 species. The genus consists of the six subgenera, among which *C.* subg. *Carex* is the largest with 70% of all of the *Carex* species, and focused on in this study. The early diverging lineages of *C.* subg. *Carex* are distributed mainly in East Asia and Southeast Asia, and thus the early diversification of the subgenus can be considered to have occurred in the Asian region. However, the phylogenetic relationships and taxonomy of these lineages are still unclear due to their great morphological diversity and the lack of ample materials from Asian region in the earlier DNA analyses. Here, we conducted the phylogenetic analysis of the early diverging lineages of *C.* subg. *Carex* (including *C.* sects. *Cryptostachyae*, *Debiles*, *Decorae*, *Graciles*, *Grallatoriae*, *Indicae*, *Japonicae*, *Mapaniifoliae*, *Mitratae* and *Mundae*) collected from Japan, China, Thailand and the Himalaya regions, using the plastome sequences. Based on the results of the phylogenetic analysis and morphological observation, we reexamined the evolutionary history and taxonomy of *C.* subg. *Carex*.

P.0279 Cryptic intraspecific diversity of a polyploid complex of Abildgaardia ovata (Cyperaceae): evidence from molecular, cytological, and ecological data

Okihito Yano[1], Yuki Tamura[1], Yukiko Saito[2], Hiroshi Ikeda[3], Kyong-Sook Chung[4], Hyoung-Tak Im[5], Yu Ito[6]

1 Faculty of Biosphere-Geosphere Science, Okayama University of Science, Okayama, Japan. 2 Faculty of Education, University of Ryukyu, Okinawa, Japan. 3 The University Museum, the University of Tokyo, Tokyo, Japan 4 Department of Medicinal Plant Science, Jungwon University, Goesan, Korea. 5 Department of Biology, Chonnam National University, Gwangju, Korea. 6 Faculty of Pharmaceutical Sciences, Setsunan University, Osaka, Japan.

Abildgaardia ovata (Cyperaceae) is a perennial herb widely distributed in the world's tropical to warm-temperate regions, including Asia, Pacific, Australia, Africa, and Central and South America. Polyploidy is known in the species, i.e., $2n = 10$ (2x) from India and Thailand and $2n = 20$ (4x) from India, Japan, Mexico, and USA. Our previous molecular study using nrITS found two ribotypes, indicating further intraspecific diversity in *A. ovata*, in which polyploidy may be involved. Here we investigated genetic variations and phylogeographic patterns and conducted chromosome observations of *A. ovata* using samples from Japan, Korea, Nepal, and Taiwan. Our molecular analysis using cpDNA and nrITS data discerned distinct two major lineages with slightly overlapped geographical structures, one in Japan's Honshu, Kyushu, and Nansei, Korea's Jeju, and Nepal while the other restricted to Nansei and Taiwan. Ecological niche modeling suggested apparent ecological differentiation between the two lineages. Samples that have heterogeneous nrITS sequences were also found in Japan; those were considered as consequences of hybridization between either the above mentioned two lineages or the latter and an unknown one. Given chromosome numbers revealed in this study, the former found in Nansei is considered as a homoploid hybrid between 2n = 20 (4x) lineages while the latter endemic to a part of Kyushu as an allopolyploid with 2n = 40 (8x). The homoploid hybrid included two types of haplotypes, indicating that hybridization events have occurred bilaterally. The overall results lead us to infer unrecognized cryptic taxa within the widespread polyploid species complex, although the apparent lack of unambiguous diagnostic characters currently precludes formal description. Further taxon sampling and additional genetic analyses may unveil whether the narrowly distributed lineage is derived from the widely distributed one in Asia and how the homoploid hybrid and allopolyploid occur with either of the lineages in Japan.

S.033. LET PEOPLE COME TO BOTANY I: NEW METHODS TO ENGAGE PEOPLE WITH PLANT DIVERSITY

P.0280 University campuses as botanical classrooms: ten years of innovative teaching

Cèsar Blanché[1], Joan Simon[1], Carles Benedí[1], Maria Bosch[1]

1 Teaching innovation group GIBAF, Faculty of Pharmacy and Food Sciences, University of Barcelona, Barcelona, Spain.

A case study on the use of plant materials from university campus gardens as a pedagogical tool in botanical education is presented. The analysis is based on the initiatives developed by the Botany Teaching Innovation Group (GIBAF 2024) at the University of Barcelona (UB) during the period from 2014 to 2024. 25 activities have been organized as part of pedagogical innovation projects for students of Botany in the Pharmacy degree at UB. Projects have been integrated into the evaluation processes. Working spaces include the Garden of the Faculty of Pharmacy and the historical Garden Ferran Soldevila (main UB building), hosting together around 350 species. We briefly highlight the botanical areas covered in the activities with students: a) Service Learning: development of botanical guides, labelling with QR codes providing information on species (nomenclature, description, distribution, uses, etc.), dissemination through faculty and UB websites, organization of guided botanical tours, and publication of student works in the UB Digital Repository. b) Organography and botanical morphology of spermatophytes: creation and publication of an illustrated glossary in the UB Digital Repository. c) Development of educational resources for students: creation and use of collaborative e-Textbooks in self-assessment and peer-assessment processes. d) Curricular environmentalization: integration of the value of plant biodiversity in teaching plans (via videos, apps, etc.). e) Promotion of the heritage value of the campuses: both at a local (faculty, UB) and international level (LERU). f) Sustainable Development Goals (SDGs): incorporation of concepts related to goals 2, 3, 6, 11, 12, 13, and particularly 15, focusing on the value of biodiversity as a source of health within the One Health context. In conclusion, the study demonstrates the effectiveness of using plant resources from university campuses as a valuable educational tool in botanical teaching. References: GIBAF (2024). Blog of the Botanical Innovation Group Applied to Pharmacy, http://gibaf.org/.

S.033. CITIZEN SCIENCE INITIATIVES FOR THE PROMOTION OF BOTANY

P.0281 Ecological restoration and maintenance processes plant material planted through pollinator corridors, in Suba, Colombia

Carrillo R. Diana[1]

1 Alcaldía Local de Suba, Universidad Pedagógica y Tecnológica, Suba-Bogotá, Colombia.

The general objective of this project is to develop strategies to restore and maintain new degraded hectares in the Main Ecological Structure EEP of Suba, Colombia, giving continuity to a project that corresponds to maintenance actions that contribute to the restoration, strengthening of the Main Ecological Structure generating new pollinator corridors in three strategic sectors for conservation: 1l Mirador los Nevados Park, 2. hydraulic round, management and environmental preservation of the Córdoba wetland and the Quebrada la Salitrosa in the town of Suba. The project is divided into four components: 1. Planting with Restoration Criteria in new areas of intervention through enrichment modules 2. Maintenance and enrichment of plant material in new areas and restored by the ALS 3. Pollinator Monitoring 4. Social Component- Citizen Science.

P.0282 Application of City Biodiversity Index to the fast-expanding city of Delhi, India for urban sustainability and resilience

Chandan Das[1], Satish C. Garkoti[1], Shalini Dhyani[2]

1 School of Environmental Sciences, Jawaharlal Nehru University, New Delhi, India. 2 Water Technology and Management Division, CSIR-National Environmental Engineering Research Institute, Nehru Marg, Maharashtra, Nagpur, Maharashtra, India.

Rapidly expanding cities with simultaneous increase in the population has put an immense pressure on the existing green spaces and biodiversity in the cities. The increasing air pollution, high carbon emissions and increased intensity of flash floods and urban heat island effects in the fast-growing metropolitan cities of India especially National Capital Territory (NCT) Delhi have put an alert on the human well-being of the urban residents. Planning and implementing site specific and cost-effective nature-based solutions become a prerequisite for improving the livability and developing resilient cities as per Sustainable Development Goal (SDG) 11. ‘City Biodiversity Index’ was assessed to understand the biodiversity concerns, efforts, and challenges for the city. The City Biodiversity Index (CBI) was assessed on recently upgraded 28 indicators. A standard protocol given in the CBI manual was followed incorporating elements of remote sensing and literature review. CBI for the NCT of Delhi scored 57 out of 100 points and was first time evaluated for the city. The different components of CBI included Native Biodiversity (including flora and fauna), Ecosystem Services, Governance and Management scored 10 out of 24 points, 5 out of 20 points and 42 out of 56 points respectively. CBI scores are crucial indicators and require attention for the state and central government officials to understand the critical situation of the city for only having a little more than 50% score. It is important that city prioritizes biodiversity conservation and local biodiversity action plan includes the results provided by the study.

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P.0283 The Ghirardi Botanic Garden as promoter of a green tourist attraction in Toscolano Maderno (Brescia, Northern Italy)

Claudia Giuliani[1,2], Martina Bottoni[1,2], Fabrizia Milani[1,2], Lorenzo Colombo[1,2], Paola S. Colombo[1,2], Gelsomina Fico[1,2]

1 Department of Pharmaceutical Sciences, University of Milan, Milan, Italy. 2 Ghirardi Botanic Garden, Department of Pharmaceutical Sciences, University of Milan, Toscolano Maderno, Brescia, Italy.

This three-year project proposal is aimed at creating, managing, and promoting educational initiatives as part of a *green tourist circuit*, in which the plant world represents the element that connects three cultural sites in Toscolano Maderno (Brescia, Northern Italy): the Ghirardi Botanic Garden (GBG), the Bernini Park, and the Papermill Valleyalong with the Paper Museum. The objective is to develop responsible and sustainable tourist flows, through offers capable of integrating the cultural attractiveness of the scientific, naturalistic, historical, and artistic features of the territory. The project represents a meeting point between the tourist's search for authenticity and beauty, perfectly embodied by the plant world, and the need to protect the historical identity and enhance the territory, in a "green" key. This overturning of tourist behaviour can succeed only by increasing the collaboration among local actors and emphasizing the "sense of belonging" to the places. Simply put, what is offered by a territory must be closely linked to the desire on its residents' part of preserving and promoting it. This is contemplated with the promotion of participative initiatives to enhance the plant resources:- the plant heritage preserved at the GBG, by scheduling training courses for guides/volunteers, promoting educational offers for local schools, and creating interpretative apparatuses that guide the visitor's attention from the GBG itself to the other target institutions, from the first year;- the centuries-old plants of the Bernini Park, with special focus on the monumental ones, starting from the second year;- the autochthonous species of the Papermill Valley, to be re-explored as a precious feature in the tourist's journey to the discovery of the Paper Museum, during the third year. The planning of the work program was possible thanks to the invaluable involvement of the Municipality of Toscolano Maderno (Brescia, Italy).

P.0284 Citizen science approach to combat plant and insect blindness and help their safeguard

Marta Galloni[1], Marta Barberis[1], Fortunato Bitonto[1], Laura Bortolotti[2], Roberto Costantino[1], Athanasia Chroni[3], Giovanna Dante[1], Jelle Devalez[3], Simone Flaminio[4], Nicola Lothar Herrmann[1], Elise Maria Keller[1], Luis Navarro[5], Annalisa Managlia[1], Umberto Mossetti[1], Theodora Petanidou[3], Marino Quaranta[2], Rosa Ranalli[6], Jose Maria Sanchez[5], Anna Traveset[7]

1 University of Bologna, Bologna, Italy. 2 Council for Agricultural Research Analysis of the Agricultural Economy, Bologna, Italy. 3 University of the Aegean, Mytilene, Greece. 4 University of Mons, Mons, Belgium. 5 University of Vigo, Vigo, Spain. 6 University of Milano-Bicocca, Milan, Italy. 7 Mediterranean Institute for Advanced Studies CSIC, Esporles, Spain.

LIFE 4 Pollinators (LIFE18/GIE/IT755) aims at involving people and key stakeholders in the conservation of wild pollinators in Mediterranean countries. To activate a virtuous circle in civil society, different audiences are involved through a general citizen science approach. The project has produced a large set of materials in 6 EU languages, including user-friendly identification tools for entomophilous plants and main pollinators. Among the main actions are the educational project "Students 4 pollinators" for secondary schools and the web platform addressed to citizens, for collecting photo records of pollinators on flowers. The former action foresees 3 phases: a preliminary education session at school; a practical activity conducted by students to record plant-pollinator interactions; a "restitution" session in which the results of practical monitoring are presented and discussed. About thousand students participated to the project across Italy, Spain and Greece, enhancing their knowledge on local flora and stimulating collective actions to help wild pollinators. Learning outcomes and project success have been assessed through questionnaires. Replies show a general increase of knowledge and awareness as well as the willingness to adopt virtuous behaviors, by both students and teachers. The web platform encourages citizen participation in biodiversity data collection: almost two thousand photos have been uploaded, half of which were taken in Natura 2000 sites thanks to bioblitzes, while pictures taken in urbanized areas were mostly collected during the educational activities. The long-term continuation of "Students 4 Pollinators" will be guaranteed in Bologna by the University Museum Network, being included within the Botanic Garden and Herbarium educational offer for schools.

P.0285 Effects of a realistic biodiversity loss scenario on the fine root structure of a semi-natural grassland.

Clara Gracia Mas[1], Aleš Lisner[2], Jules Segrestin[2]

1 Centro de Investigaciones sobre Desertificación (CSIC-UV-GVA), Valencia, Spain. 2 University of South Bohemia, České Budějovice, Czech Republic.

Biodiversity ecosystem functioning (BEF) research has shown a positive relationship between species diversity and diverse ecosystem functions, especially productivity. However, most studies have been addressing this question using artificial communities composed of a random selection of species with a main focus on aboveground productivity. Here, we used a different approach based on the removal of species from a high diversity European temperate grassland and we investigated the effect of the loss of rare and subordinate species on the belowground characteristics of the resulting communities. Particularly, we tested the effect of species loss on belowground biomass, its vertical distribution, and root traits. We also measured the resilience of plant communities in producing new roots after a soil disturbance. We found no effect of species removal on root biomass except for a small decrease in root biomass in the uppermost soil layer (0-5cm), 6 years after the experiment setup. Similarly, species loss did not affect the community root traits. Regarding resilience, we found that species removal decreased the root production after disturbance during the first 3 months. This effect, however, was no longer visible after a year, and even monocultures were able to produce as much root biomass as controls during that time. These results show that the biodiversity-productivity relationship may not be as ubiquitous as commonly thought and no interpolations from aboveground to belowground can be easily done. The lack of response found for the root vertical distribution challenges the idea that high species diversity was associated with niche partitioning and species complementarity but rather suggests that dominant species are the main determinant of belowground characteristics. However, diversity could have a positive effect in other less studied ecosystem functioning such as resilience, although in our system can just be seen in short-term.

S.033. CITIZEN SCIENCE INITIATIVES FOR THE PROMOTION OF BOTANY

P.0286 Leveraging the iconic popularity of saguaro cactus to develop conservation tools and strategies for endangered cacti

Jeny Davis[1], Kimberlie McCue[2], Tania Hernández-Hernández[2]

1 National Forest Foundation, Missoula, USA. 2 Department of Research, Conservation and Collections, Desert Botanical Garden, Phoenix, USA.

Saguaros (*Carnegia gigantea*) are columnar cactus that span and flourish in the Sonoran Desert of North America, growing exclusively in the region. There's nothing particular about saguaro ecology, physiology or genetics that makes them different from their cacti relatives, and they are not endangered. However, the importance of saguaros is tremendous for conservation purposes.

They are an iconic species included in the Cactaceae, the family with the highest number of species under severe extinction threats. The saguaro cactus is a symbol of the region, highly acknowledged in memorabilia. People hold them in high esteem, monitor them, and see them as cornerstones of urban and wild landscapes, while laws have been established to care for and preserve them. Unfortunately, given recent extreme heat waves in the metro Phoenix area, many saguaros in urban spaces have died. Desert Botanical Garden capitalizes on the social relevance of saguaro to develop a cacti conservation strategy proposal that has central components in environmental education and community involvement. With the help of the community, we developed the Saguaro Census, where people participate using the iNaturalist app to count and monitor saguaros and their health in the metro Phoenix area, raising awareness on the importance of maintaining and promoting urban green spaces and wildlife. With the Saguaros Under Stress project, we study the impact of urban heat island stress on saguaros in residential areas, where owners participate in continuously monitoring and sampling their plants. These projects sensitize the community to the potential effects of global warming on cactus extinction, and the relevance of scientific research. Finally, we developed the Saguaro Nursery, where volunteers help us propagate saguaros from a seed bank that covers the geographic range and genetic diversity of the species, acquainting with the need of early action of species preservation for future generations.

P.0287 Flora Incognita: a free App for precise and easy plant identification

Jana Wäldchen[1], Anke Bebber[1], David Boho[2], Alice Fritz[1], Jonas Hüther[2], Kevin Karbstein[1], Lara Kösters[1], Illia Korobov[2], Michael Rzanny[1], Oliver Sommer[2], Sebastian Jeschke[2], Christian Wittich[2], Patrick Mäder[2]

1 Max Planck Institute for Biogeochemistry, Jena, Germany. 2 Technische Universität Ilmenau, Ilmenau, Germany.

Being able to correctly identify plants is necessary for recognizing changes in their distribution, but knowledge of plant species is increasingly declining among the population. Flora Incognita is a tool that can counteract this loss. With intuitive usability, the application can identify over 16,000 plant species with a very high degree of accuracy. Comprehensive fact sheets provide a wealth of localized information on the species found, and curated articles regularly inform about various botanically relevant topics. Users are extrinsically rewarded with badges for finding different or specific species, increasing their motivation to engage with plant diversity repeatedly. The application is designed in such a way that citizen science projects involving the recording of species can be easily implemented. The captured plant observations and their metadata provide a rich resource for researching, monitoring and understanding plant diversity, the spread of invasive species or plant phenology. Mobile applications such as Flora Incognita stimulate the successful interplay of citizen science, conservation and education.

S.033. LET PEOPLE COME TO BOTANY I: NEW METHODS TO ENGAGE PEOPLE WITH PLANT DIVERSITY

P.0288 The xylarium BOTUw as a generator of knowledge for biodiversity sustainability

Carmen R. Marcati[1], André C. Lima[1], Julia M. N. Bidoia[1], Cleiton H. Silva[1], Juan Nicolai[1], Liliane C. Pereira[1]

1 Department of Forest Science, Soil and Environment, São Paulo State University - UNESP, Botucatu, Brazil.

Continuously deposited in successive layers throughout the life of the plant, wood records valuable environmental information that allows it to be studied for various purposes, including species identification, dendrochronological studies, climate reconstructions and sustainable forest management. Xylaria are collections of documented, organized and correctly identified wood samples, which should contain information about the specimen and the place where it was collected. With more than 2,900 specimens representing 1,600 species and 600 genera, included in 150 families, the xylarium “Profª Drª Maria Aparecida Mourão Brasil” (BOTUw) was created to expand knowledge of the Cerrado and Atlantic Forest ecosystems. It currently has around 1,500 species samples from these ecosystems, as well as contributions from international collections and more than 18,000 slides, making it possibly the largest collection of histological slides of wood and bark in Brazil. This collection was used in important publications, such as the book “Atlas of Wood Diversity of the Cerrado Paulista” and the “IAWA List of Microscopic Bark Features”, as well as several scientific papers. All the information about the samples is currently available on the *speciesLink* platform, including almost 900 macro and microscopic anatomical images of more than 100 Brazilian species. BOTUw receives visits from primary and secondary school students and undergraduates, allowing the public to have contact with the great diversity of wood in its collection. In view of current climate change and intense human pressure on natural resources, and with the rapid degradation of natural ecosystems, especially the Cerrado and the Atlantic Forest, the study and conservation of biodiversity is becoming crucial. In this way, BOTUw represents an important repository of the structural diversity and biodiversity of these ecosystems and has contributed to the dissemination of this knowledge to both the academic community and society in general.

S.033. CITIZEN SCIENCE INITIATIVES FOR THE PROMOTION OF BOTANY

P.0289 Engaging with Wikidata: Benefits and impacts for botanists and institutions

Sabine von Mering[1], Siobhan Leachman[2], Joaquim Santos[3], Heidi M. Meudt[4]

1 Museum für Naturkunde - Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany, 2 Independent researcher, Wellington, New Zealand, 3 Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal, 4 Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand

Digital outreach is an increasingly important way for scientists and institutions to communicate scientific research, including all aspects of botanical research, to audiences both inside and outside the scientific community. We will show how and why botanists can (and should) contribute biodiversity information to multiple Wikimedia projects. There are many ways that botanists can get involved in this space, including contributing research images, specimens, publications, and information about scientists, botanical collectors, taxonomic data, plant taxa, and other aspects of plants and biodiversity. Botanists can engage in multiple Wikimedia projects, with the main ones being Wikipedia, Wikimedia Commons, and Wikidata. We will focus here on Wikidata, explaining the benefits and impact of Wikidata engagement both for individuals and institutions. One of the biggest impacts of such engagement is the reuse of Wikidata data and identifiers (QIDs) in other platforms such as Bionomia, Scholia, BHL, GBIF, VIAF and others. This reuse can ensure botanists get increased acknowledgement and recognition for their contributions, such as publications, collecting and identification of specimens, and the documented use of those specimens in research. We will also discuss the opportunities and benefits of "roundtripping" Wikidata items in institutional collection management systems and natural history institution websites, as well as querying Wikidata to help answer questions of relevance to the botanical community. We will show some successful and inspiring examples of biodiversity knowledge, images and metadata that scientists, institutions and Wikimedians are adding to Wikidata and the wider Wikiverse. We will also discuss the practical steps botanists can take to engage with Wiki communities in their own countries and languages. Finally, we will share some of our personal experiences of becoming Wikimedians and engaging in such digital outreach as scientists and with scientists, including at IBC 2024 (see: https://www.wikidata.org/wiki/Wikidata:WikiProject_IBC_2024).

P.0290 School environmental project: planting to form life values.

Víctor Alfonso Mondragón Valencia[1], Liliana Ibarra[1], María Eugenia Arias[1], Oscar Molano[1]

1 Institución Educativa Metropolitano María Occidente, Popayán, Colombia.

This research analyzes the school garden as a space that helps foster school relationships, understanding that the exercise of education promotes the transformation of students from their different life environments and from various approaches such as: their socio-personal, academic, artistic processes, among others to guarantee a positive subject-environment relationship. In school gardens, topics that include food, nutrition, environmental sciences, ecology, agroecology and botany, among others, are historically worked on, hence its importance in the educational field. Environmental recycling days were formed together with the students to create eras from recycled plastics in eco-bottles: the planting of aromatic plants, aloe vera (Aloe vera), varieties of lettuce and tomato began, the students acquired interdisciplinary knowledge, such as: measurements of areas, volumes and also from biology, the morphological characteristics of plants are analyzed, they learn to recognize botanical families and types of fruits, as phenological processes. Socially, teachers' strategies were studied to create linkage mechanisms with families, with other teachers and directors, as well as with actors external to the school, to establish and provide continuity to the gardens. It is concluded that, despite the difficulties in their operation and monitoring, they represent a field of opportunities to build spaces for meeting and collaboration between teachers and students, and with other internal and external actors; although it is also recognized that much of its potential is hindered by different structural and labor factors of teaching. These factors act as barriers to the scaling up of gardens, still leaving them as a marginal activity of teachers who, for different motivations, maintain their commitment to promoting them in their schools.

S.033. LET PEOPLE COME TO BOTANY I: NEW METHODS TO ENGAGE PEOPLE WITH PLANT DIVERSITY

P.0291 Bridging Botany and society: exploring the rich legume living collection at Rio de Janeiro botanical garden, Brazil

G.C. Ottino[1], D. Cardoso[1,2], H. C. Lima[1], M.P. Morim[1], L.S.B. Jordão[1], F.L.R. Filardi[1], V.F. Mansano[1], A.M.S.F. Vaz[1], M.A. Nadruz[1]

1 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Instituto de Biologia, Universidade Federal da Bahia, Bahia, Brazil.

The Arboretum of the Rio de Janeiro Botanical Garden (JBRJ) in Brazil holds one of the World's most important and biodiverse *ex-situ* collections of tropical plants. The remarkable JBRJ Living Collection has a significant conservation value, featuring breathtaking pathways lined with towering Amazonian and Atlantic Forest trees and representative species of Brazil's unique ecosystems. This living collection offers an exceptional opportunity to engage people with a vast plant biodiversity and serves as a valuable educational experience for society. The legume family (Fabaceae), the most species-rich in the country's flora, is also particularly rich in the JBRJ living collection, providing excellent examples for knowing the Brazilian flora and phytogeographical domains. This legume living collection also plays a role in *ex-situ* conservation by housing genetically representative units of high-priority threatened species, such as the Brazilwood, *Paubrasilia echinata*, and the Rosewood, *Dalbergia nigra*. By carefully reviewing the nomenclature of the JBRJ legume living collection, following recent molecular-based phylogenetic classifications, we show that it comprises 276 legume species, from which 211 are Brazilian native species, 88 are endemic of the country, and 17 are officially listed in the national red list of threatened species. Our results compose a series of online books designed to showcase for visiting communities the families of plants cultivated at JBRJ. The book enables the general public to explore the living collection independently and know its species with greater autonomy. Each entry includes photos, popular names, scientific names, distribution, location within the Arboretum, phenology, and observations on use and conservation. This ongoing project undertakes activities to foster higher integration of science, education, culture, and nature.

P.0292 It's quarter to Daisy! - Studying flower movements in a floral clock

Katja Rembold[1], Sarah Gauss[1,2], Adrian Möhl[1], Markus Fischer[1,2], Sylvain Aubry[3]

1 Botanical Garden of the University of Bern, University of Bern, Bern, Switzerland 2 Institute of Plant Sciences, University of Bern, Bern, Switzerland 3 Department of Plant and Microbial Biology, University of Zürich, Zürich, Switzerland.

Many people perceive plants as static organisms, but the plant kingdom is full of motions - often too slow for us to observe. Based on the ideas of Carl Linnaeus, we built a floral clock in the Botanical Garden of the University of Bern (Switzerland) to communicate floral movements and their ecological and physiological background to a broad public. In a playful way, visitors could observe and experience the displayed plant movements on site and 24h online to learn about how and why plants invest energy in floral movements. Simultaneously, we studied the displayed plants in accordance with their environmental conditions to learn more about the complex mechanisms and interrelationships. Are the floral movements of each species triggered by light, temperature or humidity? Or is it a combination? In June and July 2022, we studied the opening/closing times of 11 day- or night-flowering plant species. For each species, we measured light intensity, temperature and humidity during 24h and under different climatic conditions. For most species, a combination of triggers had a significant impact on flower opening/closing with light intensity being the most common trigger. Merging expertise from botany, history of science, ecology and physiology, our project proved very successful to raise societal awareness of the beauty, complexity and sensitivity of plants.

P.0293 Fostering botanical education and promoting scientific vocations at Marimurtra Botanical Garden

Anna Sans[1], Sílvia Garriga[1], Enric Barril[1], Gisela Hernández[1], Carles Burguera[1], Jaissa Obré[1], Pere Fraga[1,2], Jordi Fàbregas[1], Antonio Aguilar [1]

1 Marimurtra Botanical Garden, Fundació Privada Carl Faust, Blanes, Spain. 2 Institut Menorquí d'Estudis, Maó, Spain.

Marimurtra Botanical Garden embraces a multifaceted approach to scientific outreach, catering to diverse audiences with varied interests and backgrounds. With a historical, cultural, and natural appeal, Marimurtra welcomes visitors from around the world, providing an opportunity to engage with the rich plant diversity spanning its more than 4-hectare landscape, housing over 4,000 cataloged plant taxa from five continents. The foundation's commitment to scientific dissemination is evident in its efforts to adapt educational activities to different age groups, particularly focusing on enhancing the experience for younger audiences. Through experiential and hands-on activities, Marimurtra aims to spark curiosity and foster a deeper appreciation for botany and the environment. These initiatives not only facilitate the acquisition of knowledge but also aim to cultivate a lifelong interest in the natural world. Moreover, Marimurtra recognizes the importance of attracting school-age visitors, acknowledging them as a key demographic for impactful engagement. By offering tailored educational programs and interactive experiences, the garden strives to leave a lasting impression on young minds, igniting a passion for plant sciences and environmental stewardship. In addition to on-site activities, Marimurtra leverages online content to extend its reach and provide supplementary educational resources. Whether through guided tours, technical workshops, or manipulative activities, the garden is committed to disseminating botanical knowledge to schools, universities, families, and environmental enthusiasts alike. As Marimurtra continues to evolve its approach to scientific outreach, it remains steadfast in its mission to protect, promote, and conserve Mediterranean biodiversity. Through a blend of tradition and innovation, the garden serves as a beacon of botanical education and environmental conservation, inspiring generations to connect with the natural world.

P.0294 Lichen diversity, citizen science and biomonitoring or how to help botanical dissemination

Zulema Varela[1]

1 CRETUS, Ecology Unit, Department Functional Biology, Facultade de Bioloxía, Universidade de Santiago de Compostela, Spain.

Citizen science is a valuable tool for raising awareness of environmental issues, disseminating scientific knowledge and methodologies, and also a great strategy for helping society to learn about and value botany. With this idea in mind, a project is being carried out between the Ánxel Casal vocational school in A Coruña (Galicia, NW Spain) and the University of Santiago de Compostela with the aim of biomonitoring air quality in the city of A Coruña using lichens. To achieve this objective, the first step is for both students and teachers to learn to differentiate lichen species and their growth forms in order to calculate the lichen diversity index and thus carry out an analysis of air pollution in different areas of their city (e.g., areas with high traffic density and areas with low emissions, parks…). So far, the implementation of the project has revealed that: i) 30% did not know what lichens were and thought they were mosses; ii) 80% are able to differentiate growth forms; iii) 50% prefer to use apps instead of field guides to identify species; iv) 45% try to identify lichen species when walking on the street or in the countryside (not related to this project); and v) 91% would participate again in citizen science projects. This shows that once botany is known, it is of general interest and helps society to appreciate the organisms we live with around us. It also shows that citizen science projects are very useful to bring this discipline closer to society and that in the future they will be key to the conservation of species.

P.0295 The “Serra del Porquet” project: merging university and secondary school iNaturalist projects to expand biodiversity appreciation

José Luis Villar García[1, 2], María Ángeles Alonso Vargas[1], Mario Martínez Azorín[1], Manuel Benito Crespo Villalba[1], Elena Martínez García[3], Elisa Goytia Pasquín[4], María Caballero Torres[5]

1 Department of Environmental Sciences and Natural Resources, University of Alicante, Spain. 2 IES Jorge Juan, Alicante, Spain. 3 IES Bahía Babel, Alicante, Spain. 4 IES Antonio José Cavanilles, Alicante, Spain. 5 IES Francisco Figueras Pacheco, Alicante, Spain.

In 2022, we started the project “Serra del Porquet” to promote the use of iNaturalist among secondary school students. That first attempt included around 180 students from IES Figueras Pacheco (Alicante, Spain) and consisted in a 2-day bioblitz in which the students visited the nearby natural area of “Serra del Porquet” and recorded biodiversity in general. The following year, the project was extended to 3 other schools from Alicante and to new areas. Each school developed an iNaturalist project for each spring round. All single projects were included in an umbrella project allowing to include all observations and providing valuable statistics and comparisons between schools and events. The “Serra del Porquet” project was merged in 2023 with a project developed at the University of Alicante and aimed to Biology degree students. Instead of a single iNaturalist project in which students could upload their observations and familiarize themselves with the local flora, they were encouraged to participate in the Secondary schools’s projects in two ways: helping as identifiers of biodiversity for the observations made by the Secondary School students; and participating themselves in the Bioblitz days organised by the Secondary Schools. The initiative of merging projects had moderate success and only a small percentage of degree students engaged with secondary school students. However, with some adaptations, the idea has been promoted again for the spring of 2024. Moreover, from the Secondary School perspective, more schools are being invited to join the project and it has been also proposed as an eTwinning project (within the Erasmus+ framework) which will help other schools from other countries within the European Union to participate and add their data. At present, the secondary school students have made 2607 observations which include 343 species, 60% of which are land plants.

S.034. CLIMATE CHANGE EFFECTS ON ALPINE PLANT SPECIES AND COMMUNITIES: INSIGHTS FROM THE GLORIA NETWORK

P.0296 Limiting factors of tree performance across Northern Hemisphere forests: an approach through the Law of the Minimum

Cristina Grajera-Antolín[1], Julen Astigarraga[1], Verónica Cruz-Alonso[2], Sara Villén-Pérez[1].

1 Universidad de Alcalá, Madrid, Spain [2] Universidad Complutense de Madrid, Madrid, Spain.

Understanding which environmental factors limit the distribution and performance of plant species is a key question in botany. One classical hypothesis, attributed to Darwin, postulates that biotic factors will be more restrictive at lower latitudes, where abiotic factors are less constraining. Empirical support of this hypothesis is mixed, partly because of methodological differences. Here we suggest that Liebig’s Law of the Minimum is a perspective highly suited to test Darwin’s hypothesis. This law suggests that only one variable will limit the performance of species at any given time and location. Here, we use this principle to identify the factor limiting tree species performance along the latitudinal gradient of US forests. To this end, we fitted quantile regressions of basal area for 114 species distributed in 18,446 plots of the US Forest Inventory and identify whether the limiting factor is biotic (symmetric and asymmetric competition) or abiotic (drought, winter temperature, pH, nitrogen and organic carbon) at each plot. Our results challenge Darwin's classical hypothesis, as the probability of biotic factors limiting tree basal area increases with latitude. Specifically, competition had an approximately 20% probability of being the limiting factor at high latitudes in contrast to any other abiotic factor, which did not exceed this value. Additionally, winter temperature acted as the limiting factor mainly at low latitudes. These unexpected results could be related to the positive effects of rising temperature on tree performance at high latitudes due to climate change. Overall, our findings suggest that climate change could be altering the performance and distribution of tree species across Northern Hemisphere forests, deviating from predictions made by Darwin.

S.036. COMPARATIVE SPATIAL PHYLOGENETICS OF MEDITERRANEANTYPE FLORAS OF THE WORLD

P.0297 Convergent evolution in Mediterranean oaks

Rubén Martín Sánchez1, Andrew L. Hipp2,3, Juan Pedro Ferrio Díaz1,4, Ana López Ballesteros1, Béatrice Chassé5, Domingo Sancho Knapik1,6, José Javier Peguero Pina1[6]

1 Centro de Investigación y Tecnología Agroalimentaria de Aragón, Zaragoza, Spain. 2 The Morton Arboretum, Lisle, USA. 3 The Field Museum, Chicago, USA. 4 Aragon Agency for Research and Development, Zaragoza, Spain. 5 Arboretum des Pouyouleix, Saint-Jory-De-Chalais, France. 6 Instituto Agroalimentario de Aragón, Zaragoza, Spain. 7 Estación Experimental de Aula Dei, CSIC, Zaragoza, Spain.

Oaks (*Quercus* L.) are distributed all around the northern hemisphere occupying a wide range of different climates. Phylogenetically, genus *Quercus* is divided into two subgenera: subgenus *Quercus* (New World oaks) and subgenus *Cerris* (Old World oaks). Both subgenera are hypothesized to have very different ancestors and evolutionary histories. New World species are supposed to have originated in the northernmost part of North America and colonized this continent as far as tropical regions in Mesoamerica and some regions in Eurasia. By contrast, Old World species are likely to have arisen under tropical regions in Southeast Asia and later colonize the Himalayas, temperate regions of Asia, and, finally, the Mediterranean Basin. Our study searches leaf morphological convergences between oaks from different subgenera (even different sections) but adapted to a similar climate. Specifically, we analyzed the leaf adaptation to Mediterranean climates where oaks occur, the Mediterranean Basin and California. We have sampled 190 oaks species from around the world growing in The Pouyouleix Botanical Garden (France), and measured several leaf morphological traits, that have been summarized into an index created *de novo* for this study. We have also used occurrence data from GBIF database to extract WorldClim climatic variables from the natural distribution of each oak. We have seen that summer aridity is the best variable defining the Mediterranean climate. Finally, the phylogeny of the genus has been used to perform the phylogenetic analyses. Mediterranean species resulted to be 38. We did not find significant differences in the rate of evolution of the morphological index but we detected significant shifts in the phylogeny when modelling summer aridity. Moreover, our analyses identified two leaf syndromes in response to the Mediterranean climate. We conclude that it exists a convergent but not exclusive morphology in one leaf syndrome, those with small rounded evergreen sclerophyllous leaves.

P.0298 Evolutionary time as an underlying driver for hyperdiversity across

global and Mediterranean biodiversity hotspots

Francis J. Nge[1,2*], Sven Buerki[3], Martin W. Callmander[4], Wen-Na Ding[5,6], Tao Deng[7], Xianhan Huang[7], Elizabeth M. Joyce[8], Martha Kandziora[9], Porter P. Lowry II[10,14], Heidi M. Meudt[11], Maria Esther Nieto-Blazquez[12], Pei Qin Ng[2,13], Peter B. Phillipson[10,14], Yohan Pillon[15], Sandra Reinales[16], Hang Sun[7], Jennifer A. Tate[17], Qin Tian[18,19,20], Thais Vasconcelos[21], John M. A. Wojahn[3], Renske E. Onstein[22, 20*]

1National Herbarium of New South Wales, Botanic Gardens of Sydney, Mount Annan, Australia. 2 School of Biological Sciences, Faculty of Science, The University of Adelaide, Adelaide, Australia. 3 Department of Biological Sciences, Boise State University, 1910 University Drive, Boise, Idaho, USA. 4 Conservatoire et Jardin botaniques de Genève, Chambésy, Switzerland. 5 Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland. 6 CAS Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, China. 7 Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China. 8 Systematik, Biodiversität & Evolution der Pflanzen, Ludwig-Maximilians-Universität München, Munich, Germany. 9 Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic. 10 Missouri Botanical Garden, St. Louis, Missouri, USA. 11 Museum of New Zealand Te Papa Tongarewa, Wellington, New Zealand. 12 Senckenberg Biodiversity and Climate Research Centre (BiK-F), Frankfurt am Main, Germany. 13 SA Genomics Centre, South Australian Health and Medical Research Institute, Adelaide, Australia. 14 Muséum national d'Histoire naturel, Paris, France. 15 LSTM, IRD, INRAE, CIRAD, Institut Agro, Univ. Montpellier, Montpellier, France. 16 Departamento de Botânica, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil. 17 School of Natural Sciences, Massey University, Palmerston North, New Zealand. 18 Germplasm Bank of Wild Species, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China. 19 University of Chinese Academy of Sciences, Beijing, China. 20 German Center for Integrative Biodiversity Research (iDiv) Halle - Jena - Leipzig, Leipzig, Germany. 21 Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, USA. 22 Naturalis Biodiversity Center, Leiden, the Netherlands.

Biodiversity hotspots contain high species richness, endemism, and threat, but whether they share common evolutionary dynamics remains unknown. We inferred age, diversification rate, and species richness for 2,904 plant lineages across 21 biodiversity hotspots and biodiverse regions, including four Mediterranean regions across the globe. We applied phylogenetic comparative methods to evaluate whether age and area explain species richness variation across hotspot lineages, and whether regions that share a similar environment also share lineages with similar ages and rates. Hotspot regions differed substantially in evolutionary dynamics. Furthermore, we detected increasing species richness with lineage age and phylogenetic signal in diversification rates and environment (e.g., islands, Mediterranean climate) across hotspot lineages, among other factors. Our results suggest that hotspots with the highest species richness contain old lineages that have accumulated diversity over time, but the highest diversification rates are found in young, island-like hotspots. Furthermore, lineages within hotspots share similar ages and rates, suggesting that region-specific drivers have shaped lineages in a similar way, while phylogenetic history has predisposed certain lineages to repeatedly colonise environmentally similar hotspots and occasionally diversify in them (e.g., Rhamnaceae across Mediterranean systems)

S.037. CONNECTIONS ALONG THE ATLANTIC FRINGE

P.0299 Total recount of indigenous species of the Celtic Fringe (TRISCelt): a standarised biodiversity occurrence database of Atlantic vascular plants

González-Toral[1], Isabel Larridon[2], Jose Ignacio Márquez-Corro[2], Marcial Escudero[3], Juan Arroyo[3], Eduardo Cires[1,4]

1 Universidad de Oviedo, Oviedo, Spain. 2 Royal Botanic Gardens, Kew, Richmond, UK. 3 Universidad de Sevilla, Seville, Spain. 4 Instituto de Recursos Naturales y Ordenación del Territorio, Mieres, Spain.

The Atlantic Floristic Region comprises territories considered among the best recorded and covered in existing on-line biodiversity databases. Although this Region has controversial boundaries, there is consensus about the Celtic Fringe—North Iberian Peninsula, North and Central France and the British Islands and their surrounding Islands—, which territories are represented in numerous vascular flora checklists. Since curated biodiversity occurrence databases are fundamental and critical to assess different aspects of vascular plants biodiversity at local and global scale, we aim to generate a standardised biodiversity occurrence database of the native vascular flora of the Celtic Fringe using a fine spatial resolution (10 x 10 Km UTM grid). We chose the cosmopolitan sedge family (Cyperaceae), which comprises nearly 6,000 species distributed in 95 genera and is especially diverse in temperate regions such as the Celtic Fringe, to illustrate this process. The inventory of the native Cyperaceae taxa of the Celtic Fringe included 201 taxa belonging to 15 genera and covering 96.64% of the total Celtic Fringe area (8,373 grids). The Cantabrian Atlantic and the French Atlantic were the most taxon-rich subprovinces (>130 taxa) however, the majority of the hybrid taxa were found in the Britannic subprovince and belonged to 2 genera. The highest area coverage (>97%) and number of occurrences (204,755) were presented by the Britannic and the French Atlantic subprovinces, respectively. Nonetheless, the mostly high-mountain and Mediterranean neighbouring Orocantabrian subprovince presented the lowest surface coverage (ca. 89%). The standardization process indicates that there exists an uneven occurrence coverage among subprovinces, which would impact future biodiversity studies. Nevertheless, the TRISCelt database and checklist will allow studying the impact of biotic and abiotic factors on the spatial phylogenetic diversity patterns of large and diverse families such as Cyperaceae within the Celtic Fringe.

S.038. CONSERVATION STATUS OF MAGNOLIA IN SOUTH AMERICA

P.0300 Magnolia calimaensis: population structure and reproductive biology

Gloria D. González-Zuñiga[1], Cristian E. Rodas-Ensuncho[1], Kelly T. Bocanegra-González[1,2,3]

1 University of Tolima, Ibagué, Colombia. 2 The University of Edinburgh, Edinburgh, UK. 3 Royal Botanic Garden Edinburgh, Edinburgh, UK.

Selective logging and habitat modification threaten 87% of the species of the *Magnolia* genus in Colombia. These species are characterized by using floral biology strategies such as protogyny, thermogenesis and floral aromas, with Coleoptera (Nitidulidae, Scarabaeidae) being the main pollinators. *M. calimaensis* (Sect. *Talauma*) is endemic to the Bajo Calima region in western Valle del Cauca and is classified as Critically Endangered (CR).

Its population structure and reproductive biology have not been studied, which is essential information to know its status and establish conservation actions. Therefore, in this research all the individuals found were recorded and measured, determining their size structure and spatial distribution. In turn, 240 hours were dedicated to observing the flowering and anthesis of 8 individuals, classifying their anthesis into 5 phases: pre-pistillate, pistillate, pre-staminate, staminate, and post-staminate, in addition, its pollinator was identified by collecting flowers in interphase. 38 individuals were recorded, with a gregarious dispersal pattern and dimensions of 6-20 m in height and 3.18-49.02 cm in diameter. In addition, it was observed that: *i)* Floral development occurs between 6-8 weeks. *ii)* Two bracts protect the flower bud until it opens. *iii)* The pistillate phase was evident with the partial opening of the floral chamber (18:30 h, day-0). *iv)* On day-1, the floral aromas are pleasant, and the tepals are cream-colored, tending toward yellow. *v)* At 18:40 h the staminate phase begins, attracting great activity from floral visitors, 35 minutes later, partially open tepals are observed. *vi)* During day-2, the flower in its post-staminate phase presents tepals and stamens that wither and detach from the receptacle. *vii)* Of 5 flowers collected, 4 contained groups of 2-3 beetles. Like other species in the section, *M. calimaensis* triggers the anthesis process in the Afternoon-Night for two consecutive nights. Its pollinator belongs to the Nitidulidae family.

S.039. CONTRASTING DIVERSITY PATTERNS, BIOGEOGRAPHY, AND CONSERVATION ISSUES IN NORTHERN AND SOUTHERN HEATHERS (ERICEAE, ERICACEAE)

P.0301 Distribution and extension changes of the European Atlantic heathlands in NW Iberia during the Upper Pleistocene and the Holocene

Castro-Parada, A.[1]; Cazás, N.[1]; Gómez-Orellana, L.[2]; Ramil-Rego, P.[2]; Ferreiro da Costa, F.J.[2]; Briones, M.J.[3]; Muñoz Sobrino, C.[1]

1 Departamento de Bioloxía Vexetal e Ciencias do Solo, Universidade de Vigo, Vigo, Spain. 2 Laboratorio de Botánica e Bioxeografía, Universidade de Santiago de Compostela, Lugo, Spain. 3 Departamento de Ecología e Bioloxía Animal, Universidad de Vigo, Vigo, Spain.

European Atlantic heaths develop on humid oceanic climates and their natural occurrence may be limited by cold temperatures and summer droughts. Throughout different periods during the Pleistocene and the Holocene, the shrublands and heathlands represented the climax vegetation in NW Iberia. This may be related to the noticeable diversity of genera and species of Ericaceae, Empetraceae and Pyrolaceae (*Erica, Calluna, Daboecia, Vaccinium, Arbutus, Corema*) currently existing in the area, which form habitats and landscapes of great ecological value. We reviewed the evidence of coastal heathland on the Cantabrian coasts, in the *Rías Baixas* and on several nearby oceanic mountains, dated from the end of the Pleistocene to present, to understand modern heathlands history in NW Iberia. Due to the climatic improvement a general expansion of broad-leaved deciduous forests occurred in NW Iberia after the end of the last glacial period. Thus, forests partially replaced heathlands and other open habitats, both on the coasts and in many mountain areas. Besides, coastal heathlands from NW Iberia retreat during the Holocene due to the sea-level rise, but various studies carried out in mountain peatbogs and lakes also suggest that changes in the vegetation composition occurred during the Holocene, with heathland increasing during the colder episodes but declining in favour of deciduous forest during the warmer episodes. From the Bronze Age onwards, the extent of heathlands peaked asynchronously in NW Iberia, as well as in different areas of Western Europe, a phenomenon that has been attributed to the combination of changing climate and the landscape transformation into agrosystems. Besides, anthropic influence must also contribute to the disappearance of heathlands in some localities, as occurred in some islands of the Galician coasts during the last 3000 years.

P.0302 Conservation issues of the endemic chasmophytic species of low altitude in the Mediterranean: case of Silene sect. Siphonomorpha

Melilia Mesbah[1], Farid Bekdouche[1,2], Keyssa Laidi[3], Errol Véla[4],Mohamed Sahnoune[1]

1 Laboratoire d'Ecologie et Environnement, Faculté des Sciences de la Nature et de la Vie, Université de Bejaia, Bejaia, Algérie. 2 Département d'Ecologie et Environnement, Faculté des Sciences de la Nature et de la Vie, Université de Batna II, Batna, Algérie. 3 Département des Sciences Agronomiques, Faculté des Sciences Biologiques et des Sciences Agronomiques, Université Mouloud Mammeri de Tizi Ouzou, Tizi Ouzou, Algérie. 4 Université de Montpellier, Montpellier, France.

The Mediterranean low-altitude limestone cliffs are known for their exceptional diversity and richness in endemics, often insufficiently assessed in Algeria. The present study is an analysis and a synthesis of individual IUCN assessments of three endemic Algerian chasmophytic species, Silene sessionis, S. aristidis and S. auriculifolia. The aim is to understand the various threats to this kind of habitat and the conservation issues of the species that grow on it. These assessments were carried out in five littoral or sublittoral areas in the north of the country. Their conservation status was established according to the IUCN recommendations and approved by the official Red List process. New sites were discovered for S. sessionis and S. aristidis with, respectively, 23/103 and 152/1174 young/total individuals, an extent of occurrence (EOO) / area of occupancy (AOO) of 2/12 and 2.6/32 km^2. The identified threats are quarries, sport climbing and shotcrete. A single site was found for S. auriculifolia (absent in three other historical sites) with only six individuals, all senescent and sterile, an EOO and an AOO of only 0 and 4 km respectively. Threats are poorly identified. The new adopted statuses for the three species are, respectively, "Endangered", "Vulnerable" and "Critically Endangered". In situ conservation measures are highly recommended for S. sessionis and S. aristidis; ex situ conservation of S. auriculifolia appears urgent. The heritage issues of these cliffs in Algeria, often located close to cities and/or transport infrastructures, deserve a reinforcement of regulatory measures (legal protection of species, ban of some development technologies) and preventive measures (pre-project impact assessments).

P.0303 Cold tolerance evolution in southern grasses (Danthonioideae): effects of snow cover and acclimation ability

Sofia Nilsson[1], Marian Schubert[1,2], Aelys M. Humphreys[1]

1 Stockholm University, Stockholm, Sweden. 2 Norwegian University of Life Sciences, Ås, Norway.

S.040. CRYOBIOTECHNOLOGY: BROADENING THE SCOPE OF PRESERVING PLANT BIODIVERSITY FOR THE FUTURE

P.0304 Stress tolerance and longevity of oak pollen: basis for the creation of a Global Oak Pollen Bank (GOPB)

Daniel Ballesteros[1, 5]*, Jose L. Canón-Prieto[1], Hugh W. Pritchard[2], Yu Tu[2], Hongying Chen[2], Raquel Folgado[3], Max Winkeljohn[4], Valerie Pence[4].

*1 University of Valencia, Burjassot, Spain. 2 Chinese Academy of Sciences, Kunming Institute of Botany, China. 3 The Huntington Library, Art Museum, and Botanical Gardens, San Marino-California, USA. 4 Center for Conservation and Research of Endangered Wildlife, Cincinnati Zoo and Botanical Garden, USA. 5 Royal Botanic Gardens, Kew, UK. *daniel.ballesteros@uv.es.*

Oak (*Quercus* spp.) seeds are not conserved for the long-term in any conventional seed bank due to their recalcitrance: their sensitivity to drying and freezing. While important efforts are put in cryopreservation research of diverse plant tissues, the implementation of these high-tech approaches is still very limited. Hence, no back-up copy exists of the genetic diversity of most oak species in the world. One route to immediately strengthen oak conservation is to establish a pollen bank. Pollen of a few oak species tolerate drying and freezing. If these attributes are shared among all species reported, a bank of dry pollen would be a low-tech method for the long-term conservation of paternal lines within oak species. The "Global Oak Pollen Bank" (GOPB), funded by the International Oak Society, aims to: (1) conduct basic research on stress tolerance and longevity in a diversity of oaks, and (2) create the first pollen bank for oak species from a global perspective. We aim to collect, research and bank pollen from at least 50 oak species in a global context, including 10 of the most endangered taxa in some of the most important oak hotspots. So far, we have found that pollen from all species tested (4 from USA, 4 from China and 5 from Spain) tolerate drying up to 11% relative humidity (RH) and storage at sub-zero temperatures after drying to 11-30% RH. Longevity studies indicate that dry storage at 30% RH seems the most suitable condition. These results set the basis for optimal oak pollen storage and are being used to create the collection conserved in the GOPB. We expect that the GOPB will not only act as a back-up of the rich oak genetic diversity but will become a fundamental conservation tool in oak restoration projects through Assisted Reproduction Technology.

P.0305 Unlocking seed functional trait diversity and stress resilience of trees to enhance ex situ conservation using cryobiotechnology

Namrata Pradhan[1], Anne Visscher[1], Louise Colville[1]

1 Royal Botanic Gardens, Kew, London, United Kingdom.

The world's forests are under threat and 30% of the world's trees are at risk of extinction. Whilst *in situ* conservation is key to the protection of species and ecosystems, *ex situ* conservation provides an insurance policy against biodiversity loss when climate change, habitat destruction and geopolitical instability threaten *in situ* conservation efforts. The Global Tree Seed Bank: Unlocked programme is working with partners in Africa, South America, Europe/Caucasus, Australasia and Asia to conserve tree seeds and restore diverse forest areas. Within this programme our research is addressing the challenge of conserving tree species that cannot be preserved in conventional seed banks because their seeds do not survive drying (recalcitrant) or their seeds are short-lived in seed bank storage at -20°C. For these "exceptional species" alternative methods for long-term *ex situ* conservation using cryobiotechnology must be developed. This requires an in depth understanding of the response of plant cells and tissues to desiccation and low temperature stress to optimise their survival and recovery following cryopreservation. This three-year project will build upon previous research to deliver: (1) Greater understanding of tree seed stress tolerance to identify species requiring cryopreservation for their long-term *ex situ* conservation; (2) successful cryopreservation of tree seeds and pollen in The Kew Cryobank; (3) enhanced knowledge of the stress resilience of tree seeds and seedlings and the interacting effects of maternal environment and cryopreservation on post-storage recovery and stress tolerance; (4) Sharing and dissemination of research findings through publications, presentations at conferences, and delivery of a training course on the cryopreservation of trees. Through advancing our understanding of the cryopreservation and post-storage recovery of tree species we will establish effective cryobiotechnological approaches for the long-term *ex situ* conservation of trees to protect against biodiversity loss and provide options for forest restoration in the future.

P.0306 Effect of maturity, provenance, and the use of cryoprotectant solutions on the cryopreservation of Quercus suber and Quercus ilex

Ana Fernández T.[1], Daniel Ballesteros[2,3]

1 Pontifical Catholic University of Chile, Santiago, Chile. 2 Universitat de València, Burjassot, Spain. 3 Royal Botanic Gardens, Kew, United Kingdom.

Quercus is a large, widespread and important tree genus in the north hemisphere. However, anthropic intervention and biotic and abiotic stress associated with climate change added to a poor regenerative capacity, maintain various *Quercus* species seriously threatened with extinction. For example, the oak decline syndrome (aka "*la seca*") is a global phenomenon with a high impact on some Iberian oaks, like *Q. ilex* and *Q. suber*. Conserving the genetic diversity housed in the wide geographical distribution of these species is crucial, particularly to secure genotypes resistant to this syndrome. Whether for ecological, economic or sociocultural interest, the ex-situ conservation of *Quercus* species has attracted particular attention worldwide, which comes up against the difficulty imposed by its seeds' recalcitrant nature (*i.e.*, desiccation sensitivity). This difficulty has been overcome for various plant species through the storage of their tissues in liquid nitrogen (cryopreservation); however, various incident factors must be examined to develop successful protocols in oak species. In this study, we have investigated the effect of seed maturity of *Q. ilex* and the provenance of seeds of *Q. suber* on post-thaw survival after cryopreservation. In both species, we have also compared the effect of using cryoprotectant solutions, such as PVS3 or glycerol alone. The responsiveness of embryonic axes excised and partially dried ultra-fast for different times and exposed to liquid nitrogen with or without applying cryoprotectant solutions was evaluated after six weeks of in-vitro culture. The central hypothesis is that the maturity stage and the latitudinal location of wild populations could be associated with different tolerance to desiccation and low temperatures, exhibiting different aptitudes to tolerate cryopreservation protocols. The approach of this study increases the knowledge of factors associated with cryopreservation success for these important recalcitrant species.

P.0307 Conservation of a rare medicinal plant Thottea siliquosa (Lamk.) Ding Hou through indirect organogenesis

Thomas Thuruthiyil, Dennis[1]

1 Department of Plant science, Central University of Kerala, Kasaragod, Kerala, India.

Thottea siliquosa (Lamk.) Ding Hou is a rare medicinal shrub belonging to the family Aristolochiaceae. It is distributed in the Western Ghats region of peninsular India and Sri Lanka. The root of this plant is used for the treatment of diarrhea, dysentery, fever, stomach-ache and as an antidote to snakes and scorpion bites. Roots of *Thottea siliquosa* were excised from in vitro grown shoots and cultured on MS medium supplemented with various plant growth regulators and the optimum callus induction was observed on MS medium supplemented with 3.0 mg/l Kinetin (KN) and 1.0 mg/l 2, 4-Dichlorophenoxyacetic acid (2, 4- D). Here, 93% cultures produced calli with good proliferation rate. The calli were multiplied and maintained on MS medium supplemented with 0.5 mg/l 2, 4-D. For shoot organogenesis, the calli were subcultured on MS medium supplemented with 0.5

mg/l N6–Benzyladenine (BA) and 0.2 mg/l α-Naphthaleneacetic (NAA). On this medium 100% cultures responded with a mean number of 20.3 shoots per unit calli. The small shoots were isolated and subcultures on MS medium supplemented with 1.0 mg/l BA for shoot elongation. The shoots measuring a length of about 1.5-2.0 cm were excised and cultured on half-strength MS medium supplemented with 1.0 mg/l Indole- 3-butyric acid (IBA) for root induction. Here, an optimum 90% cultures responding with a mean number of 20.8 roots per shoot. The rooted shoots were carefully removed from culture vials and washed thoroughly to remove agar and transferred to paper cups containing autoclaved garden soil: organic manure: cocopeat in the ratio 1:1:1 and kept in a plant growth chamber for acclimatization. Overall 93% plants survived during acclimatization. The acclimatized plants were eventually transferred to field. The protocol standardized here could be utilized for the efficient propagation of this rare medicinal plant.

S.041. CULTIVATED PLANT TAXONOMY: BRIDGING THE DIVIDE

P.0308 Taxonomic implications of some foliar organic compounds in selected Capsicum L. species.

Adeyinka O. Adepoju[1], Abiola G. Femi-Adepoju[2]

1 Research Institute for Innovations, African Methodist Episcopal University, Monrovia, Liberia. 2 Biology Department, African Methodist Episcopal University, Monrovia, Liberia.

The Nigerian *Capsicum* L. varieties and species are closely related so much that there has been some confusion among different taxonomists on their taxonomic status. The focus of this study was to investigate the taxonomic position of members of the*Capsicum* L. genus in Nigeria so as to evaluate the genetic discrepancies and closeness between them to shed some light on their identification and the infrageneric classification (INC) of the genus as well. Seeds of five cultivars of *Capsicum* spp., collected from various sources and authenticated, were regenerated and nurtured to fruiting. Variations in their foliar organic compounds were identified quantitatively using Gas Chromatography Mass Spectroscopy (GCMS). 16 organic chemical characters were compiled for *Capsicum*. The cultivars of each genus were hierarchically clustered as operational taxonomic units (OTUs) using squared Euclidean distance computed through PASTatistics software (Ward's method). Artificial keys were also constructed for the identification of the species in the genus. The categories of chemical characters adopted gave useful insights into the INC of the genus, as their combinations were sufficiently diagnostic of the species, as evidenced by the artificial keys. Taxonomic status was successfully clarified in the members of the genus *Capsicum* L. in Nigeria with relation to the distribution of their fruit capsaicin content (FCC), similar to those reported for morphology and phytochemicals in *Capsicum*. However, the challenge of vague infrageneric boundaries had only been partially resolved in the Nigerian *Capsicum* spp. studied.

P.0309 Potential of maternally inherited genomes in conservation genetics of crop wild relatives: Olea europaea L. as a case study

Andrés Barea Márquez[1], Rafael Rubio de Casas[1], Miguel G. Ximenez-Embun[1], Carlos García-Verdugo[1], Guillaume Besnard[2]

1 Universidad de Granada, Granada, Spain. 2 Laboratoire Évolution & Diversité Biologique, CNRS, Toulouse, France.

Crop wild relatives (CWRs) represent a unique reservoir of genetic and phenotypic diversity. In particular, the so-called "pool one" CWRs (those related to crops at the intra-specific level) are of increasing interest to breeders as reservoirs of genes and traits of interest. CWRs are thus crucial to prevent genetic erosion & increase crop resilience, especially in the context of global change.

However, to date, there are very few programmes and strategies specifically aimed at the conservation and management of CWRs. Population genetics and phylogeography have proven useful in informing conservation strategies and defining conservation units and can improve CWR conservation efforts by highlighting wild populations that may harbour genetic resources that are not included in the cultivated pool. However, crops and their intra-specific wild counterparts often have overlapping distributions. As they are interfertile, continuous admixture poses challenges in accurately discerning genuine CWRs from feral plants. Cytoplasmic genomes, such as plastomes and mitogenomes, are generally of exclusive maternal inheritance and therefore provide a strong and reliable phylogeographic signal. This makes them useful for identifying potentially untapped genetic resources or distinguishing between genuinely wild and feral populations. Here, we present a new phylogeny of the Olea europaea complex based on complete plastomes and mitogenomes, which supports previous hypotheses and helps to describe the complex evolutionary history of this species. We also discuss the potential of maternally inherited genomes to inform conservation measures and present a practical case integrating plastome-based phylogeography with eco-geographic approaches to establish a network of conservation sites for this taxon. Our methodology could be potentially applied to any other taxon of interest and combines genetic and ecological/agronomic criteria to prioritize in-situ preservation of wild diversity.

P.0310 Sakurab season: on the peculiar flowering and proper identification of Allium chinense G.Don in the Philippines

Michael Cedric B. Bartolome[1], Renerio P. Gentallan Jr.[1], Kristine Joyce O. Quiñones[1], Teresita H. Borromeo[1], Juan Rodrigo A. Vera Cruz[1], Emmanuel Bonifacio S. Timog[2]

1 Institute of Crop Science, University of the Philippines Los Baños, Laguna, Philippines. 2 Department of Forest Biological Sciences, University of the Philippines Los Baños, Laguna, Philippines.

Japanese scallions (Rakkyō), commonly known in the southern Philippines as sakurab or sibujing, is a minor crop frequently overlooked both in terms of economic potential and taxonomic identity. Despite its cultural significance and long history of cultivation, its non-flowering had hampered appropriate attribution to this crop species. Hence, herein is presented the first documentation of complete inflorescence and flower development of *Allium chinense* G.Don in the Philippines along with the observed peculiarities in comparison with published descriptions especially of cultivars documented in major cultivation areas. The *ex situ* conserved accession collected from Marawi conformed with the general dimensions of the inflorescence and floral parts, especially with the conspicuous exsertion or filaments and style but exhibited noteworthy distinctiveness. Contrary to the usual unpredictability, regularity in flowering was notable, initiating from the onset of the northeast monsoon and coinciding with the fall flowering in California and Japan. The development of multiple long teeth crowding both sides of the filament base is of particular interest since the character had long been regarded as variable but proved significant in the sectional classification of the subgenus Cepa. Most importantly, the potential of this accession to develop secondary umbels is a first to be reported in the genus *Allium*. This suit of characters provided compelling evidence and support for the recent molecular identification of this crop as *A. chinense* and settle the longstanding misapplication of various taxon names following its nomenclatural history of obscurity. Likewise, this discovery puts the Philippines to the map of the regions of introduction and cultivation and offers substantial insight into the disputed domestication history of the species and put forward the proper classification of the different cultivars and strains along with their phylogenetic relationships and tracing of possible natural hybridization events.

P.0311 Evolutionary history of the Allium ampeloprasum L. complex and related horticultural groups evidenced by karyological and molecular data

Thinhinan Khedim[1]

1 Departement of Biology and Physiology of Organismes, BPO Laboratory. University of Sciences and Technology Houari Boumediene, Algiers, Algeria.

The *Allium ampeloprasum* L. polyploid complex, comprising hexa- and octoploid horticultural cultivars (6*x*-8*x*) and several traditional tetraploid varieties (4*x*), represents an economically relevant group. This study aims to explore the diversity and origin of polyploidy in this complex with particular focus on its poorly investigated North-African wild representatives. Natural populations were sampled in contrasted bioclimatic sites, then subjected to karyological and molecular analysis based on nuclear rDNA *ITS* region and chloroplast *trnL-trnF* and *trnD-trnT* intergenic spacers. Comparative phylogenetic analyses were performed with available Genbank accession sequences representing old-world relatives. The results proved original data on the geographical distribution of the wild diploid (2n = 16) and polyploid (2n = 32) Algerian populations and new insights on their relationships and systematic position. The study provides novel and robust evidence demonstrating that the North African *A. ampeloprasum* genetic pool widely contributed as a source of progenitors in the formation of the GHG and Leek cultivated allopolyploids. Consequently, the North African populations emerge as an important reservoir of new wild genetic resources for tracing the origin of crop domestication and for breeding programs of cultivated varieties.

P.0312 Wild fruit and nut species in the living collection of the Armenian biodiversity information and education centre

Anush A. Nersesyan[1]

1 Institute of Botany after A. Takhtajyan of the National Academy of Sciences of the Republic of Armenia, Yerevan, Republic of Armenia.

The flora of Armenia is very rich in wild crop relatives. Armenian Biodiversity Information and Education Centre (Ecoepicenter) of the A. Takhtajyan Institute of Botany NAS RA conducts research, *ex situ* conservation and educational activities. The living collection of the Ecoepicenter exhibits several models of different vegetation types and landscapes of Armenia. Wild fruit and nut species of the Collection are represented by: wild pear, *Pyrus caucasica, P. gergerana* (endemic to Armenia; globally CR)*, P. hajastana* (endemic to Armenia; globally EN)*, P. salicifolia, P. sosnovskyi* (endemic to Armenia; globally EN), *P. tamamschiannae* (globally EN); almond, *Prunus fenzliana*, wild cherry, *Prunus incana, P. mahaleb*; plum, *Prunus cerasifera subsp. divaricata;* hawthorn, *Crataegus pontica*; Caucasian persimmon, *Diospyros lotus;* apple-tree *Malus orientalis;* common medlar, *Mespilus germanica;* European bird cherry, *Prunus padus;* wild rose, *Rosa boissieri, R. canina, R. hemisphaerica, R. pulverulenta, R. spinosissima;* raspberry: *Rubus idaeus;* mountain-ash and rowan, *Aria orbiculata, Hedlundia luristanica, H. roopiana, Sorbus aucuparia, S. hajastana, Torminalis glaberrima;* common barberry, *Berberis vulgaris;* cornelian cherry, *Cornus mas;* wild cobnut and hazelnut, *Corylus avellana, C. colurna;* oleaster, *Elaeagnus angustifolia;* sea buckthorn, *Hippophae rhamnoides;* wild fig, *Ficus carica; gooseberry, Ribes uva-crispa subsp. uva-crispa;* currant, *Ribes alpinum, R. orientale;* common walnut, *Juglans regia;* pomegranate *Punica granatum;* wild pistachio tree, *Pistacia atlantica subsp. mutica;* black elder, *Sambucus nigra;* common bladdernut, *Staphylea pinnata*. Five species are included in the Red Data Book of Armenia (2010). A.Takhtajyan Institute of Botany's partnership to the HORIZON EUROPE FRUITDIV Project 10113396 supported by EU will promote further development of the collection. The knowledge, observations and data obtained through establishment and maintenance of wild fruit and nut species at the Ecoepicenter will be used in the framework of the Project.

P.0313 Morphometrics and phylogenomics of the cultural keystone crop coca (Erythroxylum spp.) illuminate challenges to its taxonomy

Natalia A. S. Przelomska[1,2,3], Rudy A. Diaz[2], Fabio Andrés Ávila[4], Gustavo A. Ballen[5], Rocío Cortés-B[6], Logan Kistler[3], Daniel H. Chitwood[7], Martha Charitonidou[8], Susanne S. Renner[9], Oscar A. Pérez-Escobar[2], Alexandre Antonelli[2,10,11]

1 University of Portsmouth, Portsmouth, UK. 2 Royal Botanic Gardens, Kew, Richmond, UK. 3 National Museum of Natural History, Smithsonian Institution, Washington DC, USA. 4 The New York Botanical Garden, New York, USA. 5 Queen Mary University of London, London, UK. 6 Universidad Distrital Francisco José de Caldas, Bogotá, Colombia. 7 Michigan State University, East Lansing, USA. 8 University of Ioannina, Ioannina, Greece. 9 Washington University, Saint Louis, USA. 10 Gothenburg Global Biodiversity Centre, University of Gothenburg, Göteborg, Sweden. 11 University of Oxford, Oxford, UK.

South American coca (*Erythroxylum coca* and *E. novogranatense*) has been a keystone crop for many Andean and Amazonian communities for at least

8,000 years. However, over the last half century, global demand for cocaine has placed this plant in the centre of armed conflict, deforestation and the explosion of illicit economies. While national and international agencies progress from a 'war on drugs' policy model towards locally appropriate, data-informed strategies to tackle coca plantations, monitoring their expansion and composition remains essential. The principal means to identify coca plants is leaf morphology, yet the extent to which this is reflected in taxonomy is uncertain. Here, we analyse the consistency of the current naming system of coca and its four closest wild relatives (the 'coca clade'), using morphometrics, phylogenomics, and population genomics. We include the name-bearing type specimens of coca's closest wild relatives *E. gracilipes* and *E. cataractarum*. Morphometrics of 342 digitized herbarium specimens show that leaf shape and size fail to reliably discriminate between species and varieties. However, the rounder and more obovate leaves of certain coca varieties could be associated with domestication syndrome of this crop. Our phylogenomic data indicate gene flow involving monophyletic clades of *E. gracilipes*and the *E. coca*clade. These results add to our understanding of the evolution of coca and support a taxonomic framework where in *E. gracilipes*is retained as a single species. Our findings underscore idiosyncratic challenges to the classification of cultivated plants which are situated on a domestication spectrum yet require a reliable naming system. Once this is clearly established for coca, more complex scenarios can be tackled, namely effectively discriminating varieties of cultural significance from high-yielding cultivars that fuel the lucrative cocaine market.

P.0314 Hybridization between genetically differentiated lineages of Juncus decipiens contributed to the origin of Tatami-mat cultivars

Nana Goto[1], Kumiko Kihara[2], Akiko Soejima[1]

1 Kumamoto University, Kumamoto, Japan 2 National Institute of Technology, Kumamoto College, Kumamoto, Japan.

The tatami, a straw mat unique to Japan, is one of the distinctive and representative elements of Japanese culture. It is made of long stems of *Juncus decipiens*, each having nodes exclusively at an inflorescence node along the stem. In Japan, several cultivars were specifically developed for tatami mats and have been commercially cultivated. These cultivars were initially derived from domestic varieties, which were probably chosen from natural populations during the ancient age. To infer the origin of these cultivars, we conducted biogeographic analysis for *J. decipiens* using genome-wide MIG-seq SNP (Multiplexed ISSR Genotyping by sequencing Single Nucleotide Polymorphism) data on samples obtained from wild populations across its distribution range. As a result, we found three genetically differentiated lineages in *J. decipiens* in Japan and revealed that the cultivars have been derived from hybridization between two of them. Although the two lineages presumed to be the parents of the cultivars are sometimes sympatric in the western part of Japan, the genetic structure of the populations suggests limited natural crossbreeding. Therefore, they might be reproductively isolated to some extent. As a material for tatami mats, longer stems without inflorescence nodes are preferred. Perhaps due to incomplete reproductive isolation, hybrids between the two lineages may produce fewer flowers, resulting in longer stems without inflorescence nodes. It is plausible that ancient people favored such hybrids and cultivated them to develop the cultivars used in tatami production.

P.0315 Prospectives for sustainable use of peonies in Bulgaria

Christina Stoycheva1, Daniela Batovska[2], Ekaterina Kozuharova[1]

1 Department of Pharmacognosy, Faculty of Pharmacy, Medical University of Sofia, Sofia, Bulgaria. 2 Institute of Engineering Chemistry, Bulgarian Academy of Sciences, Sofia Bulgaria.

The genus, *Paeonia* L., consists of approximately 35 species. Peonies are famous as ornamental plants. They are also well-known medicinal plants, being part of the traditional medicine of different nations, and also used in alternative medicine. Several *Paeonia* species and hybrids have been widely used as traditional Chinese medicinal materials for more than 2,000 years in the treatment of cardiovascular, extravasated blood and female genital diseases. In Europe, for medicinal purposes, are popular *Paeonia officinalis* L and *P. peregrina* Mill. Native to Bulgaria are *P. peregrina* Mill., *P. tenuifolia* L. and *P. mascula* (L.) Mill., the last two being protected by the Bulgarian Biodiversity Act. For *P. peregrina,* every year, the Ministry of Environment and Water of Bulgaria determines the quantity (in kg) permitted for collecting. Since the petals and roots of *P. peregrina* are objects of commercial interest in Bulgaria, this study summarizes the hazards for the wild populations. A review of the secondary metabolites and biological activity of Bulgarian peonies is offered in comparison to their relatives and hybrids. Also, the possibilities for cultivation are discussed.

P.0316 Polyploidy, genome size variation, and hybridization in ornamental taxa of Spiraea (Rosaceae)

Lucie Němcová[1], Radim J. Vašut[1]

1 Department of Botany, Palacký University Olomouc, Olomouc, Czechia.

The genus *Spiraea* (Rosaceae), consisting of about 100 species distributed throughout the northern hemisphere, is best known for its great horticultural value. The popularity of small shrubs covered with tiny flowers dates back to the 16th century in Europe. In addition to natural taxa, many hybrids have since appeared in cultivation. The origin of such hybrids is usually inferred from morphology, but evidence of parentage is lacking. We therefore tested two approaches to shed more light on the origin of cultivated *Spiraea* taxa: i) to reveal the variation in ploidy level between species and their cultivars using the flow cytometry (FC), and ii) to pilot test the applicability of genome-wide DArTseq markers on 3 cultivars of putative (so far unknown) hybrid origin. Of the more than 50 taxa tested by FC, the majority of them were diploid, similar to species in related genera (*Petrophytum*, *Physocarpus*, etc.); American species were often tetraploid and several (mostly Asian) taxa were hexaploid; only one species (*S. humilis*) was confirmed to be octoploid; basic chromosome number in the genus is x = 9. Cultural hybrids were mostly confirmed to be intermediate between the expected parents, and odd ploidy levels were also confirmed (3x and 5x). Several controversial genome size values have been confirmed by counting chromosomes from mitotic spreads (e.g. *S. decumbens* or odd ploidy level hybrids). Genetic identification of parentage for 3 putative hybrids was challenging due to high differences in ploidy level, however we identified two new groups of hybrids with apparently spontaneous hybridisation (*S. betulifolia* × *S. nipponica* and *S. nipponica* × *S. ×vanhouttei*). We present here an overview of the ploidy level variation of over 50 *Spiraea* taxa cultivated in Europe and give an opinion on the parentage of some hybrid cultivars.

S.042. CURRENT RESEARCH IN BORAGINALES

P.0317 First draft genomes of two Echium species (Boraginaceae) endemic to the Canary Islands

Ji-Hyeon Jeon[1], Ui-Chan Jung[1], J. Alfredo Reyes-Betancort[2], Arnoldo Santos-Guerra[3], Seung-Chul Kim[1]

1 Department of Biological Sciences, Sungkyunkwan University, Suwon, Republic of Korea. 2 Jardín de Aclimatación de La Orotava, Instituto Canario de Investigaciones Agrarias, Puerto de la Cruz, Tenerife, Spain. 3 Calle Guaidil 16, 38280 Tegueste, Tenerife, Spain.

Oceanic islands represent a high level of endemism biodiversity in plant species, derived by rapid species divergence based on its geographic isolation and various ecological niches. The microenvironment in isolated islands allows pioneer species to adapt and evolve with phenotypic changes and increased fitness. The Canary Islands, the oceanic volcanic islands of the North Atlantic, have a large number of endemic flowering plants (ca. 40%) as a result of their geological age range (1 to 21 Myr) and geographical proximity to Africa. Owing to their high level of endemism, the Canary Islands contribute greatly to studies on the origin and evolution of island plants. Understanding genomic variation and its mechanisms along species divergence and adaptive radiation can elucidate the molecular and genetic bases of evolution and species differences. Mechanisms of parallel or adaptive evolution in plant species radiation have been poorly understood. Leveraging rapid development in genome-wide sequencing technologies, genomes in various plant species are increasingly unveiled, allowing evolutionary studies in depth. Of the genus *Echium* (Boraginaceae), 28 species are recognized in Macaronesia, including the Canary Islands, representing spectacular variation in their phenotypes, ecologies, plant habits and duration shaped by adaptive radiation. As the ideal models to understand evolutionary radiations, we sequenced, assembled, and annotated draft genomes of two *Echium* species endemic to the Canary Islands, herbaceous annual-biennial *Echium bonnetii* and rosette-forming perennial monocarpic *E. wildpretii*, for the first time. The first draft genomes of the Canarian *Echium* species will elucidate the genomic evolution and genetic bases of phenotypic and ecological variation derived by adaptive radiation in oceanic islands. This preliminary study will be a stepping stone to further understandings on evolution of *Echium* species on the Canary Islands, including insular woodiness.

P.0318 Phylogenetic contributions to the genus Omphalodes (Cynoglosseae s.l.) with the taxa distributed in Turkey

Aslı Doğru-Koca[1]*, Golshan Zare[2], Nilay Şen[1], Gül Ayyıldız[3]

1 Plant Conservation and Phylogeny Lab., Department of Biology, Faculty of Science, Hacettepe University, Ankara, Turkey. 2 Pharmaceutical Botany, Faculty of Pharmacy, Hacettepe University, Ankara, Turkey. 3 Laboratory for Microbiology and Process Engineering, Julius Kühn-Institut, Federal Research Centre for Cultivated Plants, Dossenheim, Germany.

Recently, distant lineages have been separated from the genus *Omphalodes* named as *Nihon, Memoremea, Iberodes, Mimophytum*. Thus, the genus *Omphalodes* has been delimited with the taxa distributed in Western Eurasia, Iran, Iraq, and Pakistan. However, there is no information on the phylogenetic position of *O. heterophylla*, endemic to Pakistan; *O. kusnezowii*, native to Transcaucasia; *O. luciliae* subsp. *kurdica*, distributed in Turkey Iran and Iraq; and *O. davisiana* and *O. luciliae* subsp. *cilicica*, endemic to Turkey. There are 5 species, 9 taxa in Turkey. *O. luciliae* has five subspecies. The recently published *O. nedimeae* was described in the Taurus Mountains, which constitutes the general distribution area of *O. luciliae* and its subspecies. The aim of this study was to reveal the evolutionary relationships of the taxa distributed in Turkey, and to re-evaluate the taxonomic status, of especially of the subspecies of *O. luciliae* by investigating multiple populations. We obtained DNA sequences of both ribosomal internal transcribed spacer (ITS1-5.8S-ITS2) and plastid rps16 genes from the different populations collected in Turkey. Bayesian and maximum likelihood phylogenetic trees were calculated using both markers separately. Incongruities were observed between two hypothetical evolutionary trees based on different data sets. Regarding the ribosomal dataset, the genus generated a monophyletic clade while based on rps16, many species were polytomously positioned within segregated genera. In both data sets, the different populations of *O. ripleyana* formed a monophyletic clade. The phylogenetic relationships based on the ITS data set reveal that *O. davisiana* which is known as a local endemic extends along Anatolian Diagonal. The populations of *O. luciliae* susbp. *scopulorum* form a monophyletic clade and this clade is sister to the lineage containing all other subspecies of *O. luciliae*. Our study displays that *O. luciliae* subsp. *scopulorum* should be accepted as a species.

P.0319 Discovering the unsuspected diversity helps to support Antiphytum (Boraginaceae) as an American amphitropical genus

Nidia Mendoza-Díaz[1], Hilda Flores-Olvera[2], Marina Díaz[3], José M. Bonifacino[3], Michael J. Moore[4], Helga Ochoterena[2], Daniel Piñero[1]

1 Instituto de Ecología, Universidad Nacional Autónoma de México, Ciudad de Mexico, México. 2 Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de Mexico, México. 3 Laboratorio de Botánica, Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay. 4 Department of Biology, Oberlin College, Oberlin, USA.

The Americas are an important source of endemic taxa in Boraginaceae, although its greatest diversity is concentrated in Asia and Europe. In the region, North America houses most of the genera shared with the Old World, as well as the largest number of species from the New World endemic genera. However, the South American species are key to properly understand the evolution of Boraginaceae. The American putative amphitropical *Antiphytum* DC. ex Meisn. is a great example of how basic taxonomic research is mandatory to address efforts to understand phylogenetic relationships and diversity patterns. The genus has been proposed either as having a disjunct distribution in North and South America, or the North American species have been segregated into a different genus, *Amblynotopsis* J.F.Macbr. Lacking an adequate sampling of the species and populations during many years obscured all efforts to solve this issue. Our research is the first to carry out intensive field work, careful morphological studies and molecular phylogenies including South and North American taxa. We described three new species and resurrect one taxon, recognizing in total 13 species in *Antiphytum*. The North and South American species share a most recent common ancestor, although the relationships of the South American clade with the two North American clades are unresolved. Nevertheless, we support *Antiphytum* as a genus due to the morphological mosaic revealed with the discovery of *A. charruasorum*. This Uruguayan new species noticeable shares the white flowers with the North American taxa and challenges the previous segregation. Our research increases the known diversity in South America to four species. Likewise, in North America our study increased the known diversity to nine species. With this example, we highlight the need for further efforts on basic taxonomy to achieve a thorough understanding of the Echiochiloideae classification and evolution.

P.0320 An overview of the knowledge of Heliotropiaceae (Boraginales) in Honduras

José I.M. Melo[1]

[1] *Universidade Estadual da Paraíba, Campina Grande, Paraíba, Brazil.*

Heliotropiaceae belongs to the order Boraginales including four genera: *Euploca*, *Heliotropium*, *Ixhorea* and *Myriopus*, and approximately 500 species. It encompasses predominantly herbaceous with several shrubby and climbing plants especially characterized by having a highly specialized stigmatic head; distributed especially in tropical and subtropical zones in arid, semi-arid or coastal habitats. Despite the recent efforts to document the representativeness of Heliotropiaceae in the Neotropics, there are still gaps in the knowledge of their taxonomic diversity and geographical distribution in several countries in this region, especially in Central America. In this perspective, this work includes the taxonomic study of Heliotropiaceae in Honduras; a Central American country still poorly known floristically that has 112,492 km2 and encompasses six main types of forests ecosystems. Morphological analyzes involved collections housed at regional physical herbaria (TEFH) and virtual North American (MO, NY) and European herbaria (K, P). Taxonomic determinations were based on nomenclatural types, protologues and other bibliographies (classical and modern). Three genera and 21 species were recorded: *Euploca filiformis* (Lehm.) J.I.M. Melo & Semir, *E. humilis* (L.) Feuillet, *E. lagoensis* (Warm.) Diane & Hilger, *E. procumbens* (Mill.) Diane & Hilger; *Heliotropium acutiflorum* (M. Martens & Galeotti) J.I.M. Melo*, *H. angiospermum* Murray, *H. angustiflorum* (Ruiz & Páv.) Govaerts, *H. cuspidatum* (Kunth) Feuillet, *H. funkiae* Feuillet, *H. glabrum* (L.) Feuillet, *H. gnaphalodes* L., *H. indicum* L., *H. luebertii* (Standl.) J.I.M. Melo*, *H. macrostachyum* (DC.) Hemsl., *H. mutabilis* (Vent.) J.I.M. Melo*, *H. rufipilum* I.M. Johnst., *H. transalpinum* Vell., *H. umbellatum* (Kunth) J.I.M. Melo*, *H. verdcourtii* Craven; *Myriopus maculatus* (Jacq.) Feuillet, *M. volubilis* (L.) Small. Additionally, four new combinations are proposed under *Heliotropium**, *Heliotropium luebertii* constituting a new record for the Honduran flora. Keys to genera and species, distribution, flowering and/or fruiting data, as well as notes on taxonomic affinities of the species are presented.

P.0321 Diversity and distribution of Heliotropiaceae (Boraginales) in Paraíba state, Brazilian Northeastern

José I.M. Melo[1]

[1] *Universidade Estadual da Paraíba, Campina Grande, Paraíba, Brazil.*

Heliotropiaceae (Boraginales) includes four genera (*Euploca*, *Heliotropium*, *Ixhorea* and *Myriopus*) and approximately 500 species predominantly herbaceous including shrubby and climbing representatives, distributed in tropical and subtropical zones especially associated to arid and semi-arid environments. In Brazil, several taxonomic studies were developed on this family in the last 25 years, especially for the Northeast and Southeast regions. However, there are still gaps in the knowledge of its taxonomic diversity and geographical distribution in several Brazilian states and regions. In this scenario, this work presents the taxonomic study of Heliotropiaceae in Paraíba, a state that has 56,585 km² encompassing the phytogeographic domains of the Caatinga and Atlantic Forest, located in Brazilian Northeast region. Morphological analyzes were carried out on collections housed in regional (CSTR, EAN, HACAM, IPA, JPB) and national (RB) physical herbaria and American virtual (MO, NY) and Brazilian Virtual Herbarium (Reflora), complemented by field studies to collects and observations of natural populations. For identifications, protologues, nomenclatural types and bibliography available for South America were examined, when necessary. Three genera and fifteen species were recorded: *Euploca*, with six species (*E. fruticosa*, *E. humilis*, *E. lagoensis*, *E. paradoxa*, *E. polyphylla* and *E. procumbens*); *Heliotropium*, with five (*H. angiospermum*, *H. curassavicum*, *H. elongatum*, *H. funkiae* and *H. indicum*) and *Myriopus*, with four species (*M. andrade-limae*, *M. candidulus*, *M. rubicundus* and *M. salzmannii*). *H. angiospermum*, *H. elongatum* and *E. procumbens* are the most widely distributed in Paraíba, and *E. fruticosa*, the most restricted, constitutes the first record for the study area. Keys to genera and species, distribution, flowering and/or fruiting data as well as comments on taxonomic relationships based on vegetative and reproductive characters of the species are presented.

P.0322 Boraginales in Gabon

Erik Simons[1]

1 Tropical Botany research group, Naturalis Biodiversity Center, Leiden, The Netherlands.

In the Flore du Gabon volume 57, the Boraginales were treated under the family Boraginaceae sensu lato. This group, which is mainly represented in parts of the world with drier climates, is represented by only a small number of species in Gabon, a country with a tropical wet climate largely covered by rainforest. In Gabon a total of 9 species are present, divided in 5 genera. Research on herbarium material of the tree genus *Cordia* yielded a new species: *C. letestui*. This genus now contains 4 species in Gabon, 2 of which are endemic to Gabon and southern Cameroon. Two other woody species found in Gabon are *Ehretia cymosa* and *Hoplestigma klaineanum*; the latter species is probably very rare and in danger of extinction. Three herbaceous species are present in Gabon. Of the genus *Heliotropium* only the cosmopolitan *H. indicum* is present. Two other herbaceous species that were previously in this genus now fall under the genus *Euploca*. It can be concluded that Boraginales are not strongly represented in Gabon in terms of numbers of species, but that a number of woody species do occur that are endemic and possibly endangered. Further research on this group in lowland rainforests in neighbouring countries is needed and could might reveal additional new species.

P.0323 Contribution to genus Cynoglossum species (Boraginaceae) in the Mediterranean part of the Middle East

Karel Sutorý[1]

1 Moravian Museum, Brno, Czech Republic.

The genus *Cynoglossum* in the Middle East (Syria, Lebanon, and Israel) is not as rich in species as it is on the neighboring Anatolian peninsula. Some sources only mention the presence of *Cynoglossum creticum* Mill. and some add another taxon either under the name *C. nebrodense* Guss. or *C. montanum* L. Neither of them could be found in the discussed area. *C. nebrodense*, described from Sicily, grows besides southern Italy also in Greece and Turkey. The range of *C. montanum* is dispersed from Spain up to north-western Turkey. The study of herbarium material has shown a new taxon (proposed name *Cynoglossum levanticum*) with a distribution range limited to Mt Lebanon and Mt Antilebanon mountain ridges in the eastern part of the Mediterranean.The distribution of *C. levanticum* is determined by temperature and precipitation. It is distributed in the narrow *warm temperate zone with dry and warm summers* amidst arid zones on the east coast of the Mediterranean Sea.

S.043. CYCADS AS EMERGING MODELS IN EVOLUTIONARY BIOLOGY AND SYMBIOSIS

P.0324 First record of plant-animal interactions with the Dioon edule complex in the Sierra Madre Oriental, Mexico

David Balderas[1], Laura Yañez[2]

1 Programa Multidisciplinario de Posgrado en Ciencias Ambientales, Universidad Autónoma de San Luis Potosí, Mexico. 2 Instituto de Investigación de Zonas Desérticas, Universidad Autónoma de San Luis Potosí, Mexico.

The *Dioon edule* complex encompasses the sister species *Dioon edule* Lindl. And *Dioon angustifolium* Miq. Both are endemic plants of Mexico, whose fragmented populations are distributed in the Sierra Madre Oriental (SMO). A widespread belief attributes the toxicity of cycads to the non-existence of wildlife interactions with their seeds and, therefore, their dispersal to abiotic factors. It was unknown which species were capable of preying on and dispersing their seeds. The ecological role of wildlife is essential since it modifies the structure, diversity, and functioning of habitats since these can achieve a connection between *D. edule* populations and thus avoid genetic problems. This study was carried out in the subprovince of the Gran Sierra Plegada in the SMO, in the states of Nuevo León, Tamaulipas, and San Luis Potosí, where we sampled six sites, characterizing the population structure of *D. Edule* in two 1000m transects. In addition, we used *D. edule* seed baits as olfactory stations recording with camera traps and animal tracks 21 species of mammals and birds that interacted with the seeds. We assigned the role of predator or disperser to each species. The α and β diversity indices show that sites share few species. The Kaplan-Meier survival analysis shows that 71.23% of 854 seeds were removed in 10 days. The birds and mammals were the most important species in the interaction with the propagules of *D. edule*. Finally, we determined that plant-animal interactions are one of the factors that modulate the structure of the *D. edule* complex populations.

P.0325 Geographic match of fruit-scented cone volatile compositions with genetic boundary in Cycas revoluta

Jui-Tse Chang[1,2*], Tsung-Chen Lee[3], Anna K. Valchanova[2, 4], Tomoko Okamoto[5], Pei-Chun Liao[1], Yudai Okuyama[2*]

1 Department of Life Science, National Taiwan Normal University, Taipei City, Taiwan. 2 Department of Botany, National Museum of Nature and Science, Tsukuba, Japan. 3 School of Forestry and Resource Conservation, National Taiwan University, Taiwan 4. Department of Biological Sciences, Graduate School of Science, University of Tokyo, Tokyo, Japan. 5. Laboratory of Insect Ecology, Faculty of Applied Biological Sciences, Gifu University, Gifu, Japan.

Volatile organic compounds (VOCs) are essential for plant communication with other species. Population chemical diversity across space hence influences their evolution and ecological interactions with local biological community. Cycads are one of renown gymnosperm with insect pollinations. Among the two families, while VOC study has been focused on Zamiaceae for its specialized pollination systems, there is a crucial need for Cycadaceae research due to stronger connections with insects than we thought before. Cycas revoluta Thunb. is ideal for cone scent geographic variations study due to the identified beetle pollinator, widespread distribution, and abundant populations compared to most other cycads. Also, previously reported genetic boundary raised the need to clarify its correlation with cone VOC variations to know underlying evolution mechanism. Here, we aim to know whether the cone scent VOCs match the genetic boundary, and their chemical composition difference between sexes. Using the solid-phase microextraction (SPME), we collected cone VOCs in both sexes traversing the genetic boundary. Among 29 individuals across three islands, the results demonstrated match of VOC profile with genetic boundary, showing statistically different and stronger VOCs difference between genetic boundary compared to other island comparisons. Further, the fruit-scented cone dominating by ethyl acetate together with fruiting

season of sympatric Pandanus odorifer enable the operation of mimicry by frugivory beetle pollinators such as Carpophilus and Epuraea reported before. Considering the widespread generalist pollinator in East Asia, the match of genetic boundary with cone chemo-variations would be mainly selectively neutral rather than pollinator-mediated selection. Our study is the first to reveal geographic match of chemical scent variations with genetic boundary in cycads and pave the way to study on ecological interactions with antagonist and mutualist across the genetic boundary.

P.0326 Genomics and metabolomics of the cycad microbial phyllosphere

Juan Carlos Villarreal Aguilar[1], Lilisbeth Rodríguez[2], Adriel Sierra[1], Marta Vargas[3], Rita Bethancourt[4], Ariadna Bethancourt[4], Marta Alonso García[1], Brian Sedio[5], Kristin Saltonstall[3]

1 Department of Biology, Université Laval, Québec, Canada. 2 Departamento de Biología Vegetal, Universidad de Panamá, Panamá. 3 Smithsonian Tropical Research Institute, Ancón, Panamá. 4 Universidad de Panamá, Departamento de Microbiología y Parasitología, Panamá. 5 University of Austin, Texas, United States.

Plant-microbe interactions are important factors influencing host fitness. Cycads are known for persisting in habitats under low nutrient availability due to their capacity to harbor a diverse symbiotic microbiome, with most studies focused on their coralloid roots. The leaf endophyte microbiota of cycads remains largely unexplored, as is their potential beneficial interactions with the host. Here we investigate how plant-microbe interactions mediate foliar secondary metabolite composition in *Zamia* species from Panama. By integrating microbial metabarcoding (16S, ITS), genomic and untargeted metabolomics techniques, we characterize the leaf bacterial and fungal microbial community alpha- and beta-diversity in phylogenetically related *Zamia* species with contrasting habitats (terrestrial vs epiphytic), distinct herbivory pressures and relate specific leaf endophytes to host metabolite composition. We recovered a number of nitrogen-fixing cyanobacterial lineages in the cycad endo and exo-phyllosphere raising questions about the functional redundancy of nitrogen fixers in cycads. In addition, we provide comparative transcriptomic and metabolomic evidence of the impact of elevated temperature in cycads. Our studies pave the way to further work on the role of the microbes inhabiting cycad phyllosphere and potential responses to future climatic scenarios.

P.0327 Importance of mesophyll conductance in shaping photosynthetic performance in 34 structurally diverse cycad species

Jesamine J. Rikisahedew[1*], Tiina Tosens[1], Ülo Niinemets[1,2]

*1 Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Tartu, Estonia. 2 Estonian Academy of Sciences, Tallinn, Estonia * Corresponding author: jesamine.rikisahedew@emu.ee.*

Cycads are gymnosperms that comprise species that are considered to be evolutionarily old, and yet are the most understudied plant group in terms of photosynthetic limitations. It is understood that there are biochemical and structural limitations to photosynthesis, however, the considerable variation of mesophyll conductance (gm) and related anatomical traits in particular remain evasive for this unique plant group. The aims of this study were to assess which structural traits are responsible for the variation of net photosynthesis (An) and gm in cycads, determine the diffusional limitations to CO2 drawdown at the subcellular level, and to understand the morpho-physiological basis underlying leaf economic spectrum (LES) traits in evolutionarily old species. 34 cycad species were selected; for which physiological parameters were measured using the Walz gas-exchange system, and anatomical parameters were measured from images taken using both light and transmission electron microscopy. The results show high variability of gm and corresponding structural traits across the cycad species, including between those of the same genus. This study fills the missing niche that explains which structural parameters most influence photosynthesis in cycads, and a better understanding of how these endangered cycads may respond to impending climate change.

P.0328 Morphological diversity in populations of the Dioon edule complex (Zamiaceae) endemic to eastern Mexico

Laura Yáñez-Espinosa[1], Gabriel Rubio-Méndez[2], David Balderas-González[3]

1 Instituto de Investigación de zonas Desérticas, Universidad Autónoma de San Luis Potosí, Mexico. 2 Facultad de Agronomía y Veterinaria, Universidad Autónoma de San Luis Potosí, Mexico. 3 Posgrado en Ciencias de la Vida, Universidad Autónoma de San Luis Potosí, Mexico.

The genus *Dioon* (Zamiaceae) forms species complexes, i.e., species that are very similar morphologically, but different genetically. The Dioon edule complex includes two species: *Dioon edule* Lindl. and *D. angustifolium* Miq. Its geographic distribution consists of scattered populations in the Sierra Madre Oriental (SMO) and central Veracruz. The intraspecific variability of the morphological characters of the *D. edule* complex is expected in a heterogeneous environment. In this study, we proposed to analyze a) morphological variation throughout its distribution area, b) the environmental filter with effect on morphology adjustment processes and c) to define its geographic distribution. Stem height, stem diameter, number of leaves, and leaf length of adult plants were measured in 39 populations. Principal component analysis (PCA) was applied to explore the variability of morphology traits. Another 29 populations were classified with a classification discriminant analysis (CDA) based on geographic and climatic characteristics. Redundancy analysis (RA) was applied to explore the association among environmental variables and morphological traits. The morphological data obtained allowed us to evaluate the phenotypic differences of populations. The PCA defined three phenotypic groups: (TS) tall stem, wide diameter, long and numerous leaves; (MS) medium stem and diameter, sparse and short leaves; (SS) short stem, narrow diameter, scanty and short leaves. 99-100% populations were correctly classified. Morphological traits are linearly related to geographical, environmental and geological variables, mainly latitude, longitude, geological province, average temperature and precipitation of the coldest quarter. Most SS populations are distributed north of 22°N parallel where humidity is sporadic during the summer and winter, but the polar air masses produce abundant rainfall on the slopes below 600 m asl. Towards the south, rainfall is abundant during summer and winter, where MS and TS populations are found.

P.0329 A tale of two threatened species: Crax rubra as a predator and disperser of the cycad Dioon edule seeds in Mexico

Laura Yáñez-Espinosa[1], David Balderas-González[2], Gabriel Rubio-Méndez[3]

1 Instituto de Investigación de Zonas Desérticas, Universidad Autónoma de San Luis Potosí, Mexico. 2 Posgrado en Ciencias de la Vida, Facultad de Ciencias, Universidad Autónoma de San Luis Potosí, Mexico 3 Facultad de Agronomía y Veterinaria, Universidad Autónoma de San Luis Potosí, Mexico.

Mexico's seasonal tropical forest presents high diversity and endemism, making it highly vulnerable to perturbation. Mainly, two species in this ecosystem attract attention because they are threatened due to overharvesting, hunting, illegal trade, deforestation, and land-use change. The cycad *Dioon edule* (Zamiaceae) is categorized as near threatenedby the IUCN. The primary dispersal method is autochory, although secondary dispersal is zoochory. *Crax rubra* (Craciformes: Cracidae) is an omnivorous large bird categorized as vulnerable by the IUCN. Both species have a broad and highly fragmented distribution in eastern Mexico. In the Huasteca region of San Luis Potosi, *Crax rubra* approaches the seeds of *Dioon edule* when foraging. However, the question ofwhether *C. rubra* eats and disperses the seeds or only preys on them remains. We studied *D. edule* population structure and demography. We established photo-trapping stations during January, June, and September toclassify their interactions, assess the type and frequency of the interactions, determine the seasonality and frequency of these interactions, and calculate the density of seeds removed. The survival curve in the *D. edule* population fitted the inverted "J" curve typical of most cycads, with a high mortality rate in the early stages. Previous studies attribute seed mortality to desiccation and predation by insects and rodents. However, *Crax rubra* activities and seasons of the year are associated with adult females (50%) and juveniles (100%) during June, as well as adult males (67%) in September and most adult males (100%) and females (80%) in January. Seed predation (33%) is the most common activity, followed by dispersal (15%). Adult males and females removed most seeds (80%) in January. Association of *C. rubra* and the dominant plant species at the sites based on their fruiting phenology showed adults associated with *D. edule*, *Ficus cotinifolia*, and *Beaucarnea inermis*.

S.044. DISSECTING THE EVOLUTION OF SEDGES (CYPERACEAE): PERSPECTIVES FROM MULTIPLE LINEAGES

P.0330 Phylogenetic analyses of Korean Eleocharis (Cyperaceae)

Kyong-Sook Chung[1], Chae Eun Lim[2], Chunghee Lee[3], Chang Shook Lee[4]

1 Jungwon University, Goesan, Korea. 2 National Institute of Biological Resources, Incheon, Korea 3 National Arboretum, Pocheon, Korea. 4 Department of Science Education, Ewha Womans University, Seoul, Korea.

Eleocharis R. Br. exhibits cosmopolitan distribution with more than 250 species, occurring mainly in wet habitats such as swaps, riversides, and seashores. The genus is characterized with unbranched culms, single spikes, and bisexual reduced flowers with perianth bristles. To estimate phylogenetic relationships of 15 Korean *Eleocharis* taxa, nrDNA (ITS and ETS) and cpDNA (*trnC-ycf6*) were utilized. Somatic chromosomes were also investigated to evaluate chromosome characters in a phylogenetic framework. Cyperaceae is known to have holocentric chromosomes, which miss constricted centromeres during cell division and contribute to dynamic speciation in the family. In the phylogenetic analyses, three major lineages were identified: *E. congesta+E. attenuate+E. wichurae*, *E. valleculosa+E. ussuriensis +E. kamtschatia*, and *E. kuroguwai +E. dulcia*. The linage of *E. kuroguwai+E. dulcia* is basal on the genus, which shares thick culms with transverse septa. Holocentric chromosomes were observed in five taxa: *E. attenuata* f. *laeviseta* (Nakai) H. Hara ($2n=20$), *E. parvula* (Roem. & Schult.) Link ex Bluff, Nees & Schauer ($2n = 10$), *E. ussuriensis* Zinserl. ($2n=16$), *E. valleculosa* var. *setosa* Ohwi ($2n=16$), and *E. kuroguwai* Owhi ($2n=$ca.180). The chromosome sizes vary from ca.0.6 µm to ca. 6 µm categorized into two types, gradient and bimodal karyotypes. Further discussions on cytological and morphological characters analyzed in a phylogenetic framework will be made in the presentation.

P.0331 Integrating systematics and biogeography of Carex L. clade Castanea (Cyperaceae): A multidisciplinary approach in the Neotropic

Luis González-Gallego[1], Anton A. Reznicek[2], Robert F. C. Naczi[3], M. Socorro González-Elizondo[4], Carmen Benítez-Benítez[5], Pedro Jiménez-Mejías[1]

1 Universidad Pablo de Olavide, Sevilla, Spain. 2 University of Michigan Herbarium, Ann Arbor, USA. 3 New York Botanical Garden, New York, USA. 4 Centro Interdisciplinario de Investigación para el Desarrollo Integral Regional Unidad Durango, Instituto Politécnico Nacional, Durango, Mexico. 5 Universidad de Sevilla, Sevilla, Spain.

The genus *Carex* L. (Cyperaceae), with over 2000 described species, is one of the most diverse plant genera in the world, boasting a cosmopolitan distribution that extends to all continents except Antarctica. The evolutionary history and the diversification of this genus encompass various colonization routes influenced by the geoclimatic events of each continent and the lineages that expanded into these new regions. In the Neotropic the genus has above 200 species and there is significant taxonomic and systematic complexity. The phylogenetic knowledge of the group in the area is still limited and the adscription of species to clades is sometimes unclear, with known examples of polyphyly at sectional and species rank. We conducted a taxonomic study of 16 species described in Andes, Central America, and Mexico, and made the morphological characterization of eight of them described in different locations of the Andes. All these species have been variously placed in sects. *Porocystis* Dumort. and *Longicaules* Mackenzie ex Reznicek, both in turn now reported as nested in the so-called Castanea clade. In addition, we carried out a molecular study based on Sanger and genomic DNA sequencing to elucidate the main phylogeographic patterns and the evolutionary history of this group. The main results obtained from this multidisciplinary approach revealed the polyphyly of what is called sect. *Longicaules* and the transferring of several of its species to sect. *Porocystis*. With these results we aim to set grounds to study the natural history of *Carex* in the Neotropic and unravel the biogeographical patterns in this group of sedges in one of the regions of the world where it is less understood.

P.0332 Stomatal presence on the utricles of Carex (Cyperaceae) species

Lorna J. Halliwell[1], Jasmine Morgan[1], Paul A. Ashton[1]

1 Department of Biology, Edge Hill University, Ormskirk, UK.

Utricles are the propagule of the *Carex* species. This structure has often been utilised to address taxonomic questions using light microscopy, however the additional information on utricle ultrastructure obtained with a Scanning Electron Microscope (SEM) has had limited investigation. This study describes intra and inter-specific utricle stomata characteristics observed via a SEM and thus elucidates their potential taxonomic value using a sample set of *Carex*species found within the UK. It also considers whether such stomata have a pre- or post-dispersal function or are a vestigial relic of prophyll origin. Potential functional roles were considered by comparing stomatal size and density against utricle size and utricle density on the flowering spike. Stomata were observed on a significant proportion of the taxa with variation between species. Stomatal length varies between species, though the location of stomata when present is uniform.

P.0333 Systematics and evolution of Bulbostylis (Cyperaceae) in the neotropical region

Juliene Maciel-Silva[1,2,3], André S. B. Gil[3], Isabel Larridon[1]

1 Royal Botanic Gardens, Kew, Richmond, UK. 2 Federal Rural University of Amazon, Belém, Brazil. 3 Museu Paraense Emílio Goeldi, Belém, Brazil.

Bulbostylis (hairsedges) is a speciose lineage of sedges with about 230 accepted extant species worldwide. Recent molecular phylogenetic work has provided support for a monophyletic genus *Bulbostylis*, but species delimitation remains problematic in areas of high species-richness. *Bulbostylis* is an example where limited availability of molecular data impedes clarification of evolutionary relationships and hampers the study of character evolution and biogeographical history of the genus. This notoriously taxonomically complex Cyperaceae genus is in urgent need of revision using an integrative taxonomic approach combining molecular and morphological data. The Neotropics is one of the centres of diversity for *Bulbostylis* with about 70 currently accepted species, however, the taxonomy continues to be poorly understood. Numerous specimens have not been identified to species level, and probably species remain undescribed to science. The main objective of this project is to carry out a systematic and evolutionary study of the neotropical *Bulbostylis*. We aim: (1) to prepare a taxonomic revision of the neotropical species of *Bulbostylis*; (2) to obtain a highly resolved phylogeny based on phylogenomic data with extensive sampling of species complexes; and (3) to investigate possible speciation events which may have contributed to the current distribution patterns of *Bulbostylis* species. Preliminary results include: (1) analysing almost 2000 specimens of neotropical *Bulbostylis* deposited in herbaria; (2) undertaking fieldtrips in the Amazon and Cerrado areas of Brazil to collect herbarium specimens and DNA samples; (3) discovering of new species to science, recording new occurrences, and rediscovering *Bulbostylis tenella*(Link) C.B.Clarke in Brazil after 179 years.

P.0334 Diversity and evolution of Cyperaceae in Madagascar with focus on Bulbostylis

Fitiavana Rasaminirina[1,2]Vonjison Rakotoarimanana[1], Mijoro Rakotoarinivo[1], Hélène Ralimanana[2], Isabel Larridon[3]

1 University of Antananarivo, Antananarivo, Madagascar. 2 Kew Madagascar Conservation Centre, Antananarivo, Madagascar. 3 Royal Botanic Gardens Kew, Richmond, UK.

Identified as the third largest monocot family in the world, the Cyperaceae family represent one of the most species-rich plant families in Madagascar with around 310 native species placed into 24 genera including one monotypic endemic genus Trichoschoenus. Our research focusses on the genus Bulbostylis or hairsedges with 24 accepted species in Madagascar to investigate the link between sedge diversity and endemicity and ecosystems in the Central Highland of Madagascar because it represents the only large endemic radiation of a sedge group using the C4 photosynthetic pathway linked with a preference for open canopy habitats. The results of our study may provide further evidence, independent from data on the Poaceae or grass family to reply to the broader question whether the grasslands of the Central Highlands of Madagascar are natural or man-made. Soils characteristics effects on the diversity and distribution of sedges in open canopy and forest habitat are expected to be explained, which will also provide baseline data for species- and area-based conservation management.To resolve relationships between the Madagascan Bulbostylis species, DNA sequence data from 102 accessions sampled during fieldwork in Madagascar (Itremo, Isalo, Morondava, Tsaratanana) and in herbaria (TAN, P, K) were generated using the Angiosperms353 targeted sequencing probes. Our results will be used to reconstruct the evolutionary history of sedges in Madagascar. It will also be used to complete a taxonomic treatment of the genus Bulbostylis which will include an identification key, descriptions, illustrations, distributions maps and IUCN Red List assessments for each species.Since 2019, our efforts to study the Cyperaceae in Madagascar have already resulted in the publication of a new species to science, i.e. Bulbostylis itremoensis. Additionally, an updated version of the Flora of Cyperaceae from Madagascar at generic level was published in English and French versions to aid identification.

P.0335 Carex muricata agg. A reassessment of the section within the UK

Lorna J. Halliwell[1], Michelle L. Davis[1], Paul A. Ashton[1]

1 Department of Biology, Edge Hill University, Ormskirk, UK.

The *Carex muricata* aggregate (section *Phaestoglochin*) is a difficult to classify group of sedges (Cyperaceae). Globally, there are approximately 37 taxa within the section, however nomenclature typically focusses upon regional taxa without any global overview. There is also significant debate over rank and recognition. The majority of current treatments are based upon morphological studies therefore a reassessment is long overdue. The work being undertaken aims to classify the group utilising a combination of genetic and novel morphological approaches to fully understand the section. Using both nuclear and chloroplast DNA markers, the relatedness of the taxa will be determined and a phylogeny produced. Utilising scanning electron microscopy, the ultrastructure of the plants is being examined to identify microscopic differences related to a revised molecular taxonomy. This will provide modern genetic and morphological data which will clear up the confusion of the section and lead to improved treatment in floras.

S.045. DIVERSIFICATION IN LARGE DOMINANT PLANT LINEAGES: INTEGRATION OF PHYLOGENY, ECOLOGY, PHYSIOLOGY, AND BIOGEOGRAPHY

P.0336 Diversification and biogeography of North American thistles (Cirsium: Carduoideae: Compositae): drivers of a rapid continent-wide

Carolina M. Siniscalchi,[1] Jennifer R. Ackerfield,[2] Ryan A. Folk[1]

1 Department of Biology, Mississippi State University, Mississippi State, USA. 2 Denver Botanic Gardens, Denver, USA.

Cirsium ("thistles"), is the most speciose genus in the Compositae (Asteraceae) subfamily Carduoideae native to North America, consisting of a rapid endemic radiation. Hummingbird pollination is rare in Compositae, but approximately 10% of all *Cirsium* in North America are adapted to this pollination syndrome. Although *Cirsium* is an example of a continent-wide evolutionary radiation, the biotic and abiotic factors contributing to this remarkable diversification have never been studied. Sixty-four taxa of *Cirsium* representing its distribution each major geographic range in North America were sequenced using the MYbaits–Compositae-1061 1kv1 kit. These results were used to infer a time-calibrated phylogeny to estimate divergence times and diversification rates. Ancestral area reconstructions for eight biogeographical areas and ten habitats were performed with BioGeoBEARS. A model fitting approach was used to test whether: 1) different environmental variables were related to diversification, 2) pollinator type was related to differences in environment, and 3) pollinator type was related to diversification. Phylogenetic least squares models of environmental variables against diversification rates were used to test if environmental variables, pollinator type, or morphological traits influenced diversification. *Cirsium* in North America originated approximately 2 mya, with the majority of the diversification occurring in three nearly simultaneous bursts during the onset of the Pleistocene ice age. Precipitation and semi-aridity were the main catalysts for diversification. Hummingbird pollination was associated with near-significant lower rates of diversification than insect pollination. The integrated effects of niche conservatism and glacial-interglacial cycles played a role in shaping current distributional patterns. Although hummingbird pollination was associated with lower rates of diversification in *Cirsium*, the switch to this syndrome may have facilitated expansion across post-Pleistocene fragmented landscapes. Ultimately, this study offers important insights into the drivers of a rapid, continent-wide radiation and the impact of Pleistocene glaciation cycles on the flora of North America.

P.0337 Ecological and evolutionary insights into savanna-related traits in African acacias (Senegalia and Vachellia, Fabaceae)

Joseph Charboneau[1], Arjun B. Potter[2], Scott Cory[2], Charles Luchagula[3], Ellen Weinheimer[2], Issakwisa Ngondya[3], T. Michael Anderson[2], James B. Pease[2], Stephen A. Smith[1]

1 Department of Ecology and Evolutionary Biology, University of Michigan; Ann Arbor, USA. 2 Department of Biology, Wake Forest University; Winston-Salem, USA. 3 Nelson Mandela African Institute of Science and Technology; Arusha, Tanzania.

Acacia species are found throughout Africa in habitats ranging from deserts to savannas to tropical woodlands. These ca. 140 acacia species (*Acacia* s.l.) are now about evenly split between two genera: *Senegalia* Raf. and *Vachellia* Wight & Arn. The most recent common ancestors of both genera date from about 5-8 Mya, after which the rise of C4 grasses and increasing diversity of large mammalian herbivores led to today's African savannas. The acacias that have become the dominant woody species in many savannas did so by overcoming many stressors including competition with grasses, herbivory by large herbivores, fires, and periodic drought. We are investigating how responses to these stressors and variation in ecological and phenotypic traits shape species distributions at landscape and regional scales using data ranging from physiological and ecological to transcriptomic and phylogenomic. Ecophysiological and gene expression data from greenhouse drought experiments are helping us to understand how species respond to water stress differently, and a common garden experiment with a set of focal species in Arusha, Tanzania has also been revealing species-specific responses to combinatorial treatments of drought, simulated herbivory, and fire. We will compare these responses with climatic and other ecological tolerances estimated from species occurrence data and niche models. Using newly assembled transcriptomes, genomes, and phylogenomic data, we are also working to understand the genetic basis for responses to savanna stressors, and to put these savanna-related traits in African species into phylogenetic and biogeographic context within the pantropical genera *Senegalia* and *Vachellia*.

P.0338 Strong Taylor's Power Law effects in plant communities across the globe

Clara Gracia Mas[1], Francesco de Bello[1,2], Jules Segrestin[2], Lars Götzenberger[2,3], The LOTVS Consortium, Jan Lepš[2,3]

1 Centro de Investigaciones sobre Desertificación (CSIC-UV-GVA), Valencia, Spain. 2 University of South Bohemia, České Budějovice, Czech Republic. 3 Czech Academy of Sciences, Průhonice, Czech Republic.

Taylor's power law (TPL), also known as fluctuation scaling, is one of the most pervasive empirical patterns in ecology. It states that the variance (V) of a nonnegative random variable (e.g., population abundances) is a power function of its mean (M) (i.e., $V = aMb \rightarrow log(V) = log(a) + b*log(M)$). While known, its exploration in the context of temporal stability of communities has been very limited. Sample exponent (*b*), TPL's log-log slope, is mathematically predicted to fluctuate around *2*. Deviation from this value imply either higher or lower variance than expected for a given mean value. In a plant community context, this exponent *(b)* is describing how stability is changing with increasing abundance and therefore it can be interpreted as an indicator of the dominance structure and the stabilization caried out by dominant species, with slopes lower than 2 suggesting dominants being relatively more stable than subdominants. In this study we aim to explore how common is TPL in real plant communities, how it relates to dominant species characteristics and which factors can predict its exponent value. We used LOTVS (https://lotvs.csic.es/) database of permanent plots worldwide to describe the power relationship between the temporal mean and variance of the populations of more than 11,000 plant communities sampled over 6-99 years across the globe. The results show strong TPL effects (R2>0.8 in 95% of the communities). More than 88% of communities show a TPL exponent significantly lower than the expected $b = 2$, with sampling methodology, climate variables and species functional traits affecting the TPL slope. These outcomes underscore the overlooked prevalence of TPL in temporal community ecology and suggest a driving effect of dominants and their traits on temporal stabilization of community abundance.

P.0339 Into Mesoamerica: convergence of Quercus functional traits across environmental gradients

Matthew A. Kaproth[1,2], Jeannine Cavender-Bares[1], Alex Kirsch[2], Antonio González-Rodríguez[3], Marlene Hahn[4], Andrew L. Hipp[4,5]

1 University of Minnesota, St. Paul, USA. 2 Minnesota State University Mankato, Mankato, USA. 3 Universidad Nacional Autónoma de México, Morelia, México. 4 Center for Tree Science and Herbarium, The Morton Arboretum, Lisle, USA. 5 The Field Museum, Chicago, USA.

The sympatric nature of *Quercus* (oak) clades in the Americas offers insights into evolutionary dynamics and environmental adaptations across broad environmental conditions. While species occupy similar regions, it is unknown if species use similar strategies to adapt to different ecological niche. We explored these patterns using herbarium surveys of 136 species (1820 specimens), with species represented by leaf and stem traits (e.g., leaf perimeter to area ratio, specific leaf area, leaf habit, huber value) and their correlation with climate and soil nutrients. Our study reveals convergent leaf morphology and habit patterns across clades, particularly in Mesoamerica. Both section *Lobatae* (reds) and *Quercus* (whites) show constrained adaptations to environmental conditions. The relationship between leaf density (SLA) and dissection (perimeter × leaf length per area; PLA) is coupled by region, demonstrating function is convergent across distantly related species that are occupying similar niches. For leaf habit, seasonal water and soil nutrient availability are identified as important interactive factors; deciduous species grow in seasonally dry climates and more nutrient-rich soils compared to brevideciduous or evergreen species, matching strategies that align along the leaf economic spectrum. We investigate whether there is parallel evolution of water use and cold tolerance traits among clades. Previous work demonstrates high rates of speciation, habit evolution, and adaptation along moisture gradients in the Mexico and American Southwest regions. This research expands on findings that clades are responding to patterns of resource heterogeneity in similar manners, but with evergreen species displaying higher rates of transition. This research enhances our understanding of the intricate relationships between evolutionary patterns, environmental adaptations, and convergent leaf functional traits in woody plant species. The findings underscore the importance of considering regional variations soil and climate for a comprehensive analysis of ecological strategies and species' success.

P.0340 Shining light on the evolution of Palearctic realm flora: biogeography and diversification patterns of Hypericum subg. Hypericum

Irene Masa-Iranzo[1], Irene Villa-Machío[2], Nicolai Nürk[3], Lisa Pokorny[1], Andrea S. Meseguer[1]

1 Real Jardín Botánico, CSIC, Madrid, Spain. 2 Missouri Botanical Garden, St. Louis, USA. 3 University of Bayreuth, Bayreuth, Germany.

Hypericum L. (Hypericaceae), with over five hundred species of herbs, shrubs, and trees distributed worldwide, is one of the 100 largest angiosperm genera. Recent studies have suggested the division of the genus into two subgenera, *H.* subgenus *Brathys* from the New World and *H.* subgenus *Hypericum* from the Old World. Although Sanger sequencing approaches have proved insufficient to resolve backbone and recent relationships across this large genus. Here we present a Hyb-Seq approach (combining genome skimming with target capture sequencing), implemented with a custom kit (integrating the Angiosperms353 targets with 273 single-copy nuclear orthologs specific to the Clusioid Clade, Malpighiales) to build a stable backbone for this large genus and infer phylogenetic relationships within the Old World subgenus *Hypericum*. We use this phylogeny to test macroevolutionary hypotheses on the evolution of the Palearctic flora in relation to Cenozoic climatic oscillations. For this, we have assembled the most comprehensive *Hypericum* sampling to date (including ~260 spp.; with a few Malpighiales taxa belonging to the Clusioid Clade as outgroup), and built nuclear and plastid topologies to address potential cito-nuclear incongruence, which could be obscuring key evolutionary processes. Additionally, we have used fossils to time-calibrate our topologies, and inferred the biogeographic history of Old World *Hypericum* taxa. This framework has allowed us to characterize the magnitude of extinction and speciation events (e.g., potential radiations) that have shaped the extant diversity in the subgenus, thus shining light on the evolution of the Palearctic realm flora. We have also explored the impact ploidy levels (calculated from Hyb-Seq data) have had in the diversification of the subgenus *Hypericum*.

P.0341 Phylogeny and biogeography of the genus Lobelia in the Mexican Transition Zone

Miguel A. Pérez-Pérez[1], Laura P. Lagomarsino[2], Laymon D. Ball[2], Arturo Castro-Castro[3], Tina J. Ayers[1]

1 Department of Biological Sciences, Northern Arizona University, Flagstaff, USA. 2 Shirley C. Tucker Herbarium, Department of Biological Sciences, Louisiana State University, Baton Rouge, USA. 3 CONAHCYT-Instituto Politécnico Nacional, Centro Interdisciplinario de Investigación para el Desarrollo Integral Regional, Unidad Durango, Durango, México.

The five major mountain ranges in Mexico, called the Mexican Transition Zone (MTZ), provide a unique opportunity to study the relationships of closely related species that are restricted to a single range. These mountains are a transition zone because they have a mix of organisms from the temperate parts of the Americas as well as from the tropics. The target organism for the project is the plant genus *Lobelia*. There are 90 species in the MTZ; of those, 83 are found only there. Most of the species have small, blue flowers and are insect-pollinated, but six have large, red flowers that are hummingbird-pollinated. Both groups have species with a unique floral feature, a nectar spur, found nowhere else in the world. We will present preliminary results of molecular data gathered from chloroplast genomes and a nuclear probe set developed for a closely related group that was used to build a comprehensive phylogenetic framework for *Lobelia*, focusing on the highly diverse and endemic lineages of Mexico. This framework will be used to address broad evolutionary questions about biogeography, pollinator shifts, and hybridization. We present a time-calibrated tree to test specific biogeographic hypotheses in the MTZ, including 1- geographic barriers between lineages, 2- long-distance dispersal between mountain ranges, and 3- biogeographic patterns associated with pollination syndrome or presence of nectar spurs.

S.046. DYSPLOIDY, DIPLOIDISATION AND DIVERSIFICATION: IMPACT OF POSTPOLYPLOID GENOME RESTRUCTURING ON SPECIES AND TRAIT DIVERSITY

P.0342 Phylogenomics unravels the complex relationships of autumn-flowering Iberian crocuses

Ruifang An[1], Frank R. Blattner[1], Nomar E. Waminal[1], Doerte Harpke[1]

1 Department Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany.

The Iberian autumn-flowering *Crocus serotinus* group, comprising *C. clusii*, *C. cobbii*, *C. nudiflorus*, and *C. salzmannii*, harbors several populations with unclear taxonomic affiliation. Variable genome sizes and chromosome numbers indicate the presence of hybridization, which might be one of the main reasons for the taxonomic uncertainties. Therefore, we aimed to define diploid taxonomical units, identify hybrids and unravel the karyotype evolution of this group. We employed a comprehensive approach including phylogenetic analyses of two chloroplast regions, genotyping-by-sequencing (GBS) of 279 individuals representing 110 populations, 14 nuclear single-copy genes and rDNA spacers of 49 populations, comparative analysis of repetitive DNA proportion in 20 individuals, genome size measurements and chromosome counting. This approach enabled the identification of at least three different allopolyploidizations, one homoploid hybridization and two populations where diploids and alloploids are growing side by side. Typically, diploids are characterized by a genome size ranging from 2C = 3.3 to 7.2 pg with chromosome counts of $2n = 20, 22, 24$, while alloploids exhibit genome size from 2C = 6.7 to 9.2 pg with chromosome counts of $2n = 36, 44, 48$. Our comparative analyses of repetitive DNA, along with GBS and nuclear single-copy markers data, suggest that the larger genome of *C. salzmannii* did not originate from recent polyploidization or repetitive DNA amplification, but is likely caused by an earlier polyploidization event followed by diploidization.

P.0343 The subordinate role of pseudogenization over recombinative deletion following polyploidization in Angiosperms

Ewout Crombez[1,2], Zhen Li[1,2], Yves Van de Peer[1-4]

1 Center for Plant Systems Biology, VIB, Ghent, Belgium. 2 Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium. 3 Department of Biochemistry, Genetics and Microbi-

ology, University of Pretoria, Pretoria, South-Africa. 4 College of Horticulture, Nanjing Agricultural University, Nanjing, China.

Polyploidy is most often followed by an eventual return to the diploid state, referred to as diploidisation. Diploidisation leads to several drastic genomic changes, of which extensive gene loss is a key feature. Given that there is genome-wide redundancy for all genes following polyploidization, pervasive loss of gene copies can be anticipated. However, the dominant mechanism responsible for gene loss post-polyploidization, whether through pseudogenization (i.e., the accumulation of deleterious mutations leading to the non-functionality of that gene, followed by further degradation through mutation), and/or deletion from the genome by recombination, remains largely unknown. Here, we investigated the extent of pseudogenization post-polyploidization by identifying pseudogenes in collinear blocks retained from polyploidy events in twelve angiosperms. The number of identified polyploidy-derived pseudogenes was consistently drastically lower than what would be expected if gene loss would occur predominantly through pseudogenization. However, this number may be affected by other processes, such as (1) diminished detectability of pseudogenes due to the accumulation of mutations and (2) loss of collinearity over time. These potential biases were addressed by (1) following the expected evolution of neutrally evolving (pseudo)genes through simulation and (2) investigating a neo-polyploid sugarcane genome. The simulations indicated that in the absence of deletion mechanisms, pseudogenes should be detectable for a longer evolutionary period than observed in the paleo-polyploid species. Furthermore, despite being still polyploid, the sugarcane genome has already experienced significant gene loss, with only one-third of these loss events associated with pseudogenization. Taken together, these findings imply that gene loss post-polyploidization primarily takes place via deletion through recombination. This assertion is further reinforced by the identification of an apparent initial phase of rapid gene loss, and the enrichment of pseudogenes in regions of low recombination. Lastly, we explored pseudogene functionality and discovered distinct functional categories enriched at varying levels of loss.

P.0344 Genome evolution and post-polyploid diploidization in the Microlepidieae (Brassicaceae)

Xinyi Guo[1], Terezie Mandáková[1,2], Milan Pouch[1,3], Martin A. Lysak[1,3]

1 CEITEC, Masaryk University, Brno, Czech Republic. 2 Department of Experimental Biology, Faculty of Science, Masaryk University, Brno, Czech Republic. 3 NCBR, Faculty of Science, Masaryk University, Brno, Czech Republic.

Plant genome evolution was marked by cycles of whole-genome duplication (WGD) and diploidization. Genome diploidization following WGDs can proceed with different intensities and be accompanied by speciation events. However, it remains unclear how and to what extent chromosomal diploidization including descending dysploidy, i.e., reduction of chromosome number, is associated with more fine-scaled genomic (gene-level) diploidization. The Microlepidieae species, endemic to Australia and New Zealand, form a monophyletic tribe within the mustard family (Brassicaceae). The Microlepidieae genomes originated after an ancient allotetraploidization event and subsequently evolved into different species and subclades with distinct levels of inter-subgenome reshuffling and descending dysploidy. To explore the post-polyploid genome evolution in Microlepidieae, we sequenced genomes of four species with different chromosome numbers (n = 4 to n = 10) and genome sizes (0.4 to 1.7 Gbp). Large structural differences underlying karyotype evolution were consistently supported by both sequencing-based and molecular cytogenetic results. The expansion of genome size was mainly caused by the accumulation of LTR retrotransposons, especially Athila elements. We identified genomic regions corresponding to two subgenomes based on different gene fractionation and gene tree topologies, and shared karyotype structures with closely related diploid genomes. Our genomic evidence confirms the most likely Asian origin of the allotetraploid ancestral genome. Whereas the maternal subgenome with an n = 8 genome structure conserved within the Camelinodae supertribe is sister to the Crucihimalayeae tribe, the paternal subgenome had an n = 6 karyotype identical to the extant genomes of the Yinshanieae tribe. In Australia, descendant genomes of the allotetraploid ancestor (n = 14) exhibited different extent of gene loss/pseudogenization between subclades, consistent with the previous cytogenetic observation of two-speed diploidization. Our results provide new insight into the process of post-polyploid genome evolution in plants.

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P.0345 Diversification of bamboo species induced by dynamic subgenome dominance

Peng-Fei Ma[1], Yun-Long Liu[1], Cen Guo[1,2], Guihua Jin[1], Zhen-Hua Guo[1], Ling Mao[1,3], Yi-Zhou Yang[1,3], Liang-Zhong Niu[1], Yu-Jiao Wang[1], Lynn G. Clark[4], Elizabeth A. Kellogg[5], Zu-Chang Xu[1,3], Xia-Ying Ye[1], Jing-Xia Liu[1], Meng-Yuan Zhou[1], Yan Luo[2], Yang Yang[1], Douglas E. Soltis[6,7], Jeffrey L. Bennetzen[8], Pamela S. Soltis[6], De-Zhu Li[1]

1 Germplasm Bank of Wild Species & Yunnan Key Laboratory of Crop Wild Relatives Omics, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan, China. 2 Center for Integrative Conservation & Yunnan Key Laboratory for the Conservation of Tropical Rainforests and Asian Elephants, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun, Mengla, Yunnan, China. 3 Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, Yunnan, China. 4 Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Bessey, Ames, USA. 5 Donald Danforth Plant Science Center, St. Louis, USA. 6 Florida Museum of Natural History, University of Florida, Gainesville, USA. 7 Department of Biology, University of Florida, Gainesville, USA. 8 Department of Genetics, University of Georgia, Athens, USA.

Polyploidy (genome duplication) is a pivotal force in evolution. However, the interactions between parental genomes in a polyploidy nucleus, frequently involving subgenome dominance, are poorly understood. Most previous studies have focused on recently formed polyploid crops and relatives that have not undergone extensive species diversification. Here we showcase analyses of a bamboo system (Poaceae; grass family) comprising a series of lineages with different ploidal levels, from diploid (herbaceous) to tetraploid and hexaploid (woody), with a subgenome shared by all polyploids. We analyzed 11 chromosome-level *de novo* genome assemblies and large-scale RNA-seq data from 476 biological samples representing a transcriptional landscape of the lineage. We find that bamboo subgenomes exhibit stunning karyotype stability, with parallel subgenome dominance in the two tetraploid clades and a gradual shift of dominance in the hexaploid clade. Allopolyploidization and subgenome dominance help explain the genetic basis of the evolution of such distinct biological traits as tree-like lignified culms, rapid growth, and synchronous flowering characteristic of woody bamboos as the world's largest grasses. Our work provides landmark insights into genome dominance in a remarkable polyploid system, including its dependence on genomic context and its ability to switch which subgenomes are dominant over evolutionary time.

P.0346 Accessing chromosome evolution in clade A beans from Phaseolus L. (Leguminosae) through oligo-FISH chromosome painting

Thiago Nascimento[1,2], André Marques[2], Andrea Pedrosa-Harand[1]

1 Laboratory of Plant Cytogenetics and Evolution, Department of Botany, Federal University of Pernambuco, Recife, Brazil. 2 Department of Chromosome Biology, Max Planck Institute for Plant Breeding Research, Cologne, Germany.

Phaseolus L. beans are word-wide consumed and stands out for their economic and nutritious importance. The genus comprises two phylogenetic clades, A and B, each with three or five monophyletic groups, respectively. The mechanisms that shaped *Phaseolus* chromosome evolution have been investigated through different cytogenetic approaches in previous studies, from conventional staining to oligo-FISH painting and barcoding. However, the studies so far concentrated efforts in analysing species that belong to clade B, while clade A species remained underrepresented. Here we aimed to analyse the chromosome evolution of species belonging to clade A through oligo-FISH painting in comparison to clade B species. For this, we applied chromosome-specific oligo probes for *Phaseolus vulgaris* chromosomes 2 and 3 through *in situ* hybridization to six species from all groups of clade A: *P. glabellus*, *P. microcarpus* (clade A, unassigned), *P. hintonii* (clade A, Tuerckheimii group), *P. parvulus* (clade A, Pauciflorus group), *P. neglectus*, *P. grayanus* (clade A, Pedicellatus group); compared to *P. filiformis* (clade B, Filiformis group), *P. vulgaris* (clade B, Vulgaris group), *P. leptostachyus* (clade B, Leptostachyus group) and *P. lunatus* (clade B, Lunatus group). All clade A species analysed here showed a conserved synteny for orthologs 2 and 3. The breaks of synteny, mostly represented by translocations events, were found only in clade B species, as previous described for the Filiformis and the dysploidy Leptostachyus group representatives. Our data suggest that clade B is a hotspot for chromosome rearrangements, while clade A species maintained a more conserved karyotype after the divergence of both clades ~4.6 Mya.

P.0347 Developing transcriptomic tools for genetic characterization of Musa spp. from Puerto Rico

Yairelys Rosa-Morales1, Christopher A. Sambolín-Pérez1, Cristina M. Pluguez-Medina1, Rosalinda Aybar-Batista1, Ramón E. Rivera-Vicéns1, Juan A. Negrón-Berríos1, Alok Arun1.

1 Institute of Sustainable Biotechnology, Inter-American University of Puerto Rico, Barranquitas, Puerto Rico.

Musa is a genus of important fruit crops such as plantains and bananas worldwide due to their nutritional values. Puerto Rico has few cultivar varieties which are grown commercially in the island. However, the genetic background of those commercially grow varieties is not well known. Developing RNA seq based molecular markers can help to assess the genetic identity of commercially important species of *Musa* grown in Puerto Rico. Also, conventional micropropagation (CM) and temporary immersion bioreactors (TIB) methods have been used globally to produce disease-free plantlets at commercial scale. However, their impact on plant phenotypic and genetic traits have not been explored in Puerto Rico. Our preliminary results comparing the morphological, molecular, and biochemical characteristics of explants grown under test tubes and TIB have shown that plantain plantlets regenerated under TIB show more robust phenotypic traits. Therefore, our goal is to carry out a comparative study of transcriptomes of two commercial *Musa* spp. in Puerto Rico. RNA was extracted from replicates of fleshy-frozen apical leaves tissues of two plantain *Musa* spp. grown on test tubes and the transcriptome was sequenced using Illumina (pair-end) platform. We generated approximately 210 million reads, which were then filtered to clean reads (Q20% of >97.5%). 72.2% of SNP variants were located on the exotic regions. We are currently identifying the differentially expressed candidate genes and SNPs. The study will provide a dataset for assessing the genetic diversity of plantains grown in Puerto Rico.

P.0348 Amazing Herbertia lahue (Iridaceae): how is morphologic and cytogenetic variation structured at different ploidy levels?

Tatiana T. Souza-Chies[1], Eudes M. Stiehl-Alves[1], Ariane T. Vieira[1], Caroline Trevelin[1], Alexandre C. Martins[1], Eliane Kaltchuk-Santos[1]

1 Institut of Biosciences, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil.

Polyploid series are recurring in Iridaceae species, indicating a substantial role in their evolution. *Herbertia lahue* is a geophytic and herbaceous species of grasslands from southern South America, with four ploidy levels (2*x*, 4*x*, 6*x*, and 8*x*) reported. Recognition of *H. lahue* is done mainly through floral characters, but their morphological variation is significant and extensive, making species boundaries doubtful. This study aims to examine the effect of polyploidy on the variation of *H. lahue* using an integrative approach. Thirty-eight populations of *H. lahue* were sampled *in situ* during flowering months across southern Brazil. Integrative approach included i) cytogenetic analysis (chromosome count, genome size estimation, and CMA/DAPI analysis), ii) pollen analyses (pollen grain count, size, and fertilization potential), and iii) morphometric analyses. Chromosome counts showed the occurrence of only three cytotypes, each one corresponding to a morphotype: seven populations are diploid ($2n=2x=14$), five are hexaploid ($2n=6x=42$), and nine are octoploid ($2n=8x=56$). All cytotypes presented asymmetric karyotypes with metacentric or submetacentric chromosomes. Genome size varied between cytotypes, but not within, and 2C-values increase according to ploidy level: 4.33pg (2*x*), 12.28pg

(6*x*), and 16.30pg (8*x*). Polyploids have lower monoploid 1C*x*-values than diploids, indicating genome downsizing. All cytotypes have CMA⁺/DAPI⁻ bands (2*x*: two bands; 6*x*: four and 8*x*: six). Pollen measurements show that polyploids have larger pollen grains but less pollen grains/anther compared to diploids. Differences are non-significant for pollen viability in all cytotypes. Discriminant analysis split *H. lahue* into three clusters corresponding to cytotypes (with partial overlap for polyploids). Our results highlighted an intricate pattern in organization of polymorphism for *H. lahue* cytotypes.

P.0349 Does the evolutionary time matter? A deeper look at the evolutionary dynamics of repetitive sequences in Brachypodium hybridum

Dana Trunova[1], Natalia Borowska-Zuchowska[1], Serhii Mykhailyk[1], Kai Xia[2], Ruben Sancho[4], Kai Wang[2], Pilar Catalán[4], Ales Kovarik[2], Robert Hasterok[1], Bożena Kolano[1]

1 Plant Cytogenetics and Molecular Biology Group, Institute of Biology, Biotechnology and Environmental Protection, Faculty of Natural Sciences, University of Silesia in Katowice, Katowice, Poland. 2 Department of Molecular Epigenetics, Institute of Biophysics, Czech Academy of Sciences, Brno, Czech Republic. 3 School of Life Sciences, Nantong University, Nantong, Jiangsu, China. 4 Department of Agricultural and Environmental Sciences, High Polytechnic School of Huesca, University of Zaragoza, Huesca, Spain.

Polyploidisation often results in genome rearrangements since two different genomeshave to be accommodated in one nucleus. Such changes may involve both the single copy sequences as well as the repetitive genome fraction. In this study, we performed a comprehensive comparative analysis of repetitive DNA in *Brachypodium hybridum* (2n = 4x = 30, genome composition DDSS), a model allotetraploid grass that came from a cross between two diploid species that resemble modern *B. distachyon* (2n = 10; DD) and *B. stacei* (2n = 20; SS). Taking advantage of the polyphyletic origin of *B. hybridum,* we investigated two lineages that showed a 10-fold difference (1.4 and 0.14 Ma) in evolutionary age and arose from different cross directions. Such a combination of lineages constitutes a unique model system to study the consequences of polyploidy in plants. Employing molecular (Southern Blot), cytogenetic (FISH) and bioinformatic approaches, we characterised and quantified repetitive DNA content. Unlike the transposable elements that tend to follow the global stasis, the tandem repeats, especially rDNA sequences, appear to be a more dynamic part of the genome. Acknowledgments: The research was funded by the National Science Centre, Poland (project number 2020/39/O/NZ8/00184) to BK and DT.

S.047. ECOLOGICAL AND EVOLUTIONARY DYNAMICS AT THE REAR EDGE UNDER CLIMATE CHANGE

P.0350 Study of stomata and mesophyll traits on plant adaptation to increased CO2

Cinti Eleonore[1], Cerri Martina[1], Carli Andrea[2], Centritto Mauro[2], Atzori Giulia[2], Zuluaga Diana[3], Haworth Matthew [2], Reale Lara [1].

1 Department of Agricultural, Food and Environmental Sciences, University of Perugia, Perugia, Italy. 2 National Research Council of Italy (CNR-IPSP), Sesto Fiorentino, Firenze, Italy. 3 Institute of Biosciences and BioResources (CNR-IBBR), Bari, Italy.

Based on the annual report from the NOAA Global Monitoring Lab, the global average atmospheric carbon dioxide concentration was 417.06 parts per million (“ppm” for short) in 2022, setting a new record. The increase between 2021 and 2022 was 2.13 ppm -the 11th year in a row where the amount of carbon dioxide in the atmosphere increased by more than 2 ppm (Lindsey, 2023). Therefore, it is essential to understand the impact of rising CO_2 on plant growth. With the PRIN project "Evolutionary implications for the development of climate resilient productive plants" (EvoPlant), we aim to elucidate patterns of plant evolution to promote the development of climate-resilient plants through the study of stomatal evolution, photosynthesis, and plant-atmosphere gas exchange. The purpose of our study is to analyze the correlation between leaf anatomy and stomatal patterning. We are currently completing morphological and anatomical analyses of the mesophyll and stomatal apparatus of 20 plant species representing an evolutionary pathway from lycophytes to dicotyledonous angiosperms, via ferns and gymnosperms. Specifically, we are examining the density, distribution, morphology, and size of stomata through light microscopy. These measurements will then be correlated with the surface area of the mesophyll cells exposed to the intercellular airspaces, the size of the mesophyll cells, the thickness of the mesophyll, the fraction of the volume occupied by the intercellular airspaces, and the total cross-sectional area of the cells that make up the mesophyll. A special case is represented by *Triticum* spp., in which we are studying, mesophyll conductance (G_m), i.e. the transport of CO_2 from intercellular airspace within leaves developed in different CO_2 concentration. These data will allow us to identify the most efficient combination of stomata-mesophyll traits for climate change resilience.

Reference: Lindsey R. 2023. *Climate change: atmospheric carbon dioxide*. NOAA.

P.0351 Estimation of carbon stored in the gallery forest of the campus of the Universidad Nacional de Asunción, San Lorenzo

Maura Isabel Díaz Lezcano[1], Isidoro Gabriel Benitez Nuñez[1], Cristian Andrés Britos Benítez[1], Higinio Moreno Resquín[1]

1 Universidad Nacional de Asuncion, Facultad de Ciencias Agrarias, San Lorenzo, Paraguay.

The overall objective was to determine the difference in carbon content in a gallery forest located in the university campus of the National University of Asunción, San Lorenzo. As specific objectives, to determine the floristic composition, to determine the dasometric values and the vegetal biomass, to determine the physical and chemical parameters of the soil, to determine the hydric behavior, to determine the soil survey, to determine the content of the existing necromass in the forest of study and the difference of the content of carbon in the vegetal cover, soil and necromass in a period of one year in the area of study. The work was established in four plots of 750 m² each. The forest is constituted by individuals mostly belonging to the family Meliaceae and Moraceae, both with two species, followed by Arecaceae, Annonaceae, Apocynaceae, Aquifoliaceae, Cecropiaceae, Euphorbiaceae, Fabaceae, Meliaceae, Moraceae, Myrtaceae and Sapotaceae with one species each. A forest inventory was carried out in each plot and the storage of tree carbon was estimated using IPCC equations (2006) which averaged 79.9 tC/ha, while the herbaceous vegetation averaged 2.44 tC/ha, and the COS component averaged 44.57 tC/ha. The total carbon accumulated in the three components as an average according to the IPCC (2006) is 126.91 tC/ha, in terms of carbon equivalent the average data found according to the IPCC (2006) was 463.5 tCO2/ha, with a difference of 34.44 tC/ha in the period of one year.

P.0352 Genomic variation and how isolation by environment influences population differentiation of a Mediterranean orchid

Marco G. Balducci[1], Karl J. Duffy[1]

1 Department of Biology, Complesso Universitario Monte Sant'Angelo, University of Naples Federico II, Naples, Italy.

Identifying the processes underlying gene flow and local adaptation is important, both to understand the limits to plant distributions, and predict how they respond to ongoing environmental change. While gene flow should decrease with increasing distance between populations (isolation by distance, IBD), the relative influence of decreased gene flow between shared environments (isolation by environment, IBE), rather than distance, is poorly understood. Due to their patchily distributed populations and dependence on mutualists to complete their life-cycle, orchids should show high levels of genetic differentiation, with high levels of IBD. However, as their seeds are wind-dispersed, they may overcome local constraints to gene flow and populations may be genetically similar in shared environments. To test the relative influence of IBD and IBE, we investigated the population genomic structure of the Mediterranean orchid, *Orchis italica* (Poir.). Using ddRADseq, we identified 31,909 polymorphic loci from samples from 21 populations, representing six Mediterranean regions. Outlier analysis was used to identify alleles potentially under selection to environmental variables. While admixture analysis revealed that populations were structured according to region, genetic differentiation was variable within regions, and there was no clear pattern of IBD. However, SNPs under selection were associated with annual mean temperature, precipitation regime, and soil texture, hence population differentiation may mainly result from isolation by environment (IBE). Genes associated with adaptation to local temperature and precipitation regimes may be important as the Mediterranean region experiences increasing mean temperatures in the 21st century. Quantifying the geographical and ecological factors underpinning genomic diversity, and identifying potential selective pressures driving the adaptive genetic variation, is necessary to understand how plants respond to ongoing climate change.

P.0353 The distribution pattern and modeling of climate change on Ajugoideae (Lamiaceae) as natural medicinal as well as nectariferous plants

Keshavarzi, M.[1], Farajollahi, F.[1], Mehrabian, A. R.[2], Mostafavi, H.[3]

1 Plant Sciences Dept., Faculty of Biological Sciences, Alzahra University, Tehran, Iran. 2 Department of Plant Sciences and Biotechnology, Faculty of Life Science and Biotechnology, Shahid Beheshti University, Tehran, Iran. 3 Institute of Environmental Sciences, Shahid Beheshti University, Tehran, Iran.

The Lamiaceae, with 48 genera and about 425 species, is the fourth largest family of angiosperms in Iran, containing medicinal and aromatic plants. The Ajugoideae includes woody or herbaceous perennial plants, sometimes with an unpleasant smell. Members of this subfamily have glycosidic and steroids iridoid compounds that are of medicinal and aromatic importance. In addition, they are considered a source of nectar and pollen production for feeding honey bee colonies. In Iran, Ajugoideae has two genera named *Ajuga* and *Teucrium*. The paper study compiled data on the actual dispersion of species or the examination of specimens in the herbarium, using available sources that include local and regional floras. Species distribution modelling (SDM) tools have been used to predict the dispersion of species in the coming years affected by climate change. After collecting data on the dispersion of the examined taxa, open layers of information on independent and predictive environmental and climatic factors were prepared from various local and foreign sources for modeling. Extracting climate information through statistical tests, these models were calibrated and implemented. Models reconstruct species-environment relationships by using spatial data of taxon position and environmental variables affecting dispersion. The pattern and issues of the present-day distribution of species with climate variables were used to estimate the geographical distribution of species under future climate scenarios. The accuracy of the models ' performance was also evaluated. The results of this study creates important achievements for the conservation management of these species.

P.0354 Distribution patterns and phenology in Linum bienne Mill.: Towards an understanding of its adaptation to the local environment

José R. Grande A.[1], Beatrice Landoni[2], Macarena Marín R.[1], Clara López[1], Carlos Almeida[1], Rocio Pérez Barrales[1]

1 Facultad de Ciencias, Universidad de Granada, Granada, Spain. 2 Università degli Studi di Milano, Milano, Italy.

Linum bienne Mill. (Linaceae) is a widely distributed species native to the Mediterranean region and the Atlantic province of the Euro-Siberian region, and the wild relative of linseed (*Linum usitatissimum*). Recent studies have shown that in the westernmost portion of the distribution it shows a latitudinal variation in the date of flowering initiation, partly explained by the local climatic conditions, as well as the influence of vernalization. Specifically, it has been seen that populations of Mediterranean origin require fewer days than populations of Atlantic origin to initiate flowering, while in Atlantic populations vernalization is a requirement to initiate flowering. This variation in the onset of flowering has been important in the domestication process of linseed in continental Europe. However, it is unknown to what extent *Linum bienne* may be sensitive to the increase in temperatures associated with global change. In this sense, it has been seen that the information contained in herbaria can help decipher the phenological responses of plants in the last 200 years. An understanding of historical and current flowering patterns could help explain the changes that have occurred in the past and, therefore, the key factors that have determined the adaptation of this species to different types of environments. The present study offers a synthetic view of the natural distribution area of *Linum bienne*, including an herbarium database and a distribution model, correlating climatic data and Julian day through geographic gradients with the aim of understanding how the patterns of flowering and fruiting phenology have changed in space and time. The data obtained will help determine the phenological changes that have occurred in the species, and can serve as a model for the projection of the distribution patterns of this and similar species in a context of global change.

P.0355 An interactive model to test ecological and evolutionary hypotheses on incipient polyploid species

Juan S. Schneider[1], Ana I. Honfi[1], Anna V. Reutemann[2], Diego H. Hojsgaard[3]

1 Instituto de Biología Subtropical (PEFyGV, IBS, UNaM-CONICET), Posadas, Argentina. 2 Instituto de Botánica del Nordeste (IBONE, UNNE-CONICET), Corrientes, Argentina. 3 Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany.

Polyploidization is commonly associated with reproductive changes towards self-fertility and apomixis. Both self-fertility and apomixis provide reproductive assurance and an advantage for range expansion. More recently, the transient expression of apomixis post-polyploidization has been hypothesized to have an important role in the demographic establishment of a new polyploid. To test this hypothesis, we used NetLogo, an open-source multi-agent software, and built a framework that target perennial hermaphrodite plants with overlapping generations with a command center capable of modifying different individuals' attributes and most relevant variables that affect the speed of formation, establishment and expansion of neopolyploids in a natural-like environment. A workspace with individually occupied patches was subjected to an environmental background determined by bioclimatic and soil variables. Two attributes, *i.e.* "Individual Adaptivity", and "Fitness" were summoned to control the population dynamics. We computed in two reproductive alternatives, diploid sexuals and polyploid apomicts, with specific types of inheritance of individual´s attributes and similar pollen and seed dispersal capabilities. Simulations starting with a group of diploid individuals run for a minimum 1000 iterations and were repeated 1000 times to account for stochasticity. Results show that production of unreduced gametes up to a certain minimum is key for polyploid formation. Triploids, when incorporated, enhanced the speed of the establishment of tetraploid lineages. Apomixis improved the rate of neopolyploids within the parental diploid population, and decreased the average number of generations required to demographic establishment. The present analysis provides useful information on the dynamics of diploid-polyploid populations that originates agamic polyploid complexes, and showcase the model as a user-friendly, interactive tool for interrogating ecological and evolutionary questions.

P.0356 Anatomical variation of Cactaceae (Coryphantha and Mammillaria) in greenhouse and wild conditions.

Mayte Stefany Jiménez-Noriega [1], Teresa Terrazas[2], Alejandro De la Rosa-Tilapa[1], Dalia Grego-Valencia[3]

1 Jardín Botánico FES-Cuautitlán. Facultad de Estudios Superiores Cuautitlán, Universidad Nacional Autónoma de México, Mexico. 2 Departamento de Botánica, Instituto de Biología, Universidad Nacional Autónoma de México, Mexico. 3 Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Mexico.

This study explores the possible anatomical variations of Cactaceae species (*Coryphantha cornifera, C. clavata, C. radians* and *Mammillaria magnimamma*) that were grown under greenhouse conditions from seed with plants of the same species collected in wild. Three individuals per species per condition were fixed and sectioned in three regions of the stem, processed using the conventional paraffin technique and were stained with safranin and fast green. Measurements were obtained for each of the tissues studied, to which tests of normality and homogeneity of variance were applied, followed by one-way variance and Tukey's mean pairwise comparison analyses. All species present simple epidermis, hypodermis of 1 to 3 layers depending on the species. The species grown in both conditions conserved most of the characters. For example, calcium oxalate crystals in the hypodermis in *Coryphantha*. The differences between both conditions were found in the quantitative characters and in the abundant lignification of cortex and pith which probably will be deleterious for re-introductions to the wild. With this lignification of primary walls of the fundamental tissue of the succulent stems may lose the dehydration-rehydration capacity and this would be disadvantageous for species exposed to periodic droughts. We conclude that special attention should be given to the horticultural practices (supply of nutrients and watering) to avoid structural modifications.

P.0357 Plant diversity of the climate changes monitoring Cite Kuchak

Igor V. Kuzmin[1], Anatoliy A. Khapugin[1]

1 University of Tyumen, Tyumen, Russia.

Protected nature area Guzeneevo is situated on the shores of freshwater lakes among pine and aspen-birch forests (subtaiga) in the Western Siberia. Here, we have been studying vegetation cover from 1999 to the present. In 2021, Greenhouse Gases, Climate Changes and Biodiversity monitoring cite (carbon polygon) Kuchak (57.348973, 66.056108) has been founded here, being a part of the Monitoring Cites Network in Siberia. In 2023, we have studied the first, model, site of this area represented by a triangle shape with 1-km sides. We studied vascular plant diversity on 72 10×10-m study plots. Within them, we made 2247 observations, 6693 digital photographs. 110 herbarium specimens were collected. They have been introduced to our biodiversity database. On the model site, 194 native and alien species from 136 genera and 46 families have been found. The highest frequency of occurrences has been noted for Pinus sylvestris (presented on 100% plots), Betula pubescens (96%), and Vaccinium vitis-idaea (94%). Almost all genera include one species in the study area; just Carex, Galium, Pyrola, and Trifolium include five species each. The richest families in species were Asteraceae (25 species), Poaceae (20), Rosaceae (17), Ericaceae (13), Fabaceae (12). We recorded the following species, protected in Tyumen region: Actaea spicata, Cypripedium guttatum, Hemipilia cucullata, Tilia cordata. We registered eight invasive alien species (e.g., Malus baccata, Matricaria discoidea). Four more alien species were found at the border of the model site (Acer negundo, Amelanchier spicata, Chelidonium majus), and Parthenocissus inserta, which were not known previously here. 25-year studies have demonstrated an increase in abundance and distribution of nemoral (like Daphne mezereum) and steppe (Stipa pennata) species in the study area. The vitality, abundance and number of localities of boreal species (like Abies sibirica) are decreasing. These trends are probably associated with the climate changes in Western Siberia.

P.0358 The determinants of the geographic variation in within-population genetic diversity

Naïs Laporte[1], Roberta Gargiulo[2], Samuel Pironon[2,3]

1 TULIP-GS University Research School, Toulouse and Perpignan, France. 2 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 3 Queen Mary University of London, London, United Kingdom.

The Convention on Biological Diversity recognizes intraspecific genetic diversity as one of the three fundamental levels of biodiversity, which serves as the raw material for evolutionary processes, facilitating adaptation, resilience, and response to changing environmental conditions. However, genetic diversity remains difficult to estimate within populations at large spatial and taxonomic scales, impeding the upscaling of conservation actions. Several models have been proposed to explain the geographic variation of within-population genetic diversity, including the "centre-periphery hypothesis", which suggests a gradual decrease of population genetic diversity from the core to the edge of species' ranges due to decreasing environmental suitability and increasing isolation. However, empirical assessments of this hypothesis have produced conflicting results, partly because of the uncertainties associated with the definition of species' ranges, and the number of centre-periphery measures employed. Based on an extensive literature review and statistical analyses including species distribution modelling, we investigate whether the distribution of within-population genetic diversity of 284 plant and animal species can be explained by the contemporary structure of species' geographic and climatic ranges, and potential historical changes in climatic suitability. By assessing geographic, climatic and historical determinants of the distribution of within-population genetic diversity, we provide a better understanding of the extent to which general rules can support the prioritization of populations for conservation and the forecasting of species' responses to future environmental change, thus bolstering strategies for biodiversity preservation and management.

P.0360 Using remote sensing in evaluation of flora and vegetation due to urban development in Tirana City

Ajola Mesiti[1], Marjol Meço[2], Ermelinda Mahmutaj[1], Petrit Hoda[1]

1 Research Center of Flora and Fauna, Faculty of Natural Sciences, Tirana, Albania. 2 Department of Biology, Faculty of Natural Sciences, Tirana, Albania.

Albania ranks 5th in the world in terms of the pollutants levels released into the air from different sectors, and mainly for air quality in urban areas. As a result, in the last ten years, the number of people who complain about breathing problems and stress has doubled. This situation is thought to be mainly caused by heavy traffic in urban areas, combined with the use of relatively old machines, which release larger amounts of gases, as well as the quality of fuel in the market. The situation is further aggravated by the pronounced lack of green spaces, which are always decreasing due to urban construction activity, often outside the requirements, as well as by the uncontrolled load of pollutants released in urban areas by many businesses. The purpose of this study is to evaluate the long-term changes in floristic diversity and vegetation, in a time frame such as 2000-2020, every five years. This time-frame corresponds with important changes of the Tirana's urban area border. Through GIS are interpolated the orthophotos and it turns out that is that the city has tripled its area while reducing habitats and threatening important plant species.

P.0361 Bee phenological patterns in tropical and subtropical regions

Paula M. Montoya - Pfeiffer[1], Leonor Patricia Cerdeira Morellato[2]

1,2 São Paulo State University and Research Center for Biodiversity Dynamics and Climate Change, Rio Claro, São Paulo, Brazil.

The temporal activity of bees in temperate regions is mainly determined by the marked seasonality of temperature throughout the year. In contrast, the phenological pattern of bees in tropical and subtropical regions is expected to be more continuous due to the reduced temperature variability throughout the year. Despite this assumption, several species of tropical and subtropical bees have shown different levels of seasonality, but the extrinsic and intrinsic factors explaining their phenological patterns are still poorly understood. In this study, we review the phenological patterns of bee species in Brazilian tropical and subtropical regions and assess their relationships with bee traits and climatic variability. Our results show that solitary bee species, nesting in the ground, have shorter activity periods compared to social species nesting in cavities. Bee activity was more continuous in warmer climates, primarily focusing on the warmer months of the year. However, activity periods did not reveal a regional pattern in response to precipitation regimes. The implications of these variable seasonal patterns and the factors driving them in the potential responses of bees to global warming are discussed.

P.0362 Distribution of genetic and phenotypic variation among and within populations of the annual plant Arabidopsis thaliana

Xavier Picó[1], Antonio R. Castilla[2], Belén Méndez-Vigo[3], Raúl de la Mata[4], Arnald Marcer[5], Carlos Alonso-Blanco[3]

1 Estación Biológica de Doñana, Sevilla, Spain. 2 Oklahoma State University, Stillwater, USA. 3 Centro Nacional de Biotecnología, Madrid, Spain. 4 Universidad de Extremadura, Plasencia, Spain. 5 CREAF-UAB, Bellaterra, Spain.

The location of populations across a species' distribution determines its evolutionary dynamics due to the combination of forces acting upon the genetic and phenotypic variation in populations from different environments. A comprehensive understanding of the evolutionary dynamics of any species requires the quantification of the amount of variation in populations and the identification of the drivers of genetic and phenotypic variation in contrasting environments. Addressing these goals require large-scale approaches tackling the distribution of genetic and phenotypic variation among and within populations, which are relevant to comprehend the response of populations in increasingly changing environments. In this contribution, we showcase research conducted on the extent of genetic differentiation among populations as well as on the spatiotemporal dynamics of genetic variation within populations of the annual plant *Arabidopsis thaliana* across its Iberian range. We highlight the role of isolation-by-distance shaping large-scale geographic patterns of genetic differentiation and the lack of relationship between the geographical location of populations and their genetic variation, which seems to be determined by variation in precipitation seasonality. In addition, we show the enormous genetic variation that *A. thaliana* populations can contain in core environments. In edge environments, we find less genetic variation, but surprisingly, all populations maintain high levels of phenotypic variation and plasticity irrespective of its core or edge location. Overall, we conclude that, although geographical and environmental factors determine the distribution of genetic variation among and within populations, the maintenance of phenotypic variation and plasticity represents an asset for *A. thaliana* populations to endure in changing environments

P.0363 Impact of extreme climate events on tree density and species richness in valley forest, in the Amazonia-Cerrado transition, Brazil

José R. R. Pinto[1,2], Jéssica D. S. Pinheiro[1], Milton S. Meira-Junior[3]

1 Department of Forestry Engineering, University of Brasília, Brasília, Brazil. 2 Reference Center for Nature Conservation and Recovery of Degraded Areas, University of Brasília, Brasília, Brazil. 3 Institute of Agricultural Sciences, Federal University of Uberlândia, Monte Carmelo, Brazil.

Global Change has made extreme climate events more frequent and intense around the world. In Central-North Brazil, warming and severe droughts, driven by El Niño, promote changes in vegetation. Here, we present the results of 27 years of vegetation monitoring in a valley forest, in the Amazonia-Cerrado biomes interface. During the study, a fire occurred in part of the forest (2010), and several warming and drought events, but we emphasize the impacts of El Niño 2015/2016 on tree density, species richness and floristic composition. We inventoried 18 permanent plots (600 m2) in 1996, 1999, 2003, 2006, 2010, 2016, and 2023 and recorded the trees with a diameter greater than 5 cm, measured at 1.3 m above the ground. Between 1996 and 2023 we observed a 16.2% reduction in tree density (1335 to 1118), with the largest decrease (-14.0%) occurring between 2010 and 2023 (before and after El Niño 15/16). In previous years, the variation in density ranged from -1.7% to +0.4%. Throughout the study we counted 212 species, with the majority (6P.%) being present all time, 14.6% was registered in a single year and the rest were present between two and six inventories. 57 species were added to the floristic list between 1996 and 2023, and 29 species were no longer recorded in the area. These changes were concentrated in species with low density (n < 3). Species richness increased between 1996 (157 species) and 2023 (168), but changed little between the years recorded (-1.2% to +5.0%), with greater species turnover between 2010 and 2023. Cyclical fluctuations, which alternate periods of increase followed by reduction in tree density and species richness, as recorded in this study, is a natural process in tropical forests. However, extreme climate events have altered this balance, increasing tree mortality and accelerating the replacement of species.

P.0364 Climatic change scenarios and land use/ land cover analysis for Asphodelus bento-rainhae subsp. bento-rainhae, a Portuguese endangered species

Alice M. Almeida [1], Fernanda Delgado[1,2,], Natália Roque [1,2], Maria M. Ribeiro [1,2,3*], Paulo Fernandez[1,2,4]

1 IPCB—Polytechnic Institute of Castelo, Polytechnic University, Castelo Branco, Portugal. 2 CERNAS—Research Center for Natural Resources, Environment *and Society, Polytechnic Institute of Castelo Branco, Castelo Branco, Portugal. 3 CEF—Forest Research Centre, Lisbon University, Lisbon, Portugal. 4 MED&CHANGE—Mediterranean Institute for Agriculture, Environment and Development & CHANGE–Global Change and Sustainability Institute, Évora University, Évora, Portugal.*

Asphodelus bento-rainhae P. Silva (Asphodelaceae), is an endemic species of the Iberian Peninsula, known in this region by abrótea, abrótega, gamão, gamon or bengala-de-são-josé, and first described in 1956 by the botanist and agronomist Pinto da Silva. Due to the ongoing decrease in the area and quality of its habitat, *Asphodelus bento-rainhae* subsp. *bento-rainhae* (AbR) was classified as "Endangered" by the Portuguese Red List of Vascular Flora and as vulnerable on the International Union for the Conservation of Nature's (IUCN) Red List of Threatened Species. This study focused on AbR, an endemic plant found only in Serra da Gardunha, Portugal. MaxEnt was used to estimate the AbR distribution for the present and the future (2050) using the Shared Socioeconomic Pathway SSP3-7. To evaluate and quantify LULC variations over time, the Portuguese LULC maps from 1951–1980, 1995, 2007, and 2018 were used. The results showed that the predicted distribution of AbR at this time is consistent with its actual distribution, which is unaffected by the projected future changes in climate. The notable shifts in LULC were noted from 1951–1980 to 1995. Given the economic significance of cherries to the area, it is assumed that future changes in LULC will result in a reduction in the species' occurrence area and an increase in the area covered by cherry orchards. It is imperative to put conservation and habitat management measures into place, as well as to support forestry and agricultural activities that are compatible with the species' conservation and habitat restoration, in order to save this rare species from going extinct in the future.

P.0365 Tree population changes in an Amazonian forest

Renato Valencia[1], Consuelo Hernández[2], Queenborough Simon[2]

1 Escuela de Ciencias Biológicas, Pontifica Universidad Católica del Ecuador, Ecuador. 2 Yale University, Yale School of the Environment, USA.

We studied population changes of >600 species of trees and shrubs over a period of 22 years (three-time intervals), in a large, terra firme forest plot (25-ha) located in Amazonian Ecuador. Because of climate warming, Amazonian forests could experience droughts and other alterations that are expected to affect population stability and produce significant population changes. We explore how large are those changes and if they are constant in the three-time intervals. We also explore if such changes are greater in the less humid ridges or in the humid valleys. We found that populations of only <1% of the species increased or decreased significantly (e.g., >5 times of the original population). Contrary to our expectations, species populations increased more in (dry) ridges than in (wet) valleys. A small portion of the species (<1%), increased systematically during the three study intervals. Our results are preliminary, but they suggest that species with wood density below the community mean are becoming more important in the forest community.

P.0366 Population genomics and adaptive evolution of the altitude-disjunct distribution of Orobanche coerulescens in Taiwan

Sih-Chen Yu[1], Akihiro Nishimura[2], Koji Takayama[2], Renata Piwowarczyk[3], Young-Dong Kim[4], Meng-Yuan Huang[1], Yu-Hsin Tseng[1]

1 Department of Life Sciences, National Chung Hsing University, Taichung, Taiwan. 2 Department of Botany, Graduate School of Science, Kyoto University, Kyoto, Japan. 3 Center for Research and Conservation of Biodiversity, Department of Environmental Biology, Institute of Biology, Jan Kochanowski University, Kielce, Poland. 4 Department of Life Science, Hallym University, Chuncheon, Gangwon, Republic of Korea.

Global warming has become the most serious threat to current ecosystems, demanding a comprehensive understanding of potential mechanisms for organisms to endure extreme climates to prevent a widespread biodiversity crisis. To detect whether climate change has led to local adaptations within a species, population structure analysis and adaptive evolution are necessary for species adapted to distinct temperature regions. *Orobanche coerulescens* (Orobanchaceae), a holoparasitic plant, mainly distributes in the temperate regions of the Eurasian continent, with Taiwan representing its southernmost distribution and being the only population capable of growing in subtropical and tropical regions. Furthermore, *O. coerulescens* populations in Taiwan exhibit an altitude-disjunct distribution, occurring in coastal areas and altitudes above 2,500 meters. However, the mechanism of natural adaptation to varying temperatures and distinctive distribution in *O. coerulescens* remains to be clarified. This study focuses on *O. coerulescens* to investigate population genomics and evolutionary adaptation under its disjunct distribution between high and low altitudes. Morphological analysis reveals an intermediate overlap among individuals in montane and coastal regions in Taiwan, suggesting a slight differentiation between two altitudes in *O. coerulescens*. Subsequently, utilizing population genomics with a ddRAD sequencing strategy, we aim to explore population structure and origin, dispersal pathways, and genetic diversity. This research contributes to formulating conservation policies for endangered plants and provides crucial insights for the global biological community facing climate change.

S.048. ECOLOGICAL DRIVERS OF PALM SPECIATION

P.0367 Interplay of soil chemistry and rainfall patterns: Understanding the ecology of canopy Palms in the Chocó Biogeographic Region

Camilo Palacios-Hurtado[1,2], Juan Carlos Copete[3], Harley Quinto[4], Riley Fortier[1], Felipe Cardona[5], Don Faber-Langendoen[6], Álvaro Duque[2]

1 Department of Biology, University of Miami, Miami, USA. 2 Departamento de Ciencias Forestales, Universidad Nacional de Colombia, Medellín, Colombia. 3 Department of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland. 4 Facultad de Ciencias Exactas y Naturales, Universidad Tecnológica Del Chocó, Quibdó, Colombia. 5 Herbario Universidad de Antioquia, Universidad de Antioquia, Medellín, Colombia. 6 NatureServe, Arlington, Vancouver, USA.

The Chocó Biogeographic region's tropical rainforest stands out as one of the globe's largest hotspots for plant diversity. Among its key inhabitants, canopy palms play a vital role, given their dominance, species richness, and varied growth forms. Despite their significance, the ecological nuances of these palms remain insufficiently explored. Across 14 one-hectare plots spanning a 450 km gradient, we delved into species abundance, dominance, growth forms, and basal area. Linear regressions scrutinized the links between these components and environmental factors like precipitation, pH, organic matter, and phosphorus content. Our study documented 878 individuals across 17 species with a DBH exceeding 10 cm, with *Oenocarpus bataua* (187 individuals), *Welfia regia* (141), and *Astrocaryum standleyanum* (138) emerging as the top three most abundant species. On average, we recorded 62 individuals and 1.24 m2 of basal area per hectare, with 97.2 % of these palms exhibiting solitary stems. Positive and significant correlations surfaced between species count, individual count, and annual precipitation alongside organic matter, while negative associations linked species count to pH. Additionally, phosphorus showed positive relationships with the number of species, and basal area (m^2), although the associations were not statistically significant Principal component analysis (PCA) explored climatic and soil variables' relationships. PC1, explaining 39.86% of the variance, is predominantly influenced by annual precipitation and annual temperature range, while PC2 (23.45% variance) is linked to variables like annual mean temperature and isothermality. Climatic variables appeared more influential in the first two components, but soil variables retain importance. This comprehensive study unveils the intricate ecological dynamics of canopy palms in the world's wettest rainforest, highlighting specific environmental factors' pivotal role in shaping their distribution and abundance.

S.049. ECOLOGY, EVOLUTION AND GENETICS OF STYLAR POLYMORPHISMS: LINKING FORM & FUNCTION

P.0368 Global distribution patterns of style-length polymorphisms

Letícia R. Novaes [1,*], Rafael Molina-Venegas [2], Violeta I. Simón-Porcar [1], Juan Arroyo [1]

*1 Universidad de Sevilla, Sevilla, Spain. *lrodrigues@us.es. 2 Universidad Autónoma de Madrid, Madrid, Spain.*

Style-length polymorphisms consist of two or three floral morphs within a population, with a reciprocal arrangement of stigma and anther heights, which enforces outcrossing in plants by contacting different parts of the pollinator's body with flower sex organs while avoiding self-fertilization. Other plant breeding systems, such as dioecy or self-incompatibility have been traditionally associated with tropical environments, biodiversity hotspots and oceanic islands. Tropical regions and biodiversity hotspots are known for their higher diversity of pollinators and plants, more complex pollination networks, and a higher level of specialization. Oceanic islands may, on the one hand, hamper colonization by self-incompatible species due to their inability to reproduce without pollination agents (Baker´s law) but, on the other hand, they host a significantly high occurrence of dioecy. Most of style-polymorphic plants are self-incompatible. In this study, we aim to unravel the distribution patterns of style-length polymorphism, which are still poorly understood. We investigated the historical and biogeographical determinants of the occurrence of style-length polymorphisms across all angiosperm genera at a global scale. Specifically, we tested for style-length polymorphism: (i) the existence of phylogenetic signal, (ii) the lower or higher occurrence in oceanic islands, and (iii) the higher frequency in tropical regions and biodiversity hotspots. Our results suggest that the occurrence of style-length polymorphism is significantly conserved in the angiosperm phylogeny. We also found a significantly higher presence in oceanic islands (similarly to dioecious plants), but its occurrence was not associated to tropicality or biodiversity hotspots. Style-length polymorphism showed a strong phylogenetic signal even when excluding the genera of the highly represented family Rubiaceae from the analyses. The parallel high occurrence of dioecy and style-length polymorphism in oceanic islands supports the hypothesis of the evolutionary transition from style-length polymorphism towards dioecy in these habitats.

P.0369 Mating patterns and genetic diversity at the S locus in populations of a distylous jasmine (Chrysojasminum fruticans, Oleaceae)

Célia Paris[1], Hervé Gryta[1], Pierre-Olivier Cheptou[2], Mathilde Dufay[2], Anne-Laure Fuchs[1], Guillaume Besnard[1]

1 Centre de Recherche sur la Biodiversité et l'Environnement, CNRS-IRD-INP-Université Toulouse 3, Toulouse, France. 2 Centre d'Ecologie Fonctionnelle et Evolutive, Université de Montpellier-CNRS-Université Paul Valéry, Montpellier, France.

Distyly, the reciprocal positioning of anthers and stigmas in flowers of different plants, is a genetic polymorphism whereby two floral morphs occur in populations. This is often associated with genetic self-incompatibility and this trait combination is thought to have evolved convergently as an adaptation favoring outcrossing in insect-pollinated Angiosperms. Distyly and self-incompatibility are often encoded by the same hemizygous supergene (hereafter the *S* locus), present in a single copy in short-styled flowers and absent in long-styled individuals. To date, the genetic basis and molecular evolution of these traits remain poorly understood. Investigating mating patterns in relation to the variation at the *S* locus in populations may allow a better understanding of the functioning of these traits, in particular by documenting crosses between floral morphs and assessing the selfing rate among individuals. Here, we investigate the Mediterranean distylous Jasmine (*Chrysojasminum fruticans*) from the Oleaceae family, whose *S* locus was inherited from its ancestor more than 80 million years ago. Thirty-four microsatellite markers were developed including a dozen located in the *S* locus to build an extensive dataset of genotyped individuals from 16 natural populations and an experimental one. Parentage analyses on progenies sampled in four populations (the experimental and three natural populations) were first conducted to describe mating patterns. Then, we investigated how the genetic diversity at the *S* locus is structured within and between populations of *C. fruticans* in southern France, in comparison with their neutral genetic diversity. Finally, the occurrence of any recombination event at the *S* locus was also investigated. Although the expected mating patterns in distylous populations (i.e., crosses between short and long-style, with no possible selfing) have been set up decades ago, this study will be one of the first testing this hypothesis using population genetics.

P.0370 Genomic and transcriptomic investigation of new self-compatible lines of common buckwheat (Fagopyrum esculentum)

Sofia R. Prokopchuk[1], Mikhail I. Schelkunov[2], Aleksey A. Penin[2], Ivan N. Fesenko[3], Nikolai N. Fesenko[3], Maria D. Logacheva[1]

1 Center for Molecular and Cellular Biology, Skolkovo Institute of Science and Technology, Moscow, Russia. 2 Laboratory of Plant Genomics, Institute for Information Transmission Problems of the Russian Academy of Sciences, Moscow, Russia. 3 Breeding Centre, Laboratory of Buckwheat Breeding, Federal State Budgetary Scientific Institution "Federal Scientific Center of Legumes and Groat Crops", Orel, Russia.

Buckwheat is a vital crop, rich in essential nutrients crucial for functional nutrition. Buckwheat is a cross-pollinated plant which outcrossing is ensured by heterostyly – the development of different floral morphs (short styled, SS and long styled, LS) - along with some self-incompatibility mechanisms that prevent fertilization between plants of the same floral morph. However, the mutants with break of self-incompatibility are known in buckwheat, they represent a valuable material for deeper investigation of self-incompatibility mechanisms. Here we report the study of three self-compatible lines, two with short-styled homostyly (HS8 and HS5) and one with long-styled homostyly. The genes controlling the dimorphism and self-incompatibility are combined into the S-locus – the non-recombining region of the genome which is hemizygous in SS plants and absent in LS plants. One of the key genes at the S-locus is S-ELF3 gene. According to current paradigm, self-fertile homostyly is usually associated with the disruption of S-ELF3. We performed transcriptome analysis of these homostyle lines and found that in the short-styled homostyle lines S-ELF3 is expressed and its ORF is intact, in contrast to the long-styled homostyle line. A more recent in-depth analysis of the HS8 line, involving chromosomal genome assembly, showed that the S-locus is disrupted in this line: S-ELF3 is located separately, on a different chromosome, away from other parts of the S-locus. This shows a one more way of degeneration of heterostyly and self-incompatibility in buckwheat, not associated with loss of S-ELF3 function.

S.050. ECOPHYSIOLOGICAL CHALLENGES IN THE ANTHROPOCENE

P.0371 Surviving mine tailings: antioxidative enzyme activities in selected plant species

Uroš Aleksić[1], Isidor Grdović[2], Milijana Kovačević[2], Tamara Rakić[2], Nikola Milanović[1], Gordana Andrejić[1]

1 University of Belgrade, Institute for the Application of Nuclear Energy, Belgrade, Serbia. 2 University of Belgrade, Faculty of Biology, Belgrade, Serbia.

Mine tailings are a specific substrate that remains after the physical and chemical processing of ores in mines. They are rich in heavy metals and lack essential macronutrients, which is extremely unfavourable for the growth and survival of plants. The aim of this study was to determine the accumulation patterns of Pb, Cu, Zn, Fe and Cd in *Silene vulgaris*, *Arrenatherum elatius* and *Lotus corniculatus* and to evaluate their effects on membrane lipid peroxidation (MDA), total antioxidant capacity, photosynthetic pigment, protein content and antioxidant enzyme activities (ascorbate peroxidase, catalase, total soluble peroxidase) in the roots and shoots of the plants. The study showed a significant accumulation of all investigated metals, especially in the roots, with the exception of *S. vulgaris*, which accumulated more Zn in the shoots. Such high metal concentrations significantly affected the biochemical parameters and led to an increase in MDA levels, disruption of pigment concentrations and altered enzyme activities. The roots of *S. vulgaris* showed a significant decrease in total soluble peroxidase activity compared to the control, indicating enzyme inhibition at very high metal concentrations as observed in the root system. This emphasises that the results showed that high metal and mineral deficiency in plants from the flotation tailings caused profound physiological stress in both below- and above-ground plant parts, causing oxidative burst and indicating the importance of the enzymatic component of the plant antioxidant system in the defence against stress caused by high metal concentrations. In addition, the metal concentrations detected in analyzed plant species indicate their potential use in phytoremediation.

P.0372 Univariate responses of certain Potamogeton species to physicochemical properties of water

Dragana Jenačković Gocić[1], Ivana Kostić Kokić[1], Danica Vukotić[1], Irena Raca[1], Danijela Nikolić[1], Gordana Andrejić[2], Tatjana Anđelković[1]

1 Faculty of Sciences and Mathematics, Niš, Serbia 2 Institute for the Application of Nuclear Energy, Belgrade, Serbia.

The main aim of this study has been to determine univariate responses of 6 *Potamogeton* species (*P. crispus*, *P. lucens*, *P. natans*, *P. nodosus*, *P. perfoliatus* and *P. pusillus*) to physicochemical water properties - minimum depth, pH, electroconductivity, concentration of nitrite, nitarte, phosphate, sulphate, fluoride, bromide, and chloride anions. The Huisman-Olff-Fresco models have been used for modeling the species response curves based on the untransformed data on species abundance and environmental variables for 270 samples. *Potamogeton crispus* is indifferent to all, while the other *Potamogeton* species are indifferent to two (*P. lucens* - nitrite and phosphate; *P. natans* - phosphate and sulphate; *P. pusillus* - nitrite and fluoride), four (*P. perfoliatus* - electroconductivity, phosphate, sulphate and bromide), and five variables (*P. nodosus* - electroconductivity, nitrite, nitrate, phosphate, fluoride and bromide). *Potamogeton lucens* shows the tendency to grow in deep, alkaline (optimum pH value: 8.6) water with low electroconductivity (103–201 µS/cm), and concentration of sulphate (2.6–10.5 mg/L), bromide (2.6–10.5 mg/L) and chloride (2.6–10.5 mg/L). *Potamogeton natans* prefers deep, strong alkaline water (optimum pH value: 9.3) with low electroconductivity (37.7–252.6 µS/cm), poor in nitrite, nitrate, and rich in fluoride, bromide and chloride. *Potamogeton nodosus* has wide ecological valences regarding minimum water depth (5–117 cm), pH (7.6–9.7), sulphate (2.6–796.2 mg/L), and chloride (359.8–3188.7 mg/L). *Potamogeton perfoliatus* has ecological affinities to deep, alkaline water with high concentration of nitrate (8.7–11.5

mg/L) and low amount of chloride, opposite to *P. pusillus* that prefers shallow, strong alkaline water with lower concentration of nitrate (0.4–1.6 mg/L) and higher amount of chloride (137.6–3527.3 mg/L). These data are a valuable basis for better understanding the ecology of the analyzed species, so they can be used in activities that are oriented towards restoration, conservation and management of freshwater habitats.

P.0373 Bryophytes of the South Patagonian Icefield, Chile: insights into biodiversity, human impacts and ecophysiology for conservation.

Victor Ardiles[1,2], Álvaro Promis[3], Enrique Zamora[4], Fernanda Gallardo[4], Jaume Flexas[2], Marc Carriquí[2]

1 Área Botánica y Herbario SGO, Museo Nacional de Historia Natural, Santiago, Chile. 2 Universitat de les Illes Balears – Instituto de Investigaciones Agroambientales y de Economía del Agua, Palma, Spain. 3 Facultad de Ciencias Forestales y de la Conservación de la Naturaleza, Universidad de Chile, Santiago, Chile. 4 Instituto Chileno de Campos de Hielo, Santiago. Chile.

The accessibility of human activities to glacial regions within the South Patagonian Icefield holds significant implications for the conservation and management of plant biodiversity in subantarctic zones. Non-vascular plants, mainly mosses and liverworts, which play a pivotal role in primary ecological succession, nitrogen fixation, and soil formation in these areas, are potentially sensitive to human trampling. This study (2015-2020) aims to characterize the moss and liverwort flora in two glacial regions situated of the South Patagonian Icefield: Jorge Montt (JM) and Pío XI (PXI) glaciers, located at S 48° and S 49°, respectively. Additionally, this research addresses potential threats and proposes monitoring measures, with a focus on "trampling" as a primary anthropogenic disturbance affecting mosses and liverworts from these areas (change in coverage by biological type and colony life's pan). The floristic study considers altitude gradients ranging from 200 to 1,100 meters above sea level. The findings reveal a total of 76 species, with 43 identified in JM and 51 in PXI, predominantly consisting of mosses and liverworts native and endemic to subantarctic areas. Three indicator species for JM and nine for PXI were identified. Three groups or associations of species were identified for JM, and five for PXI, considering the influence of environmental variables specific to each study area. Altitude and the percentage of surface rock were identified as key variables explaining these associations. Alongside the floristic results, this study introduces sustainability indicators for mosses and liverworts, specifically designed for potential tourist routes accessing the South Patagonian Icefield plateau. Finally, we suggest the urge to investigate the combined effect of alien species, global warming and the increasing influx of visitors to these ecosystems on the ecophysiology of the non-vascular plant communities from these remote areas.

P.0374 The effect of increasing Li concentrations on physiological stress parameters in Miscanthus × giganteus plants

Isidor Grdović[1], Milijana Kovačević[1], Gordana Andrejić[2], Uroš Aleksić[2], Tamara Rakić[1]

1 University of Belgrade, Faculty of Biology, Belgrade, Serbia. 2 University of Belgrade, Institute for the Application of Nuclear Energy, Belgrade, Serbia.

Ecological problems caused by increased lithium concentrations in soil and groundwater arise from lithium mine waste and the improper disposal of lithium-ion batteries, which are found in all areas of modern life – from electronic devices to electric vehicles and battery storage systems. Current scientific literature lacks comprehensive data on the physiological consequences of the accumulation of Li-ions in plants and their practical use in the phytoremediation process. The aim of this study was to determine the accumulation pattern of Li in roots, rhizome, stem and leaves of *Miscanthus × giganteus* and to investigate the effects of increasing Li concentrations on the accumulation and transport of mineral elements in the plant, electrolyte leakage, membrane lipid peroxidation (MDA) level, photosynthetic pigment content and antioxidant enzyme activities. The study showed efficient Li accumulation by Miscanthus plants, even at the highest Li concentrations, especially in roots and leaves. Accumulated Li showed significant effects on Cu and Mn accumulation, increased electrolyte leakage and MDA levels, decreased chlorophyll (*a*, *b*) and total carotenoid content, and altered antioxidant enzyme activities in roots and leaves. The results obtained showed that exposure to higher Li concentrations induces physiological stress in Miscanthus, leading to negative effects on its cellular integrity and photosynthetic processes. Despite the induced stress, the effective Li accumulation indicates its potential use in phytoremediation.

P.0375 Does hydraulic redistribution provide climate resilience to the longleaf pine ecosystem?

Thomas L. O'Halloran,[1,2], Jean-Christophe Domec[3], Jamie A. Duberstein[1], Cheng-Wei Huang[4], A. Christopher Oishi[5], Brian Viner[6], Thomas M. Williams[1]

1 Baruch Institute of Coastal Ecology and Forest Science, Georgetown, USA. 2 Department of Forestry and Environmental Conservation, Clemson University, Clemson, USA. 3 Nicholas School of the Environment, Duke University, Durham, NC/Bordeaux Sciences Agro, Bordeaux, France. 4 Portland State University, Portland, USA. 5 USDA Forest Service, Southern Research Station, Coweeta Hydrologic Laboratory, Otto, USA. 6 Savannah River National Laboratory, Aiken, USA.

Longleaf pine forests were once expansive across the southeastern United States (SEUS). Due to changing economic values in forestry, over time, longleaf forests were extensively harvested and gradually shifted to other tree species or land uses altogether. Subsequently, several plant and animal species that associated strongly with this ecosystem are now threatened or endangered. Furthermore, the longleaf understory is recognized for harboring very high levels of plant biodiversity. There is now a substantial effort underway to restore this ecosystem across its original range. One major question that has emerged from this restoration effort is whether the ecosystem will be resilient to projected future climate change. In the SEUS this is forecast to include more extreme hydrological variability, whereby total rainfall will remain relatively constant but will be delivered over fewer, more intense rain events interspersed with periods of drought. Higher temperatures are also projected to increase atmospheric vapor pressure deficit (VPD)--the driving force of evapotranspiration–which provides a stressor to plants. Longleaf pine forests are known to exhibit hydraulic redistribution (HR), a process through which the trees' large tap roots contribute to a net movement of water from deep to shallow soil layers. This can have significant implications for plants that depend on shallow soil moisture and therefore overall ecosystem function. Predicted increases in VPD may decrease nighttime HR if nocturnal transpiration consumes the majority of root water uptake or increase total HR if stomatal closure halts water flow through the trunk. In this presentation we overview a new project in coastal South Carolina designed to quantify the functional sensitivity of HR and related plant water storage dynamics to abiotic drivers. The project includes extensive in situ measurements of soil-plant-atmosphere water dynamics and modeling studies designed to forecast the ability of HR to provide climate resilience under future climate change.

P.0376 The effect of early light and water conditions for the seedlings of chamomille (Matricaria chamomilla L.)

Erika Pénzesné Kónya[1]

1 Department of Botany and Plant Physiology Eszterházy Károly Catholic University, Eger, Hungary.

It is evident that the environmental conditions during the first weeks of germination has effect for all the life span of several annual plant species. The examined species is chamomille (Matricaria chamomilla L.), an important and valuable wild medicinal plant species growing in the plain protected areas of Hungary. Tthis annual medicinal plant is known in connection with the medicinal comounds and the traditional use of it. Our aim with the experiment was to simulate different light conditions and a water flooding which occasionally occur in plain areas after winter or in autumn. The climatic chamber treatment of seeds was divided into the treatents under two different light spectra and colour temperature of LED lights with permanent light expositions of seeds using two different temperatures After the treatment the results show different growing features of the plants comparing with control individuals. The results of the experiments show the adaptability of the species to different light and water conditions of the area. It can help understanding the different productability of the species during the extreme weather conditions of last decades. Acknowledgments: The research is supported by the support of OTKA143376 application of Hungarian Academy of Sciences.

P.0377 Unraveling phenotypic divergence in polyploids as a driver of adaptive potential in response to drought

Alba Rodríguez Parra[1], Javier López Jurado[1], Jesús Picazo Aragonés[1], Mario Fernández Martínez[1], Claudia Moreno Portillo[1], Enrique Mateos Naranjo[1], Anass Terrab Benjelloun[1], Francisco Balao Robles[1]

1 University of Seville, Seville, Spain.

Polyploidy is recognized as one of the most significant factors in plant evolution. The successful establishment of polyploids is attributed to the genetic, physiological, and morphological changes that occur in polyploids would allow them to better resist environmental stresses such as drought and increased temperature, allowing them to occupy more extreme environments. These adaptations would be promoted by the greater plasticity of the genome of the autopolyploids through changes in gene expression. Consequently, understanding the role of ecological divergence and dissimilarities in phenotypic traits among neopolyploids becomes crucial for enhancing our comprehension of polyploid evolution. This study aims to elucidate the ecophysiological difference between cytotypes in response to drought, using the Mediterranean autopolyploid *Dianthus broteri* complex as a study system. This complex comprises four ploidy levels (2x, 4x, 6x, and 12x) and parapatric monocytotypic populations along an arid gradient in the Iberian Peninsula. This fact suggests that the coexistence among cytotypes is not stable and polyploids appear to have been displaced towards the most extreme niches along an aridity gradient. Therefore, we conducted an experiment to assess physiological traits linked to drought, acclimation and plant recovery in two cytotypes (2x and 6x). For this purpose, plants were subjected to lack of irrigation up to 40% soil water content ("extreme drought"). Plant water status, leaf gas exchange, chlorophyll fluorescence and photosynthetic pigments were recorded on the first day, at the peak of drought stress, and during the recovery period. By the 18th day of treatment, both cytotypes exhibited signs of water stress. In general, the 2x cytotype exhibited higher signs of water stress (a decrease in leaf relative water content). Furthermore, our results suggest that cytotypes show different photochemical strategies to cope with drought stress, which play a crucial role in determining their current distribution and their adaptation to arid conditions.

P.0378 Understanding water stress and light exposure interplay in four Atlantic Forest species used in ecological restoration projects

João P. Taranto[1, 2], Fernanda da C. G. Ferreira[1], Jerônimo Sansevero[3], Dulce Mantuano[2]

1 Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil. 3 Universidade Federal Rural do Rio de Janeiro, Rio de Janeiro, Brazil.

The predicted rise of atmospheric temperatures and the changes in rainfall patterns coupled with the inevitable stress caused by the planting of the seedlings will enhance the probability of seedlings going under stress. The drought prompts stomatal closure, limiting carbon gain to photosynthesis, potentially leading to photoinhibition and overheating. We tested the effect of water availability and light intensity on seedlings stress using chlorophyll *a* fluorescence (Fv/Fm_{50}, quantum efficiency of photosystem II,) as a proxy parameter to assess the damage intensity. We studied four species commonly used in restoration projects of the Atlantic Forest: *Calophyllum brasiliense* Cambess., *Citharexylum myrianthum* Cham., *Cordia superba* Cham. e *Myrsine coriacea* (Sw.) R.Br. ex Roem. & Schult. Additionally, we measured the total chlorophyll content, stomatal conductance, and relative water content of the leaves. To estimate the potential of recovery from photoinhibition, plants were rehydrated when they reached Fv/Fm_{50} and re-measured after five days. Under the same light and drought conditions, *C. superba* resisted only for six days but could recover from Fv/

Fm_{50} while, *C. myrianthum*, *C. brasiliense*, and *M. coriacea* resisted for 10, 11, and 17 days, respectively, but without recovery. All species demonstrated photoinhibition when soil moisture content reached around 17% at high light. Interestingly, only *C. brasiliense* exhibited photoinhibition in the shade at the same moisture level, but with less damage. These findings suggest that water restriction coupled with saturating light - which can vary according to the season - diminishes photosynthetic potential even in heliophilous-pioneer species. Expecting a future with more events of drought, we have shown that this combination will impact seedlings' physiology by hindering photosynthesis and, consequently, lowering the probability of success of the establishment of initial vegetation.

S.051. ECOSYSTEM GENOMICS: ELUCIDATING THE GENETIC DRIVERS OF NUTRIENT FLUXES IN BRYOPHYTE DOMINATED COMMUNITIES

P.0379 Bryophytes associated nitrogen-fixing microbiota in Amazonian fragmented forests

Adriel M. Sierra[1,2], Marta Alonso García[1,2], Dennis O. Escolastico[1,2], Charles E. Zartman[3], Juan Carlos Villarreal Aguilar[1,2]

1 Département de Biologie, Université Laval, Québec, Canada. 2 Institut de Biologie Intégrative et dês Systèmes, Université Laval, Québec, Canada. 3 Instituto Nacional de Pesquisas da Amazônia, Departamento de Biodiversidade, Aleixo, Manaus, Brazil.

The size and connectivity of habitat patches are key factors determining diversity patterns from genes to the ecosystem. Globally, forest fragmentation has extensively reconfigured spatial landscapes, yielding profound and enduring impacts on biodiversity. In the Amazon Forest, widespread deforestation has led to a rapid biodiversity change across the entire biome. Epiphyllous bryophytes form abundant and diverse communities in the Amazonian biome yet are highly sensitive to environmental changes making them an ideal study system for understanding biodiversity dynamics associated with forest loss. Our investigation delves into the interplay between abiotic factors (habitat size, and connectivity) and biotic factors (species identity and the host genotype) on plant-microbe associations in a fragmented forest landscape. Specifically, we integrate genomics and bioinformatics tools, to study the host population genetics and the associate nitrogen-fixing microbiota (diazotrophic) of two prevalent epiphyllous bryophyte species in forest fragments of different sizes (1-, 10-, 100-ha, and continuous forest). Results show that genotypes diverged in 1- and 10-ha fragments, compared to populations in larger 100-ha fragments and continuous forests. Additionally, both species exhibited a decrease in the number of nitrogen-fixing bacterial species as well as a shift in their composition in small 1-ha fragments. At a broader scale, our findings underscore the significant impact of fragmentation on the plant population genetics and their associated microbiota. This integrative approach illustrates the profound effects of reduced habitat size and connectivity on the plant species' ability to sustain its beneficial associated microbiota.

P.0380 A laboratory-to-field approach for determining the genetic and environmental factors underlying mutualism within a Sphagnum peatla

David J. Weston[1], Alyssa Carrell[1], Jun Hyung Lee[1], Sara Jawdy[1], Dale Pelletier[1], Jon Shaw[2], Gustaf Granath[3], Adam Healey[4], Jeremy Schmutz[4]

1 Oak Ridge National Laboratory, Oak Ridge, TN. 2 Duke University, Durham NC. 3 Uppsala University, Sweden. 4 Joint Genome Institute, Walnut Creek, CA.

The importance of plant-microbiome systems on terrestrial carbon and nitrogen processes is perhaps most pronounced in *Sphagnum* dominated ecosystems, which occupy 3% of the Earth's land surface yet store approximately 30% of terrestrial carbon as recalcitrant organic matter (i.e., peat). The foundation plant *Sphagnum* is responsible for much of the primary production in peatland ecosystems and produces recalcitrant dead organic matter. *Sphagnum* together with associated microorganisms, contributes substantial nitrogen inputs into peatlands and influences host resilience to extreme climatic events. Under changing environmental conditions, a central question about these ecosystems is whether the *Sphagnum*-microbiome will maintain its beneficial interactions, or will it shift to neutral or even antagonistic interactions that ultimately influence peatland carbon gain and storage. Here, we test the hypothesis that the thermal origin of the microbiome influence *Sphagnum* host performance and resilience to warming. Briefly, we mechanically separated the microbiome from *Sphagnum* plants residing in a whole-ecosystem warming study, transferred the component microbes to germ-free plants, and exposed the new hosts to temperature stress. Although warming decreased plant photosynthesis and growth in germ-free plants, the addition of a microbiome from a thermal origin that matched the experimental temperature completely restored plants to their pre-warming growth rates. Metagenome and metatranscriptome analyses revealed that warming altered microbial community structure, including the composition of key cyanobacteria symbionts, in a manner that induced the plant heat shock response, especially the Hsp70 family and jasmonic acid production. The plant heat shock response could be induced even without warming, suggesting that the warming-origin microbiome provided the host plant with thermal preconditioning. Together, our findings show that the microbiome can transmit thermotolerant phenotypes to host plants, providing a valuable strategy for rapidly responding to environmental change.

S.052. ETHNOBOTANY AND CONSERVATION OF MEDICINAL PLANTS

P.0381 Plant biodiversity heritage: traditional knowledge and endogenous resources of the Biosphere Reserve of Omaña and Luna Valleys

Estrella Alfaro-Saiz[1,2*], Sergio Rodríguez-Fernández[1], Blanca Cortón Gracia[1], Rebeca Díez-Antolínez[3], Ana I. Paniagua-García[3], Sandra Lobato-Pérez[3], Susana Cámara Leret[4], Ana Belén Fernández Salegui[1], Marta Eva García-González[1,2], Carmen Acedo[1]

*1 Department of Biodiversity and Environmental Management, University of León, León, Spain. 2 Herbario LEB Jaime Andrés Rodríguez, León, Spain. 3 Centre of Biofuels and Bioproducts. Agricultural Technological Institute of Castilla y León, Villarejo de Órbigo, León, Spain. 4 Independent researcher and artist. *estrella.alfaro@unileon.es*

Plants form the foundation of human life support and offer a potential solution to future supply challenges in a changing world. The revaluation of plant resources can contribute to the development of local bioeconomy, exploring applications in fields such as pharmacy, food or cosmetics in depopulated areas having a rich biodiversity. These areas can be used as laboratories for pilot experiments grounded in a commitment to respecting and caring for nature. To this end, an interdisciplinary team from the University of León (ULE), the Agricultural Technological Institute of Castilla and León (ITACyL), and the Biosphere Reserve of Omaña and Luna Valleys (RBVOyL) are actively working on a project called 'SOMOS AGUA II', in León (Castilla and León, Spain). This three-year project is developed several actions (A). A1 involves continuing the 'SOMOS AGUA I' data series, monitoring plots with aromatic and medicinal plants, mowing meadows, and managing apiaries. A2, titled "Capsules of the future," aims to locate wild plants with potential uses and involves *in-situ* and *ex-situ* conservation of plant resources in the RBVOyL. A3 focuses on valorizing the phytochemical resources of wild plants. A4, 'Biocultural probes' centres on memory, custody, and biocultural development through workshops and cultural activities. Lastly, A5 emphasises replicability and transferability, establishing a distinctive label for the territory's socially and ecologically responsible products and services. This contribution outlines the initial project findings, highlighting the territory's significance for plant biodiversity and useful wild plant resources. It also fosters collaboration with residents to design small-scale harvesting and cultivation methods that align with plant species use and conservation. Acknowledgments: The project SOMOS AGUA II is funded by Fundación Biodiversidad and Ministerio de Transición Ecológica y Reto Demográfico (MITERD) of the Spanish government in the framework of the Plan for Recovery, Transformation and Resilience funded by the European Union - NextGenerationEU.

P.0382 Ethnobotanical study and conservation of floristic diversity of Shahdag Highlands of the Greater Caucasus

Valida Ali-zade[1], Naiba Mehdiyeva[2], Rashad A. Salimov[3]

1 Natural History Museum, The Ministry of Science and Education of Azerbaijan Republic, Baku, Azerbaijan. 2 Institute of Botany, The Ministry of Science and Education of Azerbaijan Republic, Baku, Azerbaijan. 3 Faculty of the Natural Sciences, Sumgayit State University, Sumgayit, Azerbaijan.

Identification, research, conservation and sustainable use of culturally important plant resources is a strategically important issue of global importance. It is known that many important plant species are concentrated in mountain systems, and alpine meadows are the main source of medicinal and food plants. Increasing global changes may lead to significant shifts in the distribution of species, and the cultural identity of local peoples may lose traditional knowledge about the use of plants. The purpose of this work was an ethnobotanical study of the Shahdag Highlands of the Greater Caucasus. The floristic diversity and the complex of biological and socio-cultural characteristics are considered, as well as the involving traditional knowledge and practices of indigenous peoples in the conservation of biological and cultural diversity. The studied region is located in the north-east of Azerbaijan at an altitude of 2,450 meters above sea level. Currently, this region with a 5-thousand-year history has a high national historical, cultural and tourist significance. The population of this district is the Shahdag group of peoples - Khinalygs, Budugs, Gyryz, Haputs, Kekirs. As a result of research work and revision of the collected herbarium materials, it was found that 413 species and 47 infraspecific taxa belonging to 219 genera and 49 families grow on this territory. All the peoples of Shahdag have historically been engaged in cattle breeding, mainly sheep breeding. They were also partially engaged in agriculture. Crops such as barley, wheat, rye, and lentils were cultivated as the main objects. It was found that the rural population suffers most from a shortage of water, which affects the fact that they lead a seasonal nomadic lifestyle. The empirical data collected show that local perceptions form the basis on which many small societies monitor the availability and change of reserves of shared natural resources.

P.0383 Ethnobotany of the Catalan linguistic area: an up-to-date work and prospects

Canòlich Álvarez[1,2], Jacint Altimiras[1], Fuencisla Cáceres[1], Judit Català[1], Teresa Garnatje[3,4], Raquel González[1], Jon Marín[1], Maria Orriols[1], Montse Parada[1], Ester Sala[1], Joan Vallès[1,5], Sílvia Ysamat[1], Airy Gras[1]

1 Laboratori de Botànica – Unitat associada al CSIC, Facultat de Farmàcia i Ciències de l'Alimentació, Universitat de Barcelona, Barcelona, Spain. 2 Govern d'Andorra – Ministeri de Cultura, Encamp, Andorra. 3 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 4 Jardí Botànic Marimurtra – Fundació Carl Faust, Blanes, Spain. 5 Institut d'Estudis Catalans, Barcelona, Spain.

There is a lot of evidence of traditional knowledge loss in rural areas of industrialized societies, and ethnobotanical fieldwork is key to palliate the eroding process. At the same time, the return of the traditional knowledge to the people is, apart from an ethical duty, also a key piece to preserve and value this information. The Catalan linguistic area is one of the most largely studied territories in Europe from the ethnobotanical point of view, and there is still ongoing research. 'Ethnobotany of the Catalan Countries' website (https://etnobotanica.iec.cat) is an interactive tool to (re)discover plant-related traditional knowledge collected through ethnobotanical prospection since 1990. The aim of this poster is to provide an encompassing overview of both the territories already studied and those currently under study, and address the gaps in ethnofloristic research within the area. Nowadays, the website contains almost 80,000 entries with plant names and 55,000 with medicinal uses, about 30,000 entries for food uses are prepared (together with complementary data centred on plants used for beverages) and almost ready to be uploaded to the database, and work is underway to introduce, in the next two years, about 30,000 entries more for other uses and other information. We consider that this comprehensive prospection and the derived website is a good tool to feed back to society knowledge about its natural and cultural heritage, while preserving it and making it available for the new generations. Finally, in the last years, we started performing different kinds of meta-analytic work with our dataset, to compare territories or to assess different kinds of plant uses, and, more recently we have started a new approach to analyse our results on a phylogenetic framework in order, among other focuses, to detect hot nodes of traditional knowledge and natural resources for all aspects of human well-being.

P.0384 Ethnobotany and taxonomy of plants from the Emberá tribe of Colombia

Fernando Alzate-Guarin[1], Sandra Turbay[2], Javier Rosique-Gracia[2], Sneider Rojas Mora[2]

1 Grupo de Estudios Botánicos GEOBOTA, Instituto de Biología, Facultad de Ciencias Exactas y Naturales, Universidad de Antioquia, Medellín, Colombia. 2 Grupo de Investigación Medio Ambiente y Sociedad, Departamento de Antropología, Facultad de Ciencias Sociales y Humanas, Universidad de Antioquia, Medellín, Colombia.

The Emberá Amerindian people are a tribe found in northern South America and Panama. This ethnic group has some sacred sites in the Serranía de Abibe, the northwestern end of the Andes Mountain range, an area of tropical forest almost unexplored due to social and political reasons. In field work carried out, the flora of three sacred sites for this people, located in the Abibe mountain range, Colombia, was collected, described, and characterized, and the taxonomy and nomenclature used by these communities for the plants in their environment is described and presented. The characterization includes the inventory of a selected sample of the flora associated with these sites and an explanation of their ecological characteristics and cultural importance. Emphasis is placed on the nature of the knowledge that the jaibaná (traditional healers), has about plants and the ways in which they are used in the community. The botanical samples were obtained, pressed, and described for subsequent taxonomic identification in the herbarium of the University of Antioquia (HUA). The information on the use given in the community to the collected species was given by the jaibaná and other members of the indigenous community. 36 of the plants collected have names in the Emberá language, where several of these names are used at the same time to call different species, eight are named after animals and three names refer to parts of the human body. The Emberá language does not have a generic name for all plants, as it does for all animals (ninduru). For the Emberá, plants are considered female or male, depending on whether they produce fruit, and some grammatical radicals are usually added to the name that refer to characters such as timber (zarea), or toxic (neara), depending on the species.

S.052. CINCHONA: ETNOHISTORIA DE LOS USOS Y APLICACIONES ACTUALES DEL ÁRBOL DE LA QUINA

P.0385 Evaluación in vitro del efecto antiviral de extractos de Cinchona en la replicación del virus SARS-CoV-2

Miryam Palomino-Rodriguez[1], Marcos Hernández[1], Pamela Rios[1], Martin Huallanca[1], Johanna Balbuena-Torres[2], Ruben J. Arancibia Gonzales[1], Jorge L. Cabrera Melendez[3], Marco A. Bartolo-Marchena[3]

1 Área de Innovación tecnológica del Instituto Nacional de Salud. 2 Laboratorio de Virus Inmunoprevenibles del Instituto Nacional de Salud. 3 Centro Nacional de Salud Intercultural del Instituto Nacional de Salud.

The COVID-19 pandemic has caused approximately 700 million cases and nearly 7 million deaths worldwide. Pharmacological studies of likely drug candidates for the treatment of COVID'19 is a necessity as the virus currently continues to evolve, originating different lineages and becoming endemic. The aim of this study is to evaluate the in vitro antiviral effect of ethanolic and chloroformic extracts of three Cinchona species against SARS-CoV-2 virus, PE/B.1.1/28549/2020 predominant strain at the beginning of the pandemic. SARS-CoV-2 virus was inoculated into Vero 81 cells, the infected cells were treated with different concentrations of ethanolic and chloroformic extracts of three Cinchona species, and the appearance of the cytopathic effect was evaluated after 72 hours. Quantification of replicate virus was performed by plaque titration assay and real-time RT-PCR for SARS-CoV-2. Prior to treatment, a cytotoxicity test was performed to determine the optimum concentrations for treatment. The IC50 concentrations were determined to be 66, 62 and 323 µg/mL for the ethanolic extracts of C. nitida, C. pubescens and C. calisaya, respectively, and IC50s of 77, 50 and 1022 µg/mL were obtained for the chloroformic extracts in the Vero ATCC CCL-81 cell line. The chloroplast extract of C. pubescens bark showed in vitro antiviral activity against SARS-CoV-2 prototype strain PE/B.1.1/28549/2020 at the concentrations of 24-48 µg/mL of extract. The other extracts of C. nitidae and C. calisaya species did not show antiviral activity. The in vitro studies demonstrate that the extract of C. pubescens shows antiviral activity against SARS-CoV-2 virus and can be used as a candidate for treatment against this virus.

Note: This abstract was translated using IA.

S.052. ETHNOBOTANY AND CONSERVATION OF MEDICINAL PLANTS

P.0386 Sowing to grow life

Carolina Bambagüé Caícedo[1], Maribel Palechor[1], Javier Enrique Luna[1]

1 Departamento de ciencias naturales. Institución Educativa Belén. Tambo, Colombia.

Environmental education is a social educational process that raises awareness and knowledge of local, national and global environmental problems that affect the ecological balance of the planet. Given the importance of this strategy, in the Belén Educational Institution, located in the municipality of El Tambo, Colombia, the school environmental project (PRAE) was launched in 2022 with the community garden as its pillar; this space aims to train and strengthen children and adolescents in food security and food sovereignty issues. In order to start the planting process, the traditional knowledge of the community was consulted and based on the information gathered, aromatic plants were selected: camomile (*Chamaemelum* sp.), basil (*Ocimum basilicum*) y verduras: carrot (*Daucus carota*), tomate (*Solanum lycopersicum*), lettuce (*Lactuca sativa*), cucumber (*Cucumis sativus*) y onion (*Allium cepa*). In the development of the PRAE, students acquire skills to classify plants into taxonomic families, identifying morphological features such as: edges, apices and margins of leaves, shapes and structures of stems, types of fruits and flowers, as well as transformation processes. socio-political, academic and artistic processes to ensure a positive subject-environment relationship. Among the results obtained, there was a low germination of the seeds sown, which can be attributed to the physical, chemical and biological state of the soils in the study area, due to the fact that these soils have been subjected to heavy loads of agrochemicals, fumigation and monoculture plantations. In the region, the development of socio-ecological processes is highlighted through the PRAE where there is direct linkage and participation with different actors in the community. This space is a living classroom where not only natural sciences are worked on but also a process of mainstreaming is carried out.

Note: This abstract was translated with AI.

P.0387 Young researchers for ethnobotany: the project “BE ETHNO: sharing traditions, sharing plants, sharing place, sharing future”

Martina Bottoni[1,2], Fabrizia Milani[1,2], Claudia Giuliani[1,2], Gelsomina Fico[1,2]

1 Department of Pharmaceutical Sciences, University of Milan, Milan, Italy. 2 Ghirardi Botanic Garden, Department of Pharmaceutical Sciences, University of Milan, Toscolano Maderno, Brescia, Italy.

Since the 80s of the last century, immigration in Europe has always been growing. Nowadays, the multi-ethnic Italian population is integrated in pluricultural urban contexts, where immigrants retain traditional knowledge of native plants. Does their bio-cultural heritage still influence the therapeutic and culinary practices? Within the framework of the call for “Young Researchers 2023” supported by Cariplo Foundation, the project “BE ETHNO: sharing traditions, sharing plants, sharing place, sharing future” was founded (ID:2023-1454). The three-year proposal (2024-2027) aims at a multidisciplinary approach, that conceives the urban ethnobotany as a tool to reach a deeper knowledge of the plants’ traditions of use of a selected foreign community. Four workpackages are planned, starting with bibliographic research concerning the migratory phenomena in Italy, especially Lombardy region (Northern Italy), with the aim of focusing the foreign community (*reconnaissance investigation*). Within the *citizen science* polices, an ethnobotanical survey will be conducted in two urban areas, documenting the enduring traditional use of medicinal and food plants for daily needs. The same will be performed in the native country, aiming at comparing the traditional knowledge of the selected ethnic group in different geographical and cultural contexts (*ethnobotanical investigation*). Primary data will lead to the selection of 1-2 species, symbol of the foreign tradition and worthy of laboratory insights under a taxonomical, micromorphological, phytochemical, pharmacological and nutritional point of view (*laboratory investigation*). Finally, in an *open science*context, dissemination and communication actions will be organized at the G.E. Ghirardi Botanical Garden (University of Milan) by engaging key-informants (*dissemination actions*). A dedicated area will be set, hosting plants traditionally used by the foreign community with a peculiar iconographic apparatus. Thematic itineraries and a bilingual booklet (Italian-Spanish) will be realized, making the botanical garden a place of natural and cultural biodiversity.

P.0388 Ritual use of rosa de borracho (Clinopodium macrostemum Moc. & Sessé ex Benth.) in Oaxaca, Mexico

Dalay Y. Calvo-Díaz[1], Lisbeth Aguilar-Hernández[1], Mayte S. Jiménez-Noriega[2*], Alejandro Torres-Montúfar[3]

1 Instituto Tecnológico Nacional de México. Campus Instituto del Valle de Oaxaca, Oaxaca, Mexico. 2 Jardín Botánico FES-Cuautitlán, Facultad de Estudios Superiores Cuautitlán, Estado de México, Mexico. 3 Herbario FES-Cuautitlán, Facultad de Estudios Superiores Cuautitlán, Estado de México, Mexico.

In Mexico there is a close relationship between its cultural diversity and the use of plants, such as in the preparation of food as well as in spiritual and religious rituals. In this study, the uses of *rosa de* *borracho*, or *poleo*, (*Clinopodium macrostemum*) are explored via semistructured interviews with 40 members of Ocotlan de Morelos and Sola de Vega, two communities from the state of Oaxaca. The results showed that in Sola de Vega, *poleo* is used in local Soltecan weddings for a traditional dance in which it is incorporatedinto attire worn for the celebration. In the Guelaguetza annual cultural representation of the state of Oaxaca, Soltec weddings are represented. Other uses of *Clinopodium macrostemum* include as small bouquets often gifted in large celebrations which are meant to be used in the preparation of an herbal tea for curing hangovers the next morning. In Ocotlan de Morelos *poleo* can be found being used to adorn baskets and other artifacts for a ceremony called *La Llevada del Guajolote*, and is also gifted to everyone during the festivities. The same plant is also used in a procession before Christmas and New Year's Eve wherein pilgrims known as *roseros* journey to the mountain searching for the plant for use in the day's celebration. In conclusion, the plant *rosa de borracho* has many symbolic uses but are hardly limited to sacredofferings adorning altars in ceremonies and its use in the creation of complex floral arrangements at celebrations, all of which confer much importance on the plant in these Oaxacan communities.

P.0389 Flora of Rio de Janeiro: Protium Burm.f. (Burseraceae)

Silva, Débora C.[1], Sakuragui, Cássia M.[1]

1 Rio de Janeiro Botanical Garden Research Institute, Rio de Janeiro, Brazil.

Protium Burm.f. is the most diverse genus within the Burseraceae family, with approximately 70% of its species in Brazilian territory, primarily in the Amazon region. These species play a crucial role as important arboreal components in tropical forests, being frequently referenced in floristic studies and in the structural analysis of areas in the Amazon and Atlantic Forest. Popularly known as "breu" or "almecegueira", these species are morphologically often confused with other genera of Burseraceae, mainly due to the lack of taxonomic studies in the state of Rio de Janeiro. This study aimed to contribute to the taxonomic knowledge of *Protium* species in the state of Rio de Janeiro. We provided a dichotomous key for species identification, morphological descriptions, botanical illustration plates, distribution maps, and information on the conservation status of these species. The research involved visits to eight herbaria, conducted both in person and virtually, totaling approximately 500 specimens analyzed. Field expeditions covered metropolitan and rural areas of the state. Seven species were recorded for the state of Rio de Janeiro: *Protium brasiliense* (Spreng.) Engl., *P. breviacuminatum* (Swart) Byng & Christenh., *P. glaziovii* Swart., *P. heptaphyllum* (Aubl.) Marchand., *P. icicariba* (DC.) Marchand., *P. warmingianum* Marchand., and *P. widgrenii* Engl. Notable taxonomic contributions specifically include floral characteristics represented in botanical illustrations. Additionally, there was an update on the description of the leaflet margins of *P. glaziovii* and the identification of a new distribution area in the municipality of Rio Claro in Rio de Janeiro. The results of this study are of significant importance for understanding the genus *Protium* in Rio de Janeiro, contributing to a better comprehension of the morphology of these species. Furthermore, this information is valuable for other states that share the same species, such as São Paulo, Minas Gerais, Espírito Santo, and Bahia.

P.0390A look at genus Malachra L.? - Ethnobotany, phytochemistry, and pharmacological activity

Leonor Cervantes-Ceballos [1], Jorge Sánchez-Hoyos [1], Amparo Echeverry-Gómez [1], Harold Gómez-Estrada[1]

1 Grupo de Investigación en Química Orgánica Medicinal, Facultad de Ciencias Farmacéuticas, Campus de Zaragocilla, University of Cartagena, Cartagena, Colombia.

The genus *Malachra* L. belongs to the family Malvaceae and is geographically distributed in tropical and subtropical America, west tropical Africa, and Southwest Asia. It includes herbs or subshrubs of nine accepted species with approximately thirty synonyms, and it has been widely used in community folk medicine to treat health problems including inflammation, nasal obstruction, leishmaniasis, malaria, childbirth, kidney disorders, fever, and respiratory tract disease. This review was conducted using the Preferred Reporting Items for Systematic Review (PRISMA) guidelines for systematic reviews. Organized taxonomy, botanical descriptions, geographical distribution, phytochemistry, ethnobotany, pharmacological, and biological activities of plants belonging to the genus *Malachra* L. Eight species of the genus *Malachra* L. of the family Malvaceae: *Malachra alceifolia* Jacq., *Malachra capitata* (L.) L., *Malachra fasciata* Jacq., *Malachra radiata* (L.) L., *Malachra ruderalis* Gürke., *Malachra rudis* Benth., *Malachra helodes* Mart., *Malachra urens* Poit., and *Malachra urens* Poit. ex Ledeb. & Alderstam. The active phytoconstituents isolated from this genus may be useful for the evaluation and identification of molecular targets against infectious pathogens or inflammatory processes. The presence of groups of metabolites such as flavonoids, sterol-terpenoids, and phenolics, including gallic acid, caffeic acid, quercetin, and β-sitosterol associated with biological processes with activities such as antidiarrheal, antiepileptic, antiulcerogenic, antioxidant, anticonvulsant, hepatoprotective, antiviral, anticancer, antibacterial, and anthelmintic, with inflammatory activity being the most widespread. In turn, the presence of peptides with pharmacological potential contributes to the search for drugs against oncological, metabolic, cardiovascular, and neglected tropical diseases. Therefore, this review contributes to the baseline knowledge for the validation of therapeutic use and conservation of traditional and ancestral knowledge of plant biodiversity in America, Africa, and Asia. It also contributes to the basic concepts for future research aimed at the discovery of new drugs.

P.0391 Uses of Plants in an Indigenous Pijao Community of Natagaima, Tolima, Colombia

Mariano Cortés[1], Carlos A. Mendez[1], Mathusalam Pantevis[2], Diego F. Perez [2].

1 Biología Aplicada, Universidad Surcolombiana, Colombia. 2 Departamento de Psicopedagogía, Universidad Surcolombiana, Colombia.

This study is a commitment to recognize the cultural capital of the Pijao Indigenous Community of Palma Alta based on experiences, knowledge, rituals and ancestral narratives. This study addresses the relationship of the Community with plants (Ethnobotany). To carry out this objective, semi-structured interviews were carried out, surveys and dialogues were carried out that allowed recognizing the traditional knowledge and uses that they gave to the plants, then meetings were held with the boys and girls that allowed them to recognize the worldview they had regarding plant knowledge. It was found that the botanical family with the highest frequency of appearance is Malvaceae with 12% and corn (Zea mays L.) of the Poaceae family, which is an emblematic plant of the community, due to the different uses and traditional knowledge, inherited from generation to generation.

P.0392 Dittrichia spp. ethnobotanical uses in the Mediterranean basin and distribution in the Iberian Peninsula: an updated review

David Cossío-Felipe[1], Luis M. Bedoya[1], Jose A. Guerra[1], Paulina Bermejo[1], Paloma Cantó[1]

1 Department of Pharmacology, Pharmacognosy and Botany, Faculty of Pharmacy, Complutense University of Madrid.

Dittrichia spp. (Asteraceae) comprises two species: *Dittrichia graveolens* (L.) Greuter (syn. *Inula graveolens* (L.) Desf.) and *Dittrichia viscosa* (L.) Greuter (syn. *Inula viscosa* (L.) Aiton). These species grow in nitrophilous areas and anthropogenic areas in the Mediterranean basin, but both species have expanded to other countries such as South Africa, Australia or the USA as invasive species. The purpose of this work is to update the distribution of the genus in the Iberian Peninsula and compile the recorded ethnopharmacological and ethnobotanical uses of both species. To study the genus distribution in the Iberian Peninsula, we consulted *Flora iberica* and analyzed the presence of different specimens in some of the herbaria used there. FloraVeg and GBIF databases were used for the global distribution. For compiling the recorded references regarding ethnobotanical and ethnopharmacological uses, several databases were consulted: PubMed, Scopus, Web of Science and the French Society of Ethnopharmacology. Also, compilations of ethnobotanical uses like the *Spanish Inventory of Traditional Knowledge related to Biodiversity* as well as doctoral thesis concerning ethnobotanical uses were also reviewed. No distinction on the language of the sources was made. We elaborated a map comprising the distribution of the *Dittrichia* genus within the Iberian Peninsula. Regarding the ethnobotanical uses, we managed to find references throughout the Mediterranean basin. *Dittrichia viscosa* has the greatest number of references, especially in Spain, Italy and Morocco; the most extended uses of this species were related to the treatment of wounds and skin diseases, while the most used parts were its leaves. The use of *Dittrichia graveolens* was less spread, with references as an insect repellent or hemostatic among others.

P.0393 Medicines, metabolites, and pigments in the order Caryophyllales

Alex Crum[1], Zack Radford[2], Aaron Lee[1], Lisa Philander[3], Luke Busta[4], Ya Yang[1]

1 Plant & Microbial Biology Department, University of Minnesota - Twin Cities, St. Paul, Minnesota, USA. 2 Department of Biological Sciences, University of South Carolina, Columbia, South Carolina. 3 Como Park Zoo and Conservatory, St. Paul, Minnesota, USA. 4 Department of Chemistry & Biochemistry, University of Minnesota - Duluth, Duluth, Minnesota, USA.

What makes a medicinal plant medicinal? How and why we use the medicinal plants we do has been mostly studied on a case-by-case basis, and larger systemic patterns are murky. By approaching the question of what makes a medicinal plant at multiple scales, we can begin to understand the importance of cultural, biogeographic, and evolutionary factors in determining whether a plant will be selected for use. To explore evolutionary and biogeographic patterns driving medicinal plant use, we use the order Caryophyllales as a model system, which has a unique pattern of tyrosine or- phenylalanine specialized metabolism lineages, represented by the mutually exclusive betalain and anthocyanin pigments. We use this difference in metabolism types to determine whether metabolism or other factors, such as the frequency of interactions with humans across cultures, drive differences in medicinal use across the phylogeny. We found that medicinal use consistently clustered into certain lineages across types of medicinal use, regardless of metabolism type. Instead, apparency, or how noticeable a plant is to humans, is a better predictor of medicinal use. A manuscript summarizing this work is currently in review, and a version is available on Biorxiv (doi:https://doi.org/10.1101/2023.07.22.550123) At the molecular scale, we use biotic and abiotic stresses to induce tyrosine and phenylalanine specialized metabolism and explore differences in gene expression and metabolite production between two medicinal species, *Beta vulgaris* (tyrosine-dominant) and *Silene latifolia* (phenylalanine-dominant). We found different responses to different stressors, suggesting that biotic and abiotic factors likely contributed to tyrosine and phenylalanine specialized metabolism.

P.0394 An approach to the traditional knowledge of wild plants in El Campo de Agadones, Salamanca (Spain)

Luis Delgado Sánchez [1], María Vera Jiménez [1 2], Luz M. Muñoz Centeno [1]

1 Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain. 2 National University of Asunción, San Lorenzo, Paraguay.

For centuries man has maintained a very close relationship with nature using plants for different uses (food, medicinal, industrial, social…). However, in today's western society there have been profound changes in life systems that have isolated us from the natural environment, resulting in a significant loss of cultural biodiversity. In this context, an ethnobotanical study has been carried out in El Campo de Agadones (Salamanca, Spain), one of the most depopulated regions of this province (3.2 inhabitants/km2). This territory is part of the Las Batuecas-Sierra de Francia Natural Park and the El Rebollar Natural Area. Forty-five people were interviewed and reported 146 species in 56 families. The most represented families were Compositae (15 species), Labiatae (11) and Leguminosae (10). Thirteen categories of use were identified, the most represented being "Medicine" (26.7%), "Human food" (22.2%) and "Industry and handicrafts" (17.2%). The traditional knowledge of medicinal plants is remarkable since 68 species are used to treat various ailments. Most of the medicinal uses are intended to treat problems of the skin, digestive, respiratory and circulatory systems, as well as the sense organs. The most cited medicinal species were *Chamaemelum nobile* (L.) All., *Chelidonium majus* L. and *Verbascum pulverulentum* Vill. The species with the most medicinal uses were *Chamaemelum nobile*, *Hypericum perforatum* L., *Malva sylvestris* L., *Mentha pulegium* L. and *Thymus zygis* Loefl. ex L. However, the most cited species are not related to medicine but to veterinary medicine. These are *Daphne gnidium* L. and *Cistus ladanifer* L., (IC = 0.82; 0.8, respectively). In addition, popular sayings, myths and beliefs that are part of the culture of this territory were collected. It is important to rescue, conserve and promote traditional knowledge related to natural resources, since the union of scientific and traditional knowledge can help in the resolution of current problems.

P.0395 Diversity and threat status of medicinal plants in Korea district of Chhattisgarh (India)

Veenapani Dubey[1]

1 Life Science, University, Bilaspur, India.

Indian biodiversity is under serious threat. Global change has also affected India and as a consequence the biodiversity is depleting. Chhattisgarh, the 26th state of India has ample variation in physical and cultural features. The State has about 44% of its geographical area covered with forests. It enjoys a hot and humid climate. It gains rainfall from both north-east and south-west monsoon. It has about 30 small and big drainage systems. These features have an important contribution to its biological wealth. Korea district in Chhattisgarh has an average rainfall of 121.36 cm. It has a forest area of 81.23%. Annual mean temperature is 24°C with a range of variation from 16.2° to 31.8°. The district is dominated by upper Gondwana rocks which are rich in deposition of coal. The highest hill ranges occupy the northern part of Devgarh, Sonhat and Manendragarh. The district has very rich plant diversity specially the medicinal plants which are not comprehensively described. Viewing these points the present investigation was done. Present paper deals with the general diversity index and the status of threat to the medicinally important plant species of Korea. Out of 200 genera assessed 3 were found to be EW; 14- CE; 27-EN; 62-VU; 37-NT and 57 were LC.

P.0396 Indigenous knowledge on plants of Dawei district in Myanmar

Sangmi Eum[1], Thet Thet Mar Win[2], Swe Swe Aye[3], Chang Young Lee[1], Sangho Choi[1]

1 Korea Research Institute of Bioscience & Biotechnology, International Biological Material Research Center, Daejeon, Korea. 2 Department of Botany, Yangon University Yangon, Myanmar. 3 Agricultural Science Department of Taungoo University, Bago Region, Myanmar.

Biological resources have played crucial roles in mankind for centuries, especially plant species have consumed by indigenous people and ethnic groups for various daily purposes. Myanmar is one of global importance for biodiversity in the world possessing 11, 800 of vascular plant species due to the diverse landscapes and climate conditions. With 135 officially recognized ethnic groups in Myanmar, they have used the plants for various purposes such as medicines and food resources. However, only handful ethnobotanical surveys have been conducted to date. This study explores useful medicinal plants in Dawei District, southern Myanmar and documenting the traditional knowledge held by indigenous people. This research involved interviewing 89 of the ethnic group in Dawei District (M: 42, F: 47) and recording the first comprehensive documentation of their traditional medicinal plant knowledge. A total of 67 medicinal plants were reported which belong to 63 genera across 38 families, with 1332 of use reports (UR). The high number of UR for these 67 species showed that indigenous medicinal plants are still commonly used in this area for basic treatment and the richness of ethno-medicinal knowledge of the ethnic group in Dawei. A range of the Informant Consensus Factor (ICF) was between 0.833 to 1 and the highest category was related to Blood, Blood forming organs and Immune mechanism. To the best our knowledge, a potential property of *Acmella* paniculata in promoting milk production during lactation was documented in this study for the first time. Results obtained in this study revealed the significant value of medicinal plants to the indigenous people in Dawei, but further research is needed to validate and confirm their medicinal properties.

P.0397 Therapeutic plants in Freetown, Sierra Leone: an ethnopharmacological study

Adepoju O. Adeyinka[1], Femi-Adepoju G. Abiola[2], Tarawally Marian[3], Karim Abdul[3]

1 Research Institute for Innovations; African Methodist Episcopal University, Monrovia, Liberia. 2 College of Science and Allied Health, African Methodist Episcopal University, Monrovia, Liberia. 3 Department of Biological Sciences, University of Sierra Leone, Freetown, Sierra Leone.

According to literature, the use of herbal medicinal products has greatly increased over the years, with only about 75% of people worldwide still depending on some of their primary health care services. Safety, lack of enough information and improper monitoring among others remain important issues with the use of herbal medicines and the impact of their harvest on the environment. Twenty respondents who regularly practice and deal with traditional herbal medicine provided information on the constituents which make up the recipes of their products, the sources of raw material, and types of health conditions treated with the plants. A total of 92 species of medicinal plants from 41 flowering families have been used by traditional herbalists to produce herbal medicines that are indicated for the treatment of 10 different medical conditions. The most cited species out of 92 mentioned, was *Newbouldia laevis*, while the most cited family of medicinal plants was Fabaceae which had the highest value of family importance (75%). Diseases with the highest number of medicinal plant treatments included malaria, gonorrhea, dysentery and toothache. The findings of this study indicate use of herbs in the treatment of some common diseases and as promising potentials for drug discovery from the study area. Even though the raw materials are readily available, peculiarity of preparation methods are based on the types of diseases to be treated per time. Currently, there is no formal procedures of training the Traditional Herbal Medicine Practitioners in the country.

P.0398 Organization and first evaluation of the Endangered Plant Specialist Group of the mountains north of the Orinoco River, Venezuela

Ángel Fernández del Valle[1], Santos Miguel Niño[1,2], Daniela Saraí Canelón Barráez[1,2], Julián Mostacero Giannangeli[1,3]

1 Instituto Venezolano de Investigaciones Científicas, Altos de Pipe, Venezuela. 2 Universidad Nacional Experimental de los Llanos Ezequiel Zamora, Guanare, Venezuela. 3 Instituto Experimental Jardín Botánico Dr. Tobías Lasser, Caracas, Venezuela.

The flora of tropical mountain ecosystems makes up one of the most threatened biological resources on the planet, one of the most diverse and also one of those that provides the most environmental services to humanity. The mountains of Venezuela north of the Orinoco River are among these ecosystems and, in general, all their environments are strongly threatened, both by anthropogenic activity and by the effects of climate change. The area includes the Sierras de los Andes, Perijá, de la Costa, Turimiquire, Paria and the Lara-Falcón Hill System, between 400-4,990 meters above sea level, with an area of approx. of 165,000 km². Using data from the Red Book of the Venezuelan Flora (2020), the existence of 334 threatened tracheophyte species and one extinct in the area we studied was determined. We have formed a technical team (31 members so far, affiliated with universities, research institutes, government offices and herbaria) to be presented as a Specialist Group to the IUCN Species Survival Commission. In addition, a preliminary list of more than 600 species to be evaluated has been prepared and which were placed in the second version of the Red Book of Venezuelan Flora in the categories of non-threatened, with little population information, or not evaluated. The group is open to the incorporation of new members.

P.0399 BE ETHNO: Peru, the target community for an urban ethnobotanical survey

Martina Bottoni[1,2], Fabrizia Milani[1,2], Claudia Giuliani[1,2], Gelsomina Fico[1,2]

1 Department of Pharmaceutical Sciences, University of Milan, Milan, Italy. 2 Ghirardi Botanic Garden, Department of Pharmaceutical Sciences, University of Milan, Toscolano Maderno, Brescia, Italy.

Within the framework of the three-year project "BE ETHNO: sharing traditions, sharing plants, sharing place, sharing future" (2024-2027, ID:2023-1454), founded by Cariplo Foundation, an urban ethnobotanical survey, aimed at documenting the traditional uses of plants by a selected immigrant community in Italy, was planned. The survey will take place both in a pluricultural context in Lombardy (Northern Italy) and in the country of origin, thus evaluating the cultural permeation of the traditional knowledge between the two countries. Which folk heritage to select? Consulting of the Annual Reports on the Presence of Migrants of the Italian Ministry of Labour and Social Policy, as well as the Regional Observatory for Integration and Multi-ethnicity of the Lombardy Region (2021-2022), led towards the Peruvian culture, one of the largest and most integrated community in Italy. Lombardy is the first region for number of foreign residents, hosting a total of 26.1% of non-EU citizens, including Egyptians (67.6%), Ecuadorians (47.0%), and Peruvians (44.4%). These statistics are also supported by a lacking literature about Italian urban ethnobotanical investigations documenting the traditional uses of plants by the Peruvian community. Thus, first contacts were established in Italy with Italian and Peruvian associations and academic realities, involving experts in pre-Columbian civilizations, anthropologists, and linguistic mediators. Spanish language courses were planned with the Linguistic Centre of the University of Milan, a key element to foster empathy between the research group and the Peruvian informants. Finally, thanks to the close friendship between the PI and a potential Peruvian cultural mediator, the field ethnobotanical investigation in Peru was designed in Cusco, where the mediator's family still lives and preserves traditional uses of plant species. This way, first contacts with the natives were set up with the aim of meeting local *curanderos*, as well as planning naturalistic itineraries to record the autochthonous flora.

P.0400 Passiflora setacea DC. leaves: histochemical identification of phenolic compounds and ultrasound pretreatment

Mariane B. R. de Ávila[1], Rosana G. R. das Dôres[2], Naiara C. Zotti-Sperotto[1], Evandro de C. Melo[1], Analu Zanotti[1], Renata M. S. A. Meira[1], Luan B. Giovanelli[3], Raiane A. de Souza[1], Maira C. M. Fonseca[1]

1 Federal University of Viçosa, Viçosa-MG, Brazil. 2 Federal University of Ouro Preto, Ouro Preto-MG, Brazil. 3 Federal University of Jequitinhonha and Mucuri Valleys, Teófilo Otoni-MG, Brazil.

The genus *Passiflora* has been long employed in the medicine as sedative, antidepressant and anxiolytic. Therapeutic properties have been exhibited by fruits and leaves of passiflora plants genus, however, its pharmacological effects are most attributed to the leaves. *Passiflora setacea* DC., popularly known as "pérola do cerrado", is a new cultivar that has characteristics of great interest in the food and pharmaceutical industry due to its nutritional richness and high concentration of phenolic compounds. The present study aimed to conduct a histochemical study about the secretory structures in *P. setacea* as well to verify if the yield of phenolic compounds in leaves submitted to ultrasound pretreatment are afected. Samples from two sizes (7 cm and 10 cm) were subjected to anatomical and histochemical analyses. The leaves are dorsiventral, and the bundles are collateral and the total phenolic compounds being evidenced by ferrous sulfate in the form of blackened inclusions. In the central vein, subepidermal collenchyma occurs on both the adaxial and abaxial sides. In the cuttings from the fresh samples, massive idioblasts dispersed by the cortical parenchyma were observed in the central vein, both on the adaxial side and on the abaxial surface of the leaves in developing and on the completely developed leaves. Our results show that the ultrasound treatment did not cause the loss of the phenolic compounds yield in the evaluated samples but disorganization of the vascular bundle was observed. Cellular disorganization possibly occurred due to the effect of consecutive cell-to-cell compressions and expansions caused by ultrasound ("sponge effect"), which, together with the simultaneous impact of cavitations, caused cell disorder.

We conclude that have preservation of phenolic compounds and that the ultrasound processing reduces its extraction time of this medicinal compounds without interfere in the yield of these compounds in the vegetal tissue.

Acknowledgement: FAPEMIG, CNPq and CAPES for their financial support.

P.0401 Varronia curassavica Jacq.: characterization of secretory structures and essential oil yield in leaves submitted to ultrasound treatment

Naiara C. Zotti-Sperottoa[1], Evandro de C. Melo1, Michelle I.L. de Souza[1], Maira C. M. Fonseca[1], Diego A. Gonzaga[1], Mariane B. R. de Ávila[1], Antônio J. Demuner[1], Marília C. Ventrella[1], Ana C.V. Lelis[1]

1 Federal University of Viçosa, Viçosa/MG, Brazil.

Varronia curassavica is a native species from Brazil, popularly known as "erva-baleeira" and its essential oil has anti-inflammatory action. This medicinal species is promising raw materials for the development of herbal medicines. However, aiming at the continuous supply of vegetable raw material of phytochemical quality it is necessary the appropriate choice of cultivation and drying conditions to optimize the quality of the final product. This study aimed to verify the influence of the ultrasonic pretreatment combined with the drying using a heat pump, on the secretory structures, drying time and yield of essential oil of *V. curassavica*. The leaves of *V. curassavica* derived from the organic system cultivation at the Experimental Field of the Piranga Valley (20° 25′ 49″ S; 42° 48′ 20″ W). Fresh leaves were fixed in FAA50 solution (37 % formaldehyde, glacial acetic acid and 50 % ethyl alcohol) for 24 h and stored in 70 % ethanol. The leaves were cross-sectioned on a tabletop microtome and the following histochemical reactions were performed: Astra Blue and Safranin identify phenolic compounds and Sudan III for lipids (essential oils). The leaves of showed glandular trichomes on both leaf surfaces, with higher density on the abaxial surface. Besides, the glandular trichomes are above the level of the leaves' epidermal cells. Glandular trichomes are responsible for secreting, mainly, essential oils and the mesophyll also contained essential oil. The action of acoustic cavitation and the sponge effect, which resulted in reduced drying time, did not damage the glandular trichomes of *V. curassavica* and increase the essential oil yield when compared to the control. We concluded that the mechanical effects of ultrasonic waves can enhance the extraction process of essential oils, increasing the penetration of the solvent in the cellular material and facilitating the release of the cells content. Acknowledgement: FAPEMIG, CNPq and CAPES for their financial support

P.0402 Description of the use of medicinal plants traded in marketplaces in the Comunera province of Santander (Colombia).

Galvis R. Manuel[1]

1 Facultad de Ciencias de la Educación, Jardín Botánico Boyacá, Tunja Colombia.

This study describes the traditional use of more than 425 species of plants among 115 families, identifying the plant drug, its preparation and administration, the traditional medicinal purposes for which it is recommended and possible practices of inappropriate use. For methodology, 56 semi-structured interviews were applied to plant sellers in 8 marketplaces of Andean towns as follows: Socorro, Gambita, Guadalupe, Confines, Oiba, Simacota, Palmas del Socorro and Suaita. Taxonomic identification was carried out using virtual herbariums of the National University and taxonomist experts, the most reported by the vendors, who are women of legal age, were compiled and analysed, and their traditional use was compared with the pharmacological indications reported in the Colombian Vademecum of Medicinal Plants. The results showed that the most frequently cited plants among the vendors interviewed were: citron (Aloysia triphylla), calendula (Calendula officinalis) and chamomile (Matricaria chamomilla), followed by horsetail (Equisetum bogotense), rue (Ruta graveolens), basil (Ocimum basilicum), French oregano (Plectranthus amboinicus), guascas (Galinsoga parviflora), totumo (Crescentia cujete), gualanday (Jacaranda caucana) and culantro, apio sabanero (Eryngium foetidum) which had at least three reports each. It was found that some of the plants mentioned by vendors are not reported in the Colombian Vademecum of Medicinal Plants, including paico (Dysphania ambrosioides), yerba del cáncer (Petiveria alliacea), nettle and Pringamosa. Little knowledge was detected on the part of sellers about the possible contraindications or toxic effects of medicinal plants, which leads to inadequate practices. There was also a lack of knowledge of the differences between infusion and decoction preparations and the preservation of tinctures and alcoholic beverages. Medicinal plants were identified that could be therapeutically promising for new uses of medicine that has been validated for generations in the Santander peasant family heritage.

Note: This abstract was translated with AI.

P.0403 Ethnomedicinal and enhanced antifungal approach on major Lamiacean species used by the indigenous tribes of Wayanad, Kerala, India

Aswathi Ganga[1], Sunojkumar P.[1]

1 Department of Botany, University of Calicut, Tenhipalam, India.

Plants have been an integral part of traditional medicine across culture. They not only contribute to healthcare but also connect communities through shared knowledge and practices, emphasizing a vital relationship between plants, their medicinal benefits, and societal well-being. Lamiaceae, the mint family, epitomizes botanical versatility, offering a spectrum of applications from the culinary domain to various medicinal uses. Therefore, making them an indispensable group of plants within tribal communities. The tribal population in India, though numerically a small minority, represents an enormous diversity of groups, each with its own unique cultural heritage and traditions. The state Kerala, in this regard, holds a distinctive position on the tribal map of India. The present study aims to document the traditional knowledge of medicinal plants within the Lamiaceae family, which are utilized by the indigenous tribes—Kurichiyas, Kattunaikas, Kurumas, and Paniyas—residing in various pockets of the Wayanad district in Kerala. The ethnomedicinal aspects along with the enhanced antifungal activity of selected plant species using zinc oxide nanoparticles are evaluated. Furthermore, integrating this traditional knowledge with modern green nanotechnology for the findings could potentially pave the way for the development of more effective and environmentally sustainable antifungal treatments, benefiting both their healthcare and lifestyle. Thus, collecting knowledge about the richness of plant diversity in any area and understanding the extent of dependence of indigenous communities on that plant wealth not only stimulates innovation, but also emphasizes the crucial need to conserve both traditional knowledge and ecosystems for sustainable development.

P.0404 Traditional uses of plants in Tierra de Alba and Aliste (Zamora)

Claudia García Hernández[1]

1 Department of Botany, Universidad Complutense de Madrid, Madrid, Spain.

An ethnobotanical prospection has been carried out in the Tierra de Alba and Aliste regions (Zamora). The information collected includes the traditional uses and vernacular names of 88 vascular plant taxa. The objectives of the study are to study traditional knowledge, quantify the uses prevalence, and check if the uses collected are documented in the literature. 271 use-reports (UR) have been catalogued. The most important families are Lamiaceae with 44 UR and Asteraceae with 26 UR. One of the most commonly used species is Cistus ladanifer L. (9 UR), and the most cited uses are medicinal (87 UR) and food-use (66 UR). Regarding the uses prevalence, of the 57 species valued, 25 have been abandoned in all their uses. In the bibliographic comparison, have been found six records of novel use.

P.0405 Ethnobotanical survey on plants used to manage skin illnesses in communities of the department of Bolivar, Colombia

Jorge Sánchez-Hoyos[1], María Quintana-Torres[1], Erick Torres-Niño[1], Fredys Sánchez-Hoyos[1], Leonor Cervantes-Ceballos[1], Amparo Echeverry-Gómez[1], Harold Gómez-Estrada[1].

1 Grupo de Investigación en Química Orgánica Medicinal, Facultad de Ciencias Farmacéuticas, Campus de Zaragocilla, University of Cartagena, Cartagena, Colombia.

The healing practices of traditional and medicinal use of plants as a form of alternative and complementary healing have been used by communities to alleviate their health problems. Through an ethnopharmacological survey conducted among inhabitants over 40 years of age in 5 municipalities in the northern department of Bolivar (Colombia) using a closed survey format applying the TRAMIL methodology and informed consent, 523 people were surveyed and 1246 reports of medicinal plant uses were obtained. 10 plant species identified with herbal records for different skin problems with a Reporting Index (RI) greater than or equal to 20% were described: Aloe (*Aloe vera* (L.) Burm.f.), almond (*Terminalia catappa* L.), malva (*Malachra alceifolia* Jacq.), matarraton (*Gliricidia sepium* Jacq.) Kunth ex Walp), curarina (*Aristolochia anguicida* Jacq.), guasimo (*Guazuma ulmifolia* Lam.), achote (*Bixa orellana* L.), balsamina (*Momordica charantia* L.), anamu (*Petiveria alliacea* L.), and matandrea (*Alpinia purpurata* (Vieill.) K. Schum.). The family with the highest report of these species was Malvaceae, the most used part by the surveyed inhabitants was the leaf (70%), the form of preparation in remedy was poultice (62%), and the most common route of administration was topical (60%). The most common route of administration was topical (60%). 70% of the respondents have ever used these plant resources for health problems related to the skin. Skin conditions are one of the 5 problems of great interest for the communities of the northern region of Colombia. This study contributes to safeguarding ancestral and traditional knowledge of the use of medicinal plants associated with skin problems and the conservation of natural resources.

P.0406 Ethnobotany and cultivated biodiversity in Ibiza island (Balearic Islands)

Raquel González[1], Joan Vallès[1,2], Teresa Garnatje[3,4],

1 Laboratori de Botànica (UB) – Unitat associada al CSIC, Facultat de Farmàcia i Ciències de l'Alimentacio, Universitat de Barcelona, Barcelona, Spain. 2 Institut d'Estudis Catalans, Barcelona, Spain. 3 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 4 Jardí Botànic Marimurtra-Fundació Carl Faust, Blanes, Spain.

Eivissa/Ibiza, which is part of the Catalan linguistic area, is the largest of the Pityusic and the second in the Balearic Islands in terms of population. Renowned as a popular tourist destination, the tourism industry holds a pivotal role in the economic sustenance of the local population. Despite this, there is a strong relationship between people and plants on the island. The knowledge that the local society still holds regarding the names, uses, and management of plant biodiversity has been studied in this work, including information on landraces and agroecosystems through different approaches. Firstly, an extensive ethnobotanical study was conducted, representing the first of its kind on the island. This involved interviews with 101 informants, who provided information on names and uses of 251 plant taxa at specific and infraespecific levels, belonging to 71 botanical families. Concerning uses, 76 plan taxa have been reported as medicinal, 157 as food, and 107 with other uses. Secondly, focusing on cultivated plants, particularly landraces within traditional family gardens in Ibiza, information was provided by 68 informants. In this study, 99 species belonging to 33 families, comprising 204 local races, were reported. *Vitis vinifera* L., cited in nearly 9% of reports, is the most mentioned cultivated plant, thus we particularly studied it. Thirdly, genome size was estimated through flow cytometry- the first investigation in Pityusic, Balearic, and Spanish material of the species - in Ibiza and Formentera vineyard accessions, revealing a certain degree of intraespecific variability, but no interisland differentiation. Finally, we characterize Pityusic vine accessions through ethnobotanical surveys, followed by ampelographic and genetic (microsatellites) approaches, establishing synonymies and homonymies among races identifying some previously undescribed ones. With this work, Ibiza's ethnobotany finds its place among deeply studied subject worldwide, notably delving into the characterization of one of its most emblematic plants, the vine.

P.0407 Green health and Maya Q'eqchi' phytotherapy in Guatemala: plant diversity and their therapeutic uses through evidence-based ethnobotany research

Ana Isabel García-Ambrosy[1], Rafael Grajeda-Estrada[5], Francesca Scotti[2], Michael Heinrich[2], Caroline Maake[3], María Renée Álvarez-Ruano[1], José Joaquín Ché[4], Pablo Ax[4], Mónica Berger-González[1]

1 Centro de Estudios en Salud, Universidad del Valle de Guatemala, Guatemala. 2 UCL School of Pharmacy, University College London, UK. 3 Institute of Anatomy, University of Zurich, Switzerland. 4 Council of Q'eqchi' Maya Elders Releb'aal Saq'e', Petén, Guatemala. 5 Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Mexico.

Maya Q'eqchi' phytotherapy is part of the biocultural diversity in Guatemala and in the traditional healthcare services given by Ajilonel (traditional healers and herbalists). They co-exist with the national healthcare system, as a primary healthcare service in marginalized and secluded indigenous communities. These traditional practices encompass ancestral knowledge in the use of plants and treatments where the resources are obtained primarily near forests and orchards. These practices are threatened by biodiversity loss, land use change, access to forests, and loss of interest in traditional knowledge. Therefore, the Green Health Project aimed to propose a framework of access and benefit-sharing from the Convention on Biodiversity (CBD). This included ethnographic and ethnobotanical research on Maya Q'eqchi' phytotherapy, conducted by a transdisciplinary approach, with the collective participation of the Q'eqchi' Council ACGERS, Universidad del Valle de Guatemala, UCL School of Pharmacy, University of Zürich, public and private sectors. Fifteen Ajilonel from Guatemala participated by documenting 764 patient treatments in Epicultural Booklets for case registration from 2019 to 2021. A list of medicinal plants was obtained and later collected for taxonomic determination. A total of 251 specimens were sampled, 132 morphospecies determined in 92 genera and 51 families. Over 66% of the plants are located in isolated forest patches in the region. Using the International Classification of Primary Care (ICPC-3) a total of 130 physical/psychological categories were listed, and a 36-category classification was created for the energetic/spiritual ailments in their epistemology. The digestive system (17%) and Malhecho (3%) ailments, respectively, were the most mentioned overall. The Ajilonel selected 52 prioritized plant species, where *Drymonia serrulata*, *Petiveria alliacea* and *Anthurium pentaphyllum* had higher Cultural Importance and Relative Importance indexes. This project brings another scope into ethnobotanical research to foster evidence-based methodologies to help shape new insights into conservation, policies, and research.

P.0408 Plants used at the Guancasco ceremony in San Francisco de Opalaca, Honduras.

Eydi Yanina Guerrero-Medina[1]

1 Department of Biology, National Autonomous University of Honduras, Honduras.

Societies maintain collective memories, including experiences that are part of the oral tradition of people, such as rituals, legends, fables, stories, anecdotes, songs, myths, sayings and ceremonies. In this research, the "Guancasco" ritual forms the intangible heritage of the people that, due to generational circumstances, is deposited in adults that takes root throughout their lives and is transmitted orally to the next generation. The present project arises with the purpose of knowing the plants that are used and have been used in the ritual that has survived in the indigenous peoples called "Guancasco", which has been celebrated for more than 500 years, in this case we will analyze what It takes place in the community of San Francisco de Opalaca, a Lenca village located in the department of Intibucá, in western Honduras. The Guancasco is a ritual of peace among indigenous peoples, at the same time it serves as a cultural and mythological expression that transmits knowledge and teaches the importance of subsistence. Rescuing and preserving valuable ancestral knowledge linked to the use of plants in rituals such as the Guancasco in Opalaca is a crucial task. A deep knowledge of the plant species used in these ritual practices is sought, analyzing whether they are in any risk category, and then proposing concrete actions that favor their conservation. In this context, by highlighting the exceptional botanical wealth present in the region, recognizing the cultural, medicinal and ecological importance of these plants, the awareness of the population is achieved, which must acquire a fundamental role, since it seeks to create a wake up about the urgent need to conserve medicinal plants and preserve the unique biodiversity that the region has.

P.0409 Evaluation of antioxidant and analgesic activities of tubers of some species of Brachystelma

Varsha Jadhav[1], Seema More[1]

1 Department of Botany, Shivaji University, Kolhapur, India.

The Asclepiadaceae family includes the genus Brachystelma, a small under ground potato like tuber. Edible and nutrient-rich tubers and leaves are utilized in traditional medicine to relieve pain. This study's primary goal was to look into the analgesic and antioxidant properties of the tubers of three species: *Brachystelma malwanense, Brachystelma naorojii,* and *Brachystelma edule*. The acetic acid-induced writhing method was used to test the analgesic activity in mice. The antioxidant potential was assessed by a range of methods like 1,1-diphenyl-2 pricrylhydrazyl, FRAP, Ferrous ion chelating, Reducing power assay, Polyphenol, Caretonoids and Ascorbic acid. The aqueous extract of tuber of *B. naorojii* at the 500 mg/kg dose level exhibited significant activity than the others. No behavioral abnormality and mortality was seen in the rats of tubers crude medication in all selected plants. In antioxidant evaluation the carotenoid contents (0.73 ± P.57 mg/100 g) and ferrous ion chelating activity (58.25 ± 0.54 % inhibition) higher in tuber of *B. edule.* Polyphenols (52.6 ± 1.039 mg/100 g), FRAP (0.492 ± P.14 mg AAE/100 g) and Peroxidase (P.13± P.00 ΔOD min.) activities were rich in tuber of *B. naorojii.* Ascorbic acid (80.92 ± P.00 mg/100 g), DPPH scavenging activity (88.32 ± 0.56 % inhibition), Superoxide dismutase (P.04 ± P.00 ΔOD min. -1 mg-1), Catalase (0.162 ± P.02 ΔOD min.) and total antioxidant activities (0.650 ± P.01 mg AAE/100 g) more in tubers of *B. malvanensis.* The notable antioxidant properties exhibited by Brachystelma tubers may be ascribed to their polyphenol concentration and additional phytochemical components. The results of the study validated the traditional usage of the plant for pain relief by indicating that the tuber extract had potent analgesic and antioxidant properties, which may be related to its polyphenol concentration.

P.0410 Phytochemical analysis studies from Cissampelos pareira L.

Sanjay R. Biradar[1], Sarika V. Lokhande[1], Navnath Kashid[2]

1 Department of Botany, B.S.S.A.S.C. College, Makni, India. 2 Department of Botany, Baburaoji Adaskar College Kaij, Dist. Beed (MS), India.

Cissampelos pareira L. belongs to the Menispermaceae family and is a sub-erect or climbing herb, known as Laghupatha in Indian traditional medicine. It has great demand in ayurvedic medicine and is used as anti-cancer, anti-diarrhea, antifertility antihelmintic, antihyperglycemic anti-inflammatory, anti-protozoa, anti-ulcer, anti-viral, hepatoprotective, cardioprotective and immunomodulatory activities. The present work investigated an efficient method for extracting various phytochemicals from *Cissampelos pareira* by using methanol as a solvent. Various extraction methods were used like static extraction, continuous shaking extraction, and ultrasonic extraction to enhance the yield of phytochemicals. The quantification was carried out using a spectrophotometer-based assay. The findings reported that the percentage extraction of alkaloid, phenol, flavonoid, saponin, tannin, and carbohydrate was found higher in the static extraction method. Three-time intervals were optimized for static extraction, continuous shaking extraction, and ultrasonic extraction. It was noticed that the 24 h extraction reported the maximum recovery of the alkaloid (25.46 mg/g), phenol (17.23 mg/g), flavonoid (50.66mg/g), saponin (54.83mg/g), tannin (0.796/g), and carbohydrate (96.20mg/g).

P.0411 Environmental impact on the production of alkaloids in Ocimum sanctum L. and Adhatoda vasica Nees. as influenced by seasonal variation

Satishkumar M Khadia[1], Vishal P Patil[2], Piyush M Dangi[3], Zankhana N Rathod[4]

1 Department of Botany, Bhavan's Sheth R A College of Science, Gujarat University, Ahmedabad, India. 2 Centre for Atmospheric & Oceanic Sciences, Indian

Institute of Sciences, Bangalore, Karnataka, India. 3 Department of Environmental Science & Technology, ISTAR, V. V. Nagar, Gujarat, India. 4 Department of Botany, M G Science Institute, Gujarat University, Ahmedabad, Gujarat, India.

Ocimum, commonly known as Tulsi, is a huge genus within family *Lamiaceae*, comprising about 64 species of annual to perennial aromatic medicinal herbs with a long history of traditional uses. The aromatic plants of the genus *Ocimum* have long been used as flavouring agents, as well as diverse medicinal applications. Adhatoda vasica Nees is a shrub widespread throughout the tropical regions of southeast Asia. It possesses a wide spectrum of medicinal properties including positive effects on inflammatory diseases. The major chemical classes within the genus *Ocimum* include flavonoids, phenolic acids and terpenes. The bioactivities of various extracts or individual compounds, both in vitro and in vivo, include antimicrobial, cytotoxic, antinociceptive, anti-inflammatory, antihyperglycemic and antioxidant. Some of these herbs are consumed regularly by us. *Ocimum sanctum* L. (Tulsi) of family *Labiaceae* and *Adhatoda vasica* Nees. (Ardusi) of the family *Acanthaceae* are commonly used to control cough and cold. Alkaloid constituents are the photoactive components of these plants. The present study focuses on the investigation of the alkaloid contents of these important medicinal plants harvested in different seasons. It was observed that among the two varieties of Tulsi (Black and White) the white tulsi showed more active component accumulation during the winter season whereas notable variation was not recorded in Ardusi. The contents of the alkaloids were influenced by the environment.

P.0412 Ethnobotanical knowledge of some indigenous medicinal plants used by traditional healers (Vaidus) in Nandurbar district of Maharash

Swapnil M. Khare[1]

1 Department of Botany, ACS College Dharangaon, Maharashtra, India.

An ethnobotanic survey was undertaken to collect information from "Vaidu" or tribal traditional healers on use of native and indigenous medicinal plants during June 2019 to June 2020 in the Nandurbar district of Maharashtra state, India. The indigenous ethnobotanic knowledge and information related to native plants used for medicinal purposes were collected through direct personal interview of local traditional healers during field visits. Our study revealed that 51 species belonging to 48 genera and 34 families are used by these "vaidu" to treat various common diseases. The documented medicinal plants are mostly used to treat cough, dysentery, jaundice, abdominal pain, malaria, omitting and snake bite. In this study the most dominant family use was to be *Menispermaceae* and stem bark is the plant part most commonly used for treatment of diseases. The study showed that till today many tribal people of Nandurbar district are dependent on medicinal plants of native forest for treatment of various diseases. However, this traditional ethnobotanic knowledge is in danger of disappearance as these local healers are not passing their knowledge to next generation and young educated generation is also not interested to carry forward this traditional knowledge.

P.0413 'Sacred Plants': an ancient plant conservation practice

Swapnil M. Khare[1]

1 Department of Botany, ACS College Dharangaon, Maharashtra, India.

If we look at the history of Indian culture, we realize that many important plants have been given a prominent place in it. While studying Ayurveda, ancient scriptures, Upanishads, we see the mention of many trees like wad, pimpal, mango, tulsa, we get to study their importance in human life. In this study it is also noticed that the importance of these trees is only in a particular religion, but not also. In the scriptures and customs of almost all the religions found in India or living in the Indian subcontinent, the importance of these trees is highlighted in one way or another. Like tulsi, wad, pimpal, coconut, banana in Hinduism, sabja, rose in Muslim religion, bark, pimpal, mango in Buddhism and rajnigandha in Parsi religion.... And when this study approaches the tribal life, the entire tribal culture is based on this forest resource is observed. In the present research, the same has been studied.

P.0414 From seeds to skulls: assessing the bioactivity of a Medici archive recipe

Peyton Weiner[1], Emma Siegfried[1], Dr. Kyra N. Krakos[1,2], Ashley Buchanan[3]

1 Maryville University, Saint Louis, USA. 2 Missouri Botanical Garden, Saint Louis, USA. 3 Folger Institute, Folger Shakespeare Library, Washington DC, USA.

This is a historical ethnobotanical study focusing on the use of *Paeonia officinalis* and human skull to treat illness such as fevers and infant convulsions found in a recipe written by Anna Maria Luisa de' Medici (1667-1716). The translated document contains a "recipe" for this medicine which includes one ounce of peony root and seed, two ounces of human skull from an individual who died violently, but was not buried, two ounces of red and white coral, and one ounce of amber. This recipe was frequently sought after, and the active ingredients in the recipe are likely the albiflorin and paeoniflorin in the peony roots and seeds. Specifically, this study focuses on the role of bone in the preservation of the bioactivity of the albiflorin and paeoniflorin in the roots and seeds of *Paeonia officinalis* as the medicine traveled throughout Europe. This research is part of a collaboration between the Medici Archives, Maryville University, and the Missouri Botanical Gardens.

P.0415 Ethnobotany of species of the Cyperaceae family in Paraguay

Ever J. López Grau[1,3], Yenny González[1], María Fátima Mereles H.[2], Rosa Degen[2], Mirtha González[1], Sara Núñez Meza[1], Pablo García Murillo[3]

1 Departamento de Botánica, Facultad de Ciencias Químicas, Universidad Nacional de Asunción, Asunció, Paraguay. 2 Herbario FCQ, Departamento de Botánica, Facultad de Ciencias Químicas, Universidad Nacional de Asunción y Programa Nacional de Incentivo a Investigadores, PRONII, Consejo Nacional de Ciencia y Tecnología, CONACYT, Paraguay. 3 Departamento de Biología Vegetal, Facultad de Farmacia, Universidad de Sevilla, Sevilla, Spain.

Paraguay is, together with Uruguay, one of the smallest countries in South America. Between 15 and 18% of its territory is directly linked to water and about 30% indirectly, during periods of high water. One of the botanical families always present in wetlands of the country is Cyperaceae, one of the four most important in quantity. At the American level, it is one of the least known taxonomically due to the few existing studies, except in Argentina. In Paraguay the most numerous species correspond to the genera *Cyperus* L., *Rhynchospora* Vahl, and *Eleocharis* R.Br. The objective of this research was to demonstrate the uses corresponding to some species of the family. For this, we worked with herbarium material deposited in national herbaria, literature cited in ethnobotanical research in the country and those carried out directly in situ. The following uses stand out: medicinal to treat different conditions, useful, decorative, forage in its natural environment, among others. Some examples: for medicinal purposes fresh rhizomes of *Cyperus obtusatus* are used as diuretic, whole plant of *Scirpus californicus* and *Bulbostylis capillaris* as antidiabetic and for venereal diseases respectively; *Schoenoplectus californicus*, *Cyperus giganteus* and *C. bissaceus* are used in the manufacture of mats and baskets; *Eleocharis filiculmis*, *E. montana*, *E. elegans*, *E. emarginata* and other species of the genus are foragers in their natural environment; dried flowers of *Rhynchospora globosa* and *R. albiceps* are used as decorative. Ethnobotanical studies allow to keep alive the knowledge of the traditional uses, especially those related to the medicinal, since most of the species mentioned do not have chemical or pharmacological studies, they can be potential sources of active ingredients with biological activity; in addition, they allow to promote the cultivation of these species, enabling their protection, avoiding their extinction.

P.0416 The value of medicinal plants for the Kichwa indigenous community in the city of Bogotá, an approach to the perception of ecosystem services.

Victor Fabio Luna Mora[1], Mauricio Mina[2], Patricia Roncancio[3], Gerardo Garzón[4]

1 Universidad Nacional de Colombia. 2 Jardín Botánico de Bogotá, Bogotá, Colombia. 3 Secretaria de Integración Social 4 Cabildo Kichwa-Bogota, Bogotá, Colombia.

There are currently more than 25 ethnic communities in the city of Bogotá (including indigenous, Afro-descendant, Raizal, Palenquero and gypsy communities), many of which make use of the plant resources that provide them with numerous types of services that contribute to the development, well-being and good living of the community in the context of the city. Among these communities is the Kichwa community that has lived in the city of Bogotá since 1920; a city in which they carry out different types of ritual and ancestral practices that have been maintained thanks to oral tradition and which involve the use and management of medicinal and food plants. The objective of this research was to identify the medicinal species used by this community in the town of Engativá, as well as to investigate how this indigenous community perceives the ecosystem services associated with this plant resource. This study was carried out between February and September 2023. The population was randomly sampled. A qualitative methodology was used, triangulating primary and secondary sources. Exploratory activities were carried out for literature review and meetings with authorities and community leaders. Once the preliminary information was collected, semi-structured interviews were conducted with different members of the community, including families, authorities, young people and traditional doctors (Yachak) and Kichwa midwives (Mama Washa). This research is a first approach to identify how an indigenous community in a city context perceives the ecosystem services associated with a plant resource of great importance and/or relevance to them, such as medicinal plants.

Note: This abstract was translated with AI.

P.0417 Enhancing phytoimmunity in the medicinal plant Nepeta nuda through blue-red LED light exposure

Desislava Mantovska[1], Miroslava Zhiponova[1], Grigor Zehirov[2], Adriana Krasteva[1], Uroš Gašić[3], Danijela Mišić[3], Krasimir Rusanov[4], Mila Rusanova[4], Anna Zahariev[1], Valya Ganeva[1], Kiril Mishev[2], Petre I. Dobrev[5], Jozef Lacek[5], Roberta Filepová[5], Václav Motyka[5], Zhenya Yordanova[1], Ganka Chaneva[1], Valya Vassileva[2]

1 Faculty of Biology, Sofia University "St. Kliment Ohridski", Sofia, Bulgaria. 2 Institute of Plant Physiology and Genetics, Bulgarian Academy of Sciences, Sofia, Bulgaria. 3 Institute for Biological Research "Siniša Stanković", National Institute of the Republic of Serbia, University of Belgrade, Belgrade, Serbia. 4 Agrobioinstitute, Agricultural Academy of Sciences, Sofia, Bulgaria. 5 Institute of Experimental Botany, Czech Academy of Sciences, Praha, Czech Republic.

Light is a major factor affecting plant metabolism, and its quality and duration lead to major changes in the growth and development of plant species. Artificial lighting can influence the rate of photosynthesis, photomorphogenesis, and antioxidant capacity. This study investigated the effects of a blue-red LED light combination, known for inducing flowering, on the physiological state and content of biologically active substances in catmint (*Nepeta nuda* L.) grown under controlled *in vitro* conditions. We compared three lighting conditions: white light (W) as a control, and two intensities of blue-red light - high (BR) and low (BRS). We found that BR light resulted in shorter plants with more dry plant biomass and higher starch content, without altering anthocyanin levels, but reducing plastid pigments. This regime also modified the oxidative state of plants by increasing lipid peroxidation but neutralizing reactive oxygen species (ROS), enhancing total phenolic antioxidants and altering the metabolic profile. Specifically, BR light decreased the iridoid nepetalactone and increased levels of epideoxyloganic acid, rosmarinic acid and cirsimaritin. These effects appear to be regulated by the plant hormones auxin, abscisic acid and jasmonates, which are related to flowering of *N. nuda*. The BRS regime produced effects similar to the W control, increasing plant height. Both BR and BRS treatments induced the accumulation of proteins and amino acids. We conclude that BR light treatment can enhance the survival capacity of micropropagated *N. nuda* during subsequent soil adaptation, suggesting that similar light pre-treatment could improve phytoimmunity in other plant species before transfer to the field.

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P.0418 Imperative highlights of the societal reliance on indigenous plants during and post-Covid-19 era.

Mokgaetji G. Mokganya[1]

1 Science Foundation Department, Faculty of Science, Engineering and Agriculture, University of Venda, Limpopo Province, South Africa.

The outbreak of Coronavirus shocked people across the globe; inhabitants of rural villages were negatively impacted as the treatment was unknown. As a result, local people developed their traditional ways of treating any symptoms related to Influenza by using different indigenous plant species. This study investigated indigenous plant species that were used by inhabitants of the rural villages of the Vhembe region during and post-COVID-19 era. Results emerged from the semi-structured interviews conducted with 53 adults and 17 elderly participants from the four rural villages of the two selected municipalities. The study recorded a total of 13 plant species identified to have capabilities of treating symptoms related to influenza, sore throats, cough, and fever. These plants belong to 9 taxonomic families with Asteraceae at the top of the list. The treatment of these symptoms is achieved by the administration of oral decoctions, giggling by the decoctions extracted from leaves of the recorded plant species. Leaves of some plant species are boiled, and the boiling infusions are used for steaming. Some participants burnt the leaves of one plant and sniffed the smoke for the treatment of the symptoms. The continued use of these plants even post-COVID-19 era is a clear indication of their indispensability to rural communities. The traditional plant-derived medicine revealed during this study may be checked for their safety and efficacy to simply discover the new local and affordable drugs that could be used for conditions such as COVID-19.

P.0419 Isolation and characterization of novel plant-derived antimicrobial compounds from plantains

Sharelys M. Montes-Jiménez[1], Christopher A. Sambolín-Pérez[1], Glorialys Rivera-Otero[1], Juan A. Negrón-Berríos[1]

1 Institute of Sustainable Biotechnology, Inter American University of Puerto Rico, Barranquitas, Puerto Rico.

Musa spp., specifically bananas and plantains have had a variety of applications throughout the history of mankind. This crop has been key to feeding the population besides its variety of additional applications including medicinal properties. Currently, there is an emerging problem of bacterial resistance to commercially available antibiotics. Phytomedicine presents a sustainable solution to develop new compounds that can control bacterial growth. Pseudostem in bananas reportedly contains an increased concentration of organic compounds, some of which have been partially characterized. This study aimed to study the antibacterial characteristics of extracts obtained from plantain pseudostem tissues which are currently considered waste after fruit production. An organic extraction technique using the Soxhlet system was applied to produce organic extracts. Further, these extracts were characterized by infrared spectroscopy (FTIR) and Total polyphenol content was quantified. Then, the extract was applied to *Pseudomonas aeruginosa, Escherichia coli, Bacillus cereus, and Staphylococcus aureus* to analyze the antibacterial activity using Minimum Inhibitory Concentration (MIC) and Disk diffusion assays. Preliminary FTIR results show a high similarity spectrum of plantains pseudostem extract with bleomycin hydrochloride, lysozyme hydrochloride, and bacitracin zinc. MIC and disk diffusion tests indicate potential antibacterial activity of plantain pseudostem methanolic extract at 645 mg/ml on all tested bacteria with more sensitivity on Gram-negative. This study might help to identify and characterize novel sources of plant-derived antimicrobial compounds for a wider application in areas of human health.

P.0420 Medicinal plants of Paraguay. Species used in the eastern region of the country

María Vera Jiménez [1, 2], Luis Delgado Sánchez [1], Luz M. Muñoz Centeno [1]

1 Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain. 2 National University of Asunción, San Lorenzo, Paraguay.

Medicinal plants are used to treat specific ailments and maintain health. The Paraguayan population has a strong tradition in the use and consumption of medicinal plants, fresh and/or dried in infusions, decoctions, macerations or direct consumption. In Paraguay, traditional preventive and curative medicine is the first alternative in the treatment of many diseases, consuming medicinal plants in mate and tereré, although there is still not a complete knowledge of them. The objective of the research was to record the species used in the eastern region of Paraguay and to analyze them. Interviews were conducted with vendors in the municipal markets of the cities of Concepción (Concepción), Ciudad del Este (Alto Paraná), Coronel Oviedo (Caaguazú), Encarnación (Itapúa), San Lorenzo (Central) and Asunción. Forty people were interviewed (with prior informed consent) and reported on 119 medicinal species. Most of the medicinal uses are intended to treat digestive (94), genito-urinary (57), circulatory (51), skin, endocrine-metabolic, musculoskeletal, respiratory and nervous problems. Of the species mentioned, the ones used to treat a wide spectrum of conditions were: *Gonopterodendron sarmientoi* (Lorentz ex Griseb.) A.C. Godoy-Bürki (Zygophyllaceae) -palo santo-, *Urera baccifera* (L.) Gaudich (Urticaceae) -pyno guasu-, *Solanum palinacanthum* Dunal (Solanaceae) -juruveva-, *Commelina erecta* L. (Commelinaceae) -santa lucía hovy- and others. The medicinal species most cited by the interviewees were *Begonia cucullata* Willd. (Begoniaceae) -agrial-, *Equisetum giganteum* L. (Equisetaceae) -cola de caballo-, *Aloysia polystachya* (Gris.) Mold. (Verbenaceae) -cedrón Paraguay-, mainly used to treat conditions of the digestive, respiratory and circulatory systems. The families Asteraceae (21), Fabaceae (6) and Verbenaceae (6) have the largest number of medicinal species in the eastern region of Paraguay. In many cases, traditional knowledge is the basis of scientific knowledge, so it is of utmost importance to preserve and promote it.

P.0421 Enriched in phenolics callus cultures from the medicinal plant Nepeta nuda

Ana-Maria Nedelcheva[1], Anna Zaharieva[1], Desislava Raykova[1], Viktoria Vladimirova[1], Desislava Mantovska[1], Zhenya Yordanova[1], Miroslava Zhiponova[1]

1 Faculty of Biology, Sofia University "St. Kliment Ohridski", Sofia, Bulgaria.

Nepeta nuda L. (naked catmint; Lamiaceae) is a perennial medicinal plant with a wide geographic distribution in Europe and Asia. This plant is enriched in phenolic compounds with anti-proliferative, antioxidant, anti-inflammatory, antiviral, and anti-bacterial activities. Recent studies demonstrated that *N. nuda*'s metabolic content is significantly affected by the growth conditions, therefore plant biotechnological approaches could improve the directed synthesis of phytochemicals of interest. The *in vitro* propagation of *N. nuda* occurs in a hormone-free nutrition medium, however, the metabolic activity of *in vitro* plants strongly declines. This study aims to outline an approach for callus induction by administration of plant growth regulators (PGRs), which is not well explored. Among the PGRs, series of concentrations (0.1, 0.5, 1 mg/l) of four auxins (2,4-dichlorophenoxyacetic acid/2.4-D, picloram, indole-3-acetic acid/IAA, 1-naphthaleneacetic acid/NAA) and three cytokinins (6-benzylaminopourine/BAP, kinetin/KIN, thidiazuron/TDZ) have been tested for biomass production, accumulation of phenolic compounds and related antioxidant activity. The presence of picloram and TDZ induced fine callus of undifferentiated cells suitable for cell cultures, however, the phenolic antioxidants were reduced. On the other hand, combinations between IAA, NAA, and BAP, TDZ, showed a significant increase in biomass and phenolics. Petiole and stem explants demonstrated much higher proliferation ability than leaves, and dark-grown explants were much more actively dividing. In comparison to untreated in vitro plants, the callus produced from the combined application of TDZ+IAA (0.5 mg/l each) led to nearly 10-folds increase in total content of phenolics. Further studies on the corresponding biological activities would assist in the selection of the best variants and the identification of specific bioactive compounds. In conclusion, the strategy of using elicitors for increased metabolic rate of cell cultures has the perspective for upscaled accumulation of molecules of pharmacological interest.

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P.0422 Phytochemical and antioxidant potentials of Basella spp. in Nigeria

Funmilola M. Ojo[1], Taiwo A. Alakinde-Adenegan[2]

1 Department of Biological Sciences, Olusegun Agagu University of Science and Technology, Okitipupa, Nigeria. 2 Department of Biology Education, Adeyemi Federal University of Education, Ondo city, Nigeria.

Antioxidants from natural sources can be antidotes for free radical release during metabolic activities in humans. Basella spp., a commonly eaten vegetable in south-western Nigeria, may have the potential to supply antioxidants to the human diet. The study evaluated the phytochemical constituents and antioxidant properties of species and landraces of Basella spp. The forms of Basella spp. contained phytochemicals and antioxidant properties in varied amounts. Basella alba, round leaf, had the highest contents of phenol (0.22 ± P.2%) and vitamins A and C, 21.96 ± P.1% and 21.67 ± 0.90%, respectively. Basella rubra had the highest alkaloids and tannin contents, 7.68 ± 0.11 and 0.47 ± 0.17%, respectively. Basella cordifolia had the highest anthraquinone (12.50 ± P.3%) content; the highest flavonoid (96.77 ± P.3%) and saponin (0.63 ± P.1%) contents were in B. alba. Basella alba also had the highest DPPH (44.85 ± 2.11%). The Basella forms have the potential to be used as natural antioxidants needed by humans.

P.0423 Bioprospecting Indian Barleria: A treasure trove of bioactive metabolites

Shreedhar S. Otari[1], Manoj M. Lekhak[1], Savaliram G. Ghane[1]

1 Shivaji University, Kolhapur, India.

Barleria (Acanthaceae) consists of 285 species worldwide of which 32 taxa reported from India. We performed the Ultrasonic-assisted extraction (UAE) of phytochemicals such as total phenolic content (TPC), total flavonoid content (TFC), total tannin content (TTC), total iridoid content (TIC) and proanthocyanidins (Pro) from the aerial parts using methanol and water. Extracts were tested for their antioxidant activities, *viz.* DPPH (2,2-diphenyl-1-picrylhydrazyl) and ABTS (2,2′-azino-bis (3-ethylbenzothiazoline-6-sulfonic acid) radical scavenging, ferric reducing antioxidant property (FRAP), phosphomolybdenum (PMA) and metal chelating (MC). Further, bioactive compounds, shanzhiside methyl ester (SME), barlerin (BAR), verbascoside (VER) and stigmasterol (STI) were quantified using high-performance liquid chromatography (HPLC). Phytochemicals mainly TPC, TIC, Pro and TTC revealed positive correlation with ABTS (r = 0.344, 0.409, 0.368, 0.273, respectively) and MC (r = 0.504, P.22, 0.117 and 0.186, respectively). Principal component analysis (PCA) showed that all tested parameters except TFC enjoyed positive plane of component 1 (PC1). TIC, TTC, Pro, FRAP and PMA fell in positive plane of component 2 (PC2). However, negative plane of PC2 was dominated by variables like TPC, DPPH, ABTS, and MC. The positive plane of PC1 was mainly due to the variables reported from the alcoholic extract. Methanol was identified as the optimal extraction medium for extracting the studied phytochemicals. Furthermore, HPLC analysis confirmed the highest contents of SME, BAR, VER, and STI in the studied aerial parts of *B. terminalis* (51.42±0.48 mg/g DW), *B. hochstetteri* (22.11±0.48 mg/g DW*), B. gibsonii* (133.56±1.48 mg/g DW) and *B. cristata* (0.276±P.6 mg/g DW), respectively. Based on the current investigation, it is suggested that Indian *Barleria* species have a great medical potential and their conservation and further exploration for active principles, particularly iridoids is needed.

P.0424 The role of indigenous knowledge in ethnobotanical practices: a case study in Mandvi Taluka

Kavi K. Oza[1], Hasmita Fufal[1], Vinay M. Raole[1]

1 Department of Botany, Faculty of Science, The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat, India.

This study aims to document the ethnomedicinal plant species used to manage human aliments and the associated indigenous knowledge in and around the Mandvi taluka of the Kachchh district of Gujarat. Key informant interviews and participatory observations were conducted during different seasons from 2020 to 2023 involving laymen, local people, village heads (Sarpanch, Mukhiya), forest-dwelling tribes, Vaidyas, Hakims, Bhuvas, etc. During this study, a total of 103 plant species were recorded. Among all the dominant vegetation types, the average density of *Commiphora wightii* was 50-55 individuals/ha. and was recorded as the medicinally dominant species in the study area. Also, 90 noteworthy medicinal plants were also recorded. The ethnobotanical importance indices were developed to establish the main parameters needed to evaluate which are the most important plants within a culture and to determine conservation requirements.

P.0425 The art of being alone: study of secondary compounds in Rivasmartinezia cazorlana, a paleondemism in SE Spain

María I. Pozo1, Baudilio Herrero[1], Juan Andrés Oria-Rueda[1], Olaya Mediavilla[1], Alfredo Benavente[2], Alfredo Benavente Navarro[3]

1 Agroforestal Sciences, ETSIIAA, University of Valladolid, Palencia, Spain. 2 Plant Production, ETSIIAA, University of Valladolid, Palencia, Spain. 3 Centro de Capacitación y Experimentación Forestal, Vadillo-Castril, Spain.

Rivasmartinezia is a recently described genus within the Apiaceae family that accounts for only two species. Uniquely present in the Iberian Peninsula, the first species, *R. vazquezii*, inhabits a few locations in Somiedo Natural Park, in Asturias. More strickinly, the second species, *R. cazorlana*, is represented by a single population in Cazorla-Segura-las Villas Natural Park, in Jaén. The unique *R. cazorlana* population is located in a barely accessible area of 4 ha. at 1470 m.a.s.l. Despite the relic character of the species, more than 50K individuals have been estimated in the population. The plants are vigorous and grow without competing taxa, and no signs of herbivory have been observed. We hypothesize that these highly competitive skills might be explained by the presence of secondary compounds in vegetative and reproductive tissues, chemicals that mediate the interaction between the plant and the environment. We have identified plant secondary compounds from leaves and fruits of *R. cazorlana* individuals using high resolution UPLC-MS chromatography. Besides of characterizing the chemical profile of the plant species, in this contribution we test Plant Optimal Defence theory by comparing leaves and fruits from the same plant. Considering the remarkable scent of the fruits, we have compared the chemical profile of *R. cazorlana* with related Apiaceae taxa, such as coriander (*Coriandrum sativum*) and cumin (*Cuminum cyminum*) fruits, and we have added licorice (*Glycyrrhiza glabra*, Fabaceae) as external member of comparison purposes. We would like to highlight the importance of uncovering Iberian hidden plant diversity, and the defensive strategies exploited by ancient and relic species. Besides, the *species R. cazorlana* shows clear potential for useful applications for mankind, such as source of antioxidant and antimicrobial compounds, or culinary use.

P.0426 Herbal remedies for health improvements in Batak Karo people, Sumatra Utara, Indonesia

Endang C. Purba[1], Jer-Ming Hu[1,2]

1 Institute of Ecology and Evolutionary Biology, National Taiwan University, Taipei, Taiwan 2 NTU Herbarium, National Taiwan University, Taipei, Taiwan.

Indonesia is a mega-diverse country that contains many potential medicinal plants. The Batak Karo people from Sumatra, Indonesia, have traditional knowledge of curing and preventing diseases and traditional concoctions that have been used to improve health e.g. *minak, tawar* and *kuning.* Different recipes exist in various villages and families however it has never been documented thoroughly. The local knowledge of the Batak Karo is a cultural property that needs to be explored and recorded so that this traditional management does not become extinct and to fulfill the goals for the Sustainable Development Goals (SDGs). This study aims to document the medicinal plants of the traditional concoctions from Batak Karo to improve health as an alternative medicine. An ethnobotanical study was conducted in Semangat Gunung and Doulu, Karo, Sumatra, Indonesia. Six traditional healers were interviewed personally. Observation and plant surveys were carried out during the fieldwork. The voucher specimens were identified and stored at the herbarium of the University of Indonesia. A total of 47 plant species are used to prepare *minak, kuning* and *tawar.* The most frequently used family is Zingiberaceae. *Allium sativum, A. cepa, Kaempferia galangal, Piper nigrum* and *Zingiber officinale* are used in all three remedies. Herbal remedies are widely and effectively used to improve the health of Batak Karo. There is a need to extend the documentation of medicinal plants in the area and evaluate their biological activity as a basis for developing future medicines.

P.0427 Traditional botanical knowledge of Artemisia vulgaris L. (Asteraceae) from Serbia - ethnobotanical study

Maja Radulović[1], Milan Gavrilović[1], Zora Dajić-Stevanović[2], Pedja Janaćković[1]

1 Department of Morphology and Systematic of Plants, Faculty of Biology, Belgrade, Serbia. 2 Department of Agrobotany, Faculty of Agriculture, Belgrade, Serbia.

Artemisia vulgaris L., common mugwort, has a widespread distribution in the natural habitats worldwide (Europe, Asia, North and South America, and Africa). For many centuries, this species has been mainly used for treating gynecological ailments and gastrointestinal diseases. However, ethnobotanical knowledge regarding the usage of this plant in Serbia is missing. Therefore, the aim of this study was to collect information on traditional uses of common mugwort for medicinal purposes, human and animal nutrition, veterinary and miscellaneous purposes. Ethnobotanical survey was conducted from June to November, in 2023, in all regions (south, east, central, west and north) of Serbia, including 64 localities (24 cities and 40 villages). The group of 376 local inhabitants was interviewed by semi-structured interview. Twenty-two use-reports were recorded, mostly for medicinal purposes especially against stomach diseases. It was shown that common mugwort was used in all investigated regions in Serbia, mostly in southern Serbia. The most frequently mode of preparation was infusion, while tincture and balm were less utilized. Flowering aerial parts (mostly dried) were the most used plant part against different diseases, especially against digestive tract disorders. Also, dried leaves and roots are used as remedy against stomachache. Some informants mentioned that in the past they used dried herba as revetment against sore throat. We documented new folk names and recipes for tincture and balm. There are differences in the usage of this plant between regions, and between men and women. Also, some respondents mentioned that this plant is a weed in agricultural fields. We documented for the first time that shoots without leaves and inflorescences are used as a toy for children in urban area in western Serbia, a novelty for Balkan ethnobotany.

P.0428 Anti-inflammatory, anti-microbial, and anticancer activities of medicinal plants hydrocolloid extract

Mapula Razwinani1, Keolebogile SCM Motaung[1]

1 Durban University of Technology, Department of Technology Transfer and Innovation, Steve Biko Campus, Durban, South Africa.

South Africa has a high incidence rate of serious burn injuries and deaths which is the most common cause of death in children under the age of four. South African burns affect about 3.2% of the population annually. The purpose of this study is to design, formulate, and a fabricate medicinal plant hydrocolloid. The plant extract was screened for its phytochemical, antioxidant, and antimicrobial activities and then incorporated with natural polymers to design, synthesize, and characterize the hydrocolloid dressing. The plant extracts show the presence of alkaloids, saponin, and flavonoids; and inhibition of *S. aureus* and *P. putidi* bacteria The synthesized dressing SEM image exhibited irregular, smooth, interwoven, and uniform morphology with fibrous bead-shaped and FTIR spectra show that the wound dressings were successfully synthesized, with several similar peaks for each single layer hydrocolloid. The phytochemical screening of plant extracts and pre-formulation study is an essential preliminary study to ensure the successful establishment of an optimum drug delivery system before formulation of a novel modality for wound healing dressing.

P.0429 Ethnobotany in the Tecozautla municipality, Hidalgo, Mexico

Gabriela Hernández[1], Sonia Rojas[1], Carlos Castillejos[1], Reynalda Roldán[1], Carolina Rojas[1]1

1 Universidad Nacional Autónoma de México, Ciudad de México, Mexico.

In Tecozautla, Hidalgo, there is a xeric scrubland with different plant associations that belong to the Queretano-Hidalgo Arid Zone in the final portion of the Mexican Chihuahuan Desert. In this region, Otomi influence, once an important heritage, has diminished over time. This is manifested in the limited number of floristic studies carried out and in the absence of ethnobotanists. However, this field of study plays a crucial role in highlighting the intimate relationship between humans and plants. Thus, an ethnobotanical analysis of the species in the municipality was carried out, as well as a simplified description of the uses of medicinal species. 209 (43.63%) species were recorded with some use of the 479 reported for the region. The Eudicotyledons presented 161 (77.03%) species, Monocotyledons 37 (17.70%), Monilophytes 9 (4.31%) and Gymnosperms and Lycophytes, a single species each (0.48%). The families with the greatest number of useful genera were Asteraceae with 32 (15.31%) and Poaceae with 18 (8.61%) and the genera with the most species were Ipomea with 5 (2.39%) and Euphorbia with 4 (1.91%). The useful plants were classified into 10 ethnobotanical categories, the main ones being: medicinal with 124 (47.15%) species, ornamental with 63 (23.95%) and forage with 49 (18.63%); Those with the lowest percentage were:

fertilizers and wastewater treatment, both, with a single species (0.38%). Finally, specific reference is made to 124 medicinal species with ethnobotanical use data, and additional information is included such as photographs of the plant, morphological description and distribution. This work is a useful tool to facilitate taxonomic identification, mainly for people who are not related to the topic; in addition to being a compilation that brings together the available ethnobotanical information.

P.0430 Diversity and distribution of medicinal plants of the United Arab Emirates (UAE): Perspectives for sustainable utilization and future research

Salama Al Mansoori[1], Sabitha Sakkir[1], Maher Kabshawi[1]

1 Plant Genetic Resources Centre, Environment Agency - Abu Dhabi, Al Ain, UAE.

Medicinal plants are globally valuable sources of herbal and traditional medicines and products. This article provides an overview of the diversity and distribution of medicinal species of the UAE and efforts to conserve their genetic resources through in-situ and ex-situ conservation methods. The UAE is gifted with diverse habitat types occurring in the desert, plains, coastal, sabkhas and mountainous ecosystems. The UAE flora contains over 600 native plant species, which over 20% species were used in traditional medicines and product. The local knowledge associated with the conservation and use of medicinal plants is disappearing at an alarming rate. The main aim of the recently started Plant Genetic Resource Centre is to undertake and promote long-term conservation of plant genetic resources, including medicinal plants, by ex-situ conservation of seeds, in-vitro cultures, and cryopreservation techniques. Germplasm of more than 120 medicinal plant species is conserved in our ex-situ conservation facilities for various future research projects and conservational programs. As well as the current established network of protected areas in the UAE which is one among the *in-situ* conservation strategies implemented. The number of medicinal plants reported from country indicates that the people possess rich traditional knowledge, and the vegetation constitutes rich diversity of medicinal plants.

P.0431 Conservation of economically important Nigerian trees through seed dormancy release and in vitro clonal propagation

Shakira Shaik[1], Mustapha Haruna[1], Muhammad Nakhooda[2]

1 School of Life Sciences, University of KwaZulu-Natal, Durban, South Africa. 2 Department of Biotechnology and Consumer Sciences, Cape Peninsula University of Technology, Cape Town, South Africa.

Overharvesting and destruction of wild trees for medicines, fuelwood and construction have led to the decline of many economically significant species in Nigeria such as *Ziziphus spina-christi* and *Vitex doniana.* Barriers to their cultivation and conservation are seed dormancy and a lack of mass propagation methods. Hence, strategies to overcome seed dormancy, and techniques for *in vitro* clonal propagation, were presently investigated. Seeds of both species were established as non-photoblastic with an optimal germination temperature range of 25-35°C. Physical dormancy was attributed to hard testas, which, when removed and fractured in *Z. spina-christi* and *V. doniana*, respectively, improved germination to 87% in both species compared to their controls (47 and 7%). Direct shoot organogenesis protocols were established using *in vitro*-derived nodal explants. Shoot multiplication was successful in *Z. spina-christi* using MS basal salt medium containing 2 mgL^{-1} zeatin (5 shoots/explant), and with Woody Plant Medium (WPM) containing 0.3 mgL^{-1} benzylaminopurine, for *V. doniana* (4 shoots/explant). In the former, shoots were rooted *ex vitro* using a one-hour pulse treatment in 200 mgL^{-1} indole-3-butyric acid resulting in 80% rooting and 100% plantlet survival post-acclimatisation. In the latter, shoots were rooted on WPM containing 0.5 mgL^{-1} indole-3-acetic acid (IAA) resulting in 80% rooting and 93% plantlet survival post-acclimatisation. Protocol development for somatic embryogenesis (SE) was unsuccessful, as pro-embryos induced with 2,4-dichlorophenoxyacetic acid, picloram, IAA, or naphthalene acetic acid (or combinations of these), failed to develop further, largely attributable to auxin persistence. This warrants further investigation as SE can be used a means of germplasm conservation for these declining species.

P.0432 Effect of ginger aqueous extract on THP-1 tumor cells

Marcos C. Silva[1,2]*, Danilo Portela[2], Eliane Conceição[2], Camila Nascimento[1,2], Pedro Sá[1], Renata Souza[1], Thais Rocha[1,2], Olga Souza[1], Rafael Pereira[2], José Raynal[2], Roberto Meyer[2], Vera Vale[1]

*1 State University of Bahia, Bahia, Bazil. 2 Federal University of Bahia, Bahia, Brazil. *marcosilva@uneb.br.*

Zingiber officinale Roscoe (ginger) is a monocotyledon, belonging to the Zingiberaceae family of the Zingiberales order. Its tuberous rhizome is used for multiple therapeutic benefits, such as bactericidal, digestive, circulatory, respiratory, immunomodulatory action and cancer prevention. It is widely used in medicinal systems to treat a variety of diseases, including loss of appetite, indigestion and pain, as well as in the cuisine of various peoples. The ginger has main components: carbohydrates and lipids, including free fatty acids, oleoresin, volatile oils, among others. However, the main phenolic compounds in ginger are gingerols, shogaols and paradols, which can have immunomodulatory effects, including the ability to modulate inflammation and the function of components of the cellular immune response, as well as antitumor effect. This work aimed to evaluate the effect of crude aqueous ginger extract (obtained by solubilization and subsequent centrifugation of 2g of rhizome powder in 10mL of saline solution) subjected to temperatures of 25, 40, 60 and 80°C on the development of tumor monocytes of the THP-1 lineage. For this, $1x10^6$ monocytes TPH-1 were incubated in culture and each well was stimulated by one of the different extracts at a concentration of 1000 µg/mL. The entire experiment was carried out in triplicate. The material was incubated for 48h at 37°C in an oven containing 5% CO_2. After this period, the MTT assay (3-4,5-dimethylthiazol-2,5-diphenyltetrazolium bromide) was performed to verify cell viability. It was observed that the 25°C extract reduced ~70% the development of tumor cells, the 40°C extract promoted a reduction of ~50%, the 60°C extract ~30% and the 80°C extract a reduction of ~60%. These data suggest that ginger has compounds with antitumor potential and that the way and temperature in which it is consumed can influence this effect.

P.0433 Blue-red LED light-induced anatomical and physiological alterations in the leaf of micropropagated medicinal plant Nepeta nuda L.

Miroslava Stefanova[1], Tsveta Ganeva[1], Momchil Paunov[1], Miroslava Zhiponova[1]

1 Faculty of Biology, Sofia University "St. Kliment Ohridski", Sofia, Bulgaria.

The biotechnological approach for *in vitro* propagation of medicinal plants followed by *ex vitro* adaptation provides upscale multiplication in a controlled environment. Here, we aimed to test the impact of LED light on the micropropagation efficiency of *Nepeta nuda* L. Combined blue and red LED lights with high intensity (BR) and low intensity (BRS) were applied and compared to the regular white fluorescent light (W) under *in vitro* conditions. The histological and morphometric analyses revealed altered leaf anatomy. In comparison with W, the BR light enlarged the leaf area and increased the mesophyll height, while the epidermal height remained the same. Stomata on the adaxial surface and increased stomatal density on the abaxial surface were observed under BR illumination. The BRS reduced the leaf area and thickness due to the diminished height of all tissues and shrinkage of the spongy parenchyma intercellular spaces. The morphology and density of the non-glandular and glandular trichomes were not altered by the different blu-red intensities. In the following *ex vitro* adaptation in greenhouse under daylight, the BR-plantlets showed an enhanced efficiency of photosynthetic electron transport, which defines this light regime as suitable for initial cultivation of *N. nuda*. The achieved results confirmed the anatomical analysis of the *in vitro*-plantlets as an appropriate method that provides predictable and reliable data about the adaptive capability of the plantlets to overcome the demanding process of *ex vitro* adaptation, restoring their bioactive potential.

P.0434 Chemotaxonomy of plants for medicinal use from the Sierra Nororiental of the state of Puebla, Mexico

Valdés-Vásquez I. F.[1], Rojas-Chávez S.[2], Serrano-Dirvas D. L.[3], Mendoza-Cariño M.[4]

1 Unidad de Investigación en Ecología Vegetal, FES Zaragoza UNAM, Ciudad de México, México. 2 Laboratorio de Investigación Formativa, FES Zaragoza UNAM, Ciudad de México, México. 3 Unidad de Investigación en Química Computacional, Síntesis y Farmacología, FES Zaragoza UNAM, Ciudad de México, México 4 Colegio de Posgraduados, Campus Montecillo, Universidad Chapingo, Ciudad de México, México.

This research was carried out in the Region Sierra Nororiental of Puebla, Mexico, due to the historical importance of the cultural region, medicinal plants have active ingredients that carry out modifications in the human body through secondary metabolites from four families: acids, alkaloids, phenols and terpenes, with components such as carotenoids, flavonoids, mucilage and pectins. The study area is located in the central region of Mexico, surrounded by the type of vegetation of Cloud Forest, Low Subdeciduous Forest and Evergreen Tropical Forest, to determinate the biological and phytochemical diversity of the species, botanical collections were carried out, they were taxonomically identified and interviews were carried out with traditional doctors to learn about the use and preparation of each one, as well as its applications in the different health problems of the population, this served to generate a glossary for the recognition and application of phytochemical families. 75 species belonging to 43 families were identified, of which they have been described in 51 similarities, in which gastritis, diabetes mellitus Type 2 and urticaria related to apparatus and systems of the human body, stand out. Mainly the digestive system, nervous system and skin predominate, however plants for medicinal use have properties more focused on the protection of the systems: locomotor, circulatory and endocrine because the secondary metabolites inhibit the attack of pathogens. In conclusion, the use of medicinal plants constitutes an alternative to the lack of health services in several rural populations, therefore, the glossary as a resource facilitates the recognition of plants in the region and includes recommendations for their appropriate use, that provide benefits for the community.

P.0435 Cytotoxic action of Psidium bahianum essential oil on cells of the THP-1 leukemic lineage

Vera Vale[1], Olga Lara Souza[1], Renata Souza[1], Thais Rocha[2], Alexa Paes Coelho[1], Marcos Silva[1,2]

1 State University of Bahia, Bahia, Brazil. 2 Federal University of Bahia, Bahia, Brazil.

Psidium bahianum Landrum & Funch, belonging to the Myrtaceae family, has a geographical distribution restricted to some regions of the State of Bahia, mainly in the Atlantic Forest region of southern Bahia. Several species of the genus *Psidium* have been related to antitumor potential for different cell lines, including *Psidium guajava, Psidium cattleianum and Psidium guineense.* The objective of this work was to evaluate the cytotoxic potential of *P. bahianum* essential oil on cells of the human leukemia lineage, THP-1. Leaves were collected in the morning, 9 am, in the Atlantic Forest Vegetation Complex of Campus II – UNEB in the municipality of Alagoinhas - Bahia, Brazil. The young leaves were cut, weighed (350g) and the essential oil was obtained by the "water vapor drag" technique for a period of 4 hours and 30 minutes, using a Clevenger apparatus. Monocytes from the human tumor line THP-1 were cultured in DMEM/F12 supplemented with 1% penicillin/spectromycin and 10% fetal bovine serum (FBS), in a humidified environment at 37°C with 5% CO2 for 48 hours in triplicate. $1x10^{6}$ of THP-1 cells were used in each well and stimulated at concentrations of 200, 100 and 50 µg/mL. The entire experiment was carried out in triplicate. After this period, the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium (MTT) assay was performed to verify the cell viability. At a concentration of 200µg/mL, there was a 75% reduction in viable cells, at a concentration of 100µg/mL the reduction was 25% and at a concentration of 50µg/mL, the reduction was visible at 0.6% when compared to the control. These data suggest that *P. baihanum* essential oil has constituents with antitumor activity for tested cells and subsequent studies will be necessary to better understand the oil's mechanisms of action, including other tumor lineages.

P.0436 Ethnobotany and medical applications in *Acalypha*: a global review with taxonomic assessment

Lucía Villaescusa González[1], José María Cardiel Sanz[2], Iris Montero Muñoz[3], Pablo Muñoz Rodríguez[1]

1 Universidad Complutense de Madrid, Spain 2 Universidad Autónoma de Madrid, Spain. 2 Real Jardín Botánico de Madrid, Spain.

Throughout history, humans have used plants for many different purposes, including disease prevention and treatment. Understanding why and how communities have used and continue to use plants not only has an intrinsic value as part of human history but is also important as it can help identify new compounds of pharmacological interest and conservation priorities. Many plants used by humans, however, belong to groups that are only imperfectly known, and the lack of a good taxonomic knowledge makes it difficult to confirm the identity of the plants studied. This work focuses on the genus *Acalypha* L. (Euphorbiaceae). With ca. 500 accepted species and a pantropical distribution, almost a third of *Acalypha* species have reported uses by humans. The information available is, however, only of limited use since we lack a basic taxonomic knowledge for most species, specimen misidentification is frequent, and many names used in previous studies are now considered synonyms. Understanding the ethnobotanical diversity in *Acalypha* necessarily relies on a comprehensive taxonomy, which is missing for many *Acalypha* species. We present a detailed review of the ethnobotany of *Acalypha* species used by past and present human populations. We compiled, classified, and critically reviewed scientific literature on ethnobotanical research and experimental studies of *Acalypha*, at a global scale. Importantly, we assess the taxonomy of the plants studied and the reliability of the studies published and classify all recorded uses following international standards to facilitate future research. This review, part of a broader monographic study of the genus, opens the door to subsequent targeted investigation on *Acalypha* and its medicinal potential.

P.0437 Anatolian medicinal plants in respiratory diseases: A review of the ethnobotany

Golshan Zare[1], N. Yağmur Diker[1], I. Irem Tatlı Çankaya[1]

1 Department of Pharmaceutical Botany, Faculty of Pharmacy, Hacettepe University, Sıhhiye, Ankara, Turkey

Respiratory disorders are among the most common diseases worldwide and include chronic obstructive pulmonary disease, asthma, emphysema, pneumonia, or emphysema. A large part of the population experiences at least one of these disorders in a mild or severe form annually. This review aimed to evaluate the documented medicinal plants from Anatolia which are traditionally used to treat respiratory diseases. Turkey was home to many ancient civilizations geographically placed as a bridge between Asia and Europe and, during many historical periods created a transition between the continents of Europe, Asia and Africa. Consequently, throughout history, the plants have been extensively used for different purposes such as nutrition and healing. On this sense, approximately five hundred plant taxa from Anatolia were listed as traditional therapeutics for the treatment of respiratory diseases including asthma, bronchitis, colds & flu, influenzas and pneumonia. Despite 512 taxa with ethnobotanical records, our result has highlighted 33 most frequently used plants. Fruits of Rosaceae, aerial parts of Lamiaceae, flowers of Asteraceae members besides *Tilia*, are among the most used taxa. Generally, these plants are used internally for therapeutic purposes and mainly prepared with hot or cold water as decoctions, infusions and macerations. Most of these taxa have antibacterial, antiviral, antitussive, antipyretic, and anti-inflammatory activities. *Sambucus nigra*, *Glycyrrhiza glabra*, *Cydonia oblonga*, *Urtica dioica*, *Matricaria chamomilla*, *Juniperus oxycedrus*, *Plantago spp.*, *Rubus spp.* and *Pinus* with antiviral, anti-inflammatory and immunomodulatory activities can be subjected to further investigation as potential candidates against COVID-19.

S.038. CONSERVATION STATUS OF MAGNOLIA IN SOUTH AMERICA

P.0438 Cinchona nitida in critical danger: assessment, conservation strategies, and challenges in central Perú

Lizeth K. Huamán[1], Joaquina A. Albán[1], Adrián Saldaña[2]

1 Department of Ethnobotany and Economic Botany, Natural History Museum of San Marcos, Lima, Perú. 2 Seed Blessing Ethnobotanical Garden, San Ramón, Perú.

Cinchona nitida, a perennial and endemic tree of Peru, has recently been recorded in the Junín department, indicating an expansion beyond the initial records in Huánuco. Although not classified as threatened wildlife under the Peruvian current regulation (Supreme Decree N°043-2006-AG), the species faces critical risks due to its restricted distribution and threats such as land-use change and climate change. This study aims to assess the current status of the species and propose conservation strategies. Information was compiled from national and international herbariums, supplemented by over five field expeditions in various locations in Huánuco, Junín, and Pasco to collect data on density by stages and morphological characteristics observed in the field. Additionally, the area of occupancy and extent of occurrence were analyzed, and activities altering its habitat were recorded. The results indicate that *Cinchona nitida* is primarily concentrated in the locality of Malalma, Junín, particularly at altitudes between 2000 and 2100 m.a.s.l. However, a subsequent visit revealed an incident of deforestation affecting previously surveyed populations, indicating even greater vulnerability and justifying its inclusion in the nationally and internationally threatened flora list. The reduction of habitat and its limited geographical distribution (EOO $< 100\ km^2$ and AOO $< 10\ km^2$) support its classification as critically endangered. Faced with these challenges, reforestation is proposed in the Callas Palca Community or the Pampa Hermosa Reserved Zone, areas close to the registered populations in Junín. Additionally, repopulation in the districts of the Oxapampa province, Pasco, is suggested due to their altitude and similar climatic conditions. In conclusion, the urgent conservation of *Cinchona nitida* is imperative due to its critical endangered status and the vulnerability of its habitat. This underscores the pressing need to review and update conservation classifications, incorporating nursery propagation and field reintroduction protocols to ensure the effective protection of this at-risk species.

S.054. EVOLUTION AND DIVERSITY OF CARBON CONCENTRATING MECHANISMS (CCM) IN LAND PLANTS

P.0439 Patterns of phytochemical variation in populations of Amaranthus viridis in two ecological zones of Ghana

Gideon Antwi[1], Matthew Kweku Essilfie[1]

1 Department of Plant and Environmental Biology, University of Ghana, Legon-Accra, Ghana.

The study aimed to assess the patterns of variations in total phenolic content, total flavonoid content, and antioxidant activity in populations of *A. viridis* in two different ecological zones of Ghana. Matured plant leaves of A. viridis were collected at two different locations namely Aburi Botanical Gardens and Legon Botanical Gardens and were subjected to ethanolic extraction. The extracts were analyzed for antioxidant activity using 1,1-diphenyl 1,1-2 picrylhydrazyl radical scavenging, total phenolic content was analyzed using Folin-Ciocalteu reagent, and total fla-

vonoid content was also analyzed using the Aluminium chloride colorimetric technique. The correlation of total phenolic content and total flavonoid content, total phenolic content and antioxidant activity, and total flavonoid content and antioxidant activity all yielded a directly proportional association. Thus, as total phenolic content increased total flavonoid content also increased and this applies to all the scenarios above. There was a substantial difference in the phenolic content as Aburi Botanical Gardens had a higher phenolic content than Legon Botanical Gardens. The semi-deciduous forest of the Aburi Botanical Garden and the coastal savannah of the Legon Botanical Garden, two contrasting ecological contexts, have diverse effects on the phytochemical composition of A. viridis, as this study has clarified.

P.0440 Investigating the role of epigenetic inheritance in Crassulacean Acid Metabolism (CAM) photosynthesis in Cistanthe longiscapa

Dauerman, Sophie[1], Chomentowska, Anri[1], Edwards, Erika[1]

1 Yale University, Department of Ecology and Evolutionary Biology, New Haven, USA.

Cistanthe longiscapa is a charismatic annual plant in the family Montiaceae. Native to the Atacama Desert in Chile, *C. longiscapa* experiences drought stress after mass-flowering following El Niño events. This plant performs CAM photosynthesis, which involves nighttime fixation of CO_2 into malic acid and its decarboxylation during the day. This is beneficial because CAM limits daytime water loss – *C. longiscapa* is a facultative CAM plant, upregulating CAM during drought. Gas exchange monitoring revealed that the CAM cycle remains activated after rewatering, even once daytime stomatal conductance has returned to pre-drought levels. This indicates changes in expression of CAM genes that persist after the cessation of the environmental signal. One plausible explanation for the phenomenon is epigenetic changes, such as DNA methylation. In this study, we investigate the role of epigenetic modification in the regulation of functional CAM photosynthesis. We grew parental *C. longiscapa* individuals in two treatments – under drought or fully watered – and monitored plant growth. We characterized the CAM phenotypes by measuring overnight accumulation of titratable acid and tracking gas exchange data. We collected seeds from both treatments, then grew the seeds in separate batches such that F1 progeny from each treatment were grown under full-water and drought, effectively setting up four treatments. We compared CAM phenotypes of these F1 progeny, testing whether the magnitude of CAM remains upregulated in the progeny of drought plants compared to the progeny of watered plants. We also compared the timing of onset of CAM following the start of drought. In all, our experiment contributes to the literature on the role of epigenetics in conferring drought tolerance between generations by conducting the first epigenetic inheritance experiment in a facultative CAM species.

P.0441 Tropaeolaceae as a model system to study the evolution and development of morphological traits

Sebastián Martínez-Salazar[1], Yan Gong[1], Natalia Pabón-Mora[2], Elena Kramer[1]

1 Harvard University, Cambridge, USA. 2 Universidad de Antioquia, Medellín, Colombia.

The monogeneric Tropaeolaceae (Brassicales) is a family of flowering plants that encompasses about 100 species native from South and Central America. This family displays a diversity of morphological traits that are lacking or rare in the closely related Brassicaceae, to which the model plant Arabidopsis belongs. Such traits include tuber formation, a climbing growth habit, peltate leaves, bilateral floral symmetry, floral tube development, nectar spurs, complex petal sculpting, and a broad range of pollination syndromes. In turn, we are developing Tropaeolaceae as a model system to study the evolution and development of those traits. This is particularly convenient because the members of the family have relatively short life cycles, and their genetic complement lacks two rounds of whole-genome duplications that most other Brassicales, including Arabidopsis, share. To start, we have been building comparative transcriptomic resources to study gene expression in different *Tropaeolum* species. We have also been optimizing virus-induced gene silencing in the garden nasturtium, *Tropaeolum majus*, as a technique to study gene function. We have performed this technique to downregulate a gene required for carotenoid synthesis (the *PHYTOENE DESATURASE TmPDS*) as a positive control, and a gene required for anthocyanin synthesis (the *ANTHOCYANIDIN SYNTHASE TmANS*) as a reporter gene in a variety of *T. majus* high in anthocyanins. This technique will allow us to further study the function of candidate genes for the development of the morphological traits that we mentioned, and in the long term will allow us to have a better understanding on how these traits have evolved and diversified in the family.

S.055. EVOLUTION AND FUNCTION OF CONVERGENT FLORAL PHENOTYPES 1

P.0442 Floral adaptations for pollination by bats and hummingbirds in ring-gentians (Symbolanthus, Gentianaceae)

Belen Alvestegui[1], Lena Struwe[2], Nathan Muchhala[1]

1 University of Missouri-St. Louis, St. Louis, USA. 2 Rutgers University, New Brunswick, USA.

Research carried out during the last 20 years has revealed that the ring-gentians (*Symbolanthus,* Gentianaceae), a neotropical asterid genus, has a particularly high floral diversity. There are at least 38 *Symbolanthus* species (including 8 species to be described) that are present from Bolivia in the south to Costa Rica in the north, with outliers on the tepuis in Venezuela and Guyana (on the Guiana Shield) and in the Lesser Antilles in the Caribbean. Their up to 12-cm long conspicuous corollas present variable shape, symmetry, and color patterns, with basic colors ranging from green, white, and yellow to pink and red, depending on the species. Pollinator information is remarkably poor for such a large-flowered taxon, but herbarium records and new investigations have revealed primary visitation by bats and hummingbirds. We determined pollination systems for species in Bolivia, Ecuador, and Colombia. We found that some species of *Symbolanthus* concur with traditional pollination syndromes: tubular, red-flowered species with UV-reflecting nectar guides are visited by hummingbirds (e.g., *S. australis*), and white, bell-shaped species are visited by bats (e.g., *S. pterocalyx*). However, other pink-yellow-flowered species are generalized to both groups (e.g., *S. brittonianus*). By combining these pollinator observations with floral measurements taken from herbaria, we found that typical pollination syndromes are validated by distinct morphospaces but species hypothesized to be adapted to bat and hummingbird pollination are dispersed in the morphospace. This occurs because floral characteristics such as flower shape, time of blooming, and nectar volume that aid visitation by both groups need to be collected in the field. Additionally, we carried out flight cage experiments with bats and hummingbirds to determine the effect of the corona, a tube-like structure within the corolla, on pollen deposition and found that it helps to filter pollinators' access to nectar at the ovary base.

P.0443 Pollen flower classification then and now: Vogel (1978) revisited

Melo L.R.F.[1], Vasconcelos T.[2], Brito V.L.G.[3]

1 Postgraduate Program in Ecology, Conservation and Biodiversity - Institute of Biology, Universidade Federal de Uberlândia, Uberlândia, Minas Gerais, Brazil. 2 Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, USA. 3 Institute of Biology, Universidade Federal de Uberlândia, Uberlândia, Minas Gerais, Brazil.

The term "pollen flowers" describes flowers that present pollen as the main or only resource available for their pollinators. Such flowers are mainly pollinated by bees and have a series of morphological and functional adaptations, especially in their male reproductive organs, related to their close interaction with pollinators. In 1978, these adaptations led the botanist Stefan Vogel to classify pollen flowers into three types: *Magnolian*, *Papaver,* and *Solanum.* However, Vogel's classification was based on limited access to data from that time and, for that reason, it did not encompass all the variability of floral traits and ecological interactions that pollen flowers are currently known to present. In this study, we revisit the pollen flower classification by Vogel to assess whether it encompasses the currently known diversity of pollen flowers. Pollen flowers were reported in 75 of the 420 angiosperm families recognized in the APG IV, and our analysis allowed the identification of three functional groups of pollen flowers that are different from the original ones proposed by Vogel. The first group includes flowers that have anthers with longitudinal dehiscence, shed or exposed pollen grains, radial symmetry, many stamens, and commonly brush-blossom floral display. The second group also has flowers with longitudinal anthers but their flowers are mostly grouped, small, and with reduced petals and few stamens. In addition, this group presents ambophily as a reproductive strategy, a condition not analyzed in Vogel's work. The last group is characterized by poricidal anthers and pollen grains that are released in small portions. These flowers often have few stamens that contrast with the petals' colors, radial symmetry, and a shooting-star floral display. In conclusion, our research suggests a move away from Vogel's classification and encourages a more inclusive and comprehensive classification of pollen flowers based on morphological traits.

P.0444 Analysis of flower formation in two species with contrasting morphology, Disocactus speciosus and Disocactus eichlami (Cactaceae)

C. Genaro Ramírez-Castro[1,2], Estela Sandoval-Zapotitla[1], Isaura Rosas-Reinhold[1,2,3], Alma Piñeyro-Nelson[4,5], Salvador Arias[1]

[1]Instituto de Biología, Jardín Botánico, Universidad Nacional Autónoma de México, Ciudad de México, México. 2 Unidad de Posgrado, Circuito de Posgrados, Coyoacán, Ciudad de México, México. 3 Center for Genomics and Systems Biology, New York University, New York, USA. 4 Universidad Autónoma Metropolitana-Xochimilco, Ciudad de México, México. 5 Centro de Ciencias de la Complejidad, Universidad Nacional Autónoma de México, Ciudad de México, México.

Species of the Cactaceae family present adaptations related to their growth in environments under hydric stress. These adaptations have resulted in the reduction and modification of various structures such as leaves, stems, lateral branches, roots and the structuring of flowers in a so-called flower shoot or floral axis. Although the flowers and fruits of cacti have a consistent morphology, the developmental dynamics of the vegetative and reproductive tissues that comprise the reproductive unit have only been inferred through the analysis of the morpho-anatomy of the pre-anthetic buds. In this work we present a comparative analysis of flower development in two species with contrasting morphologies, *Disocactus speciosus* and *Disocactus eichlamii*. We also put forth a preliminary analysis of genes involved in the formation of the floral axis. The morpho-anatomical data show that within the areol, an apical meristem of the shoot begins to grow upward, producing lateral leaves with a spiral arrangement, quickly transitioning to a floral meristem. There is differential growth of the vegetative tissue, which covers the floral tissue and generates a graded transition between organs, as well as among internal tissues in both species. We also observed that different meristem sizes may be involved in the formation of these contrasting morphologies. Furthermore, analyzing transcriptomic data of these species, we found putative orthologous genes for*LEAFY* (*LFY*)*TERMINAL FLOWER 1* (*TFL1*), *APETALA 1* (*AP1*) and *CUP-SHAPED COTYLEDON 2* (*CUC2*). The expression dynamics of these genes during flower development could explain the formation of the floral axis. Here we present a first study that documents the first developmental stages of initial meristem determination, floral axis formation and the early differentiation of floral organs, as well as an orthology analysis of genes that could be involved in floral development in these species.

P.0445 Convergence and molecular evolution of floral scent after independent transition to selfing in the genus Capsella

Natalia Wozniak[1], Kevin Sartori[2], Christian Kappel[1], Lihua Zhao[2], Alexander Erban[3], Ines Fehrle[3], Friederike Jantzen[1], Stefanie Rosa[2], Michael Lenhard[1], Joachim Kopka[3], Adrien Sicard[2]

1 Institut für Biochemie und Biologie, Universität Potsdam, Potsdam-Golm, Germany. 2 Sverige Lantbruks Universitet, Uppsala, Sweden. 3 Max-Planck-Institut für Molekulare Pflanzenphysiologie, Potsdam, Germany.

A striking example of convergent evolution in the plant kingdom is the repeated mating system shift from cross-pollination to self-pollination. It is demonstrated that the breakdown of the self-incompatibility system triggers the relaxation of the selection on pollinator attractive traits, which induces a phenotypic transformation; the so-called "selfing syndrome". Self-pollinating species (hereinafter "selfers") have smaller and less showy reproductive organs, have smaller pollen-to-ovule ratios and produce less nectar than cross-pollinating species ("outcrossers"), while less is known about scent production. By comparing the volatile compound emissions of closely related outcrossers and selfers, we aim at identifying essential compounds for pollinator attraction that suffer relaxation of selection in the selfers. *Capsella* species represent ideal study models to address this phenomenon: the transition to selfing occurred at least two times independently through the breakdown of the self-incompatibility system of the outcrossing *C. grandiflora*-like ancestors. The two selfers, *C. rubella* and *C. orientalis* converged in the composition of scent, by a reduction of (E)-β-ocimene production. In-depth genetic analysis in *C. rubella* revealed that a point mutation, likely captured in the ancestral outcrosser population, caused a rechanneling of the *TERPENE SYNTHASE 2* out of the chloroplast to a different metabolic pathway. Interestingly, the gene was not under relaxation of selection in none of the species, likely due to its pleiotropy. This might explain why the observed phenotypic convergence does not echo a genetic convergence in the second selfer, *C. orientalis*.

P.0446 Identification of genes that regulate scent biosynthesis in Ophrys orchids

Chengwei Wang[1], Alessia Russo[1,2], Teresa Rosa Galise[3], Salvatore Cozzolino[3], Shuqing Xu[4], Philipp M. Schlüter[1]

1 Department of Plant Evolutionary Biology, Institute of Biology, University of Hohenheim, Germany. 2 Department of Plant and Microbial Biology, University of Zürich, Switzerland. 3 Department of Biology, University of Naples Federico II, Italy. 4 Institute for Evolutionary Plant Sciences, University of Mainz, Mainz, Germany.

The genus *Ophrys* is remarkable for its mimicry, with flowers closely resembling pollinator females in a species-specific manner. Floral traits, especially scent, are associated with pollinator attraction and are hence suitable models for investigating the molecular basis of adaptation to pollinators. *Ophrys sphegodes s.l.* employs a hydrocarbon profile in its scent, which is similar to that of pollinator females and is mainly composed of alkanes and alkenes. Genes encoding stearoyl-acyl carrier protein desaturases (*SAD*) are involved in alkene biosynthesis. We have identified *SAD1/2* and *SAD5/6* gene clusters in the *O. sphegodes* genome. Owing to the central role those *SAD* genes play in determining the positioning of the alkene double-bonds in *O. sphegodes*, a detailed characterization of their function and regulation is important for understanding the evolution of this specific pollination mechanism. The present study aims to investigate the regulation of gene expression of these *SAD* genes. By full-length RNA sequencing analyses combined with GC-MS, we have identified 5 transcription factors, which belong to the MYB, GTE, WRKY, and MADS families that are potentially related to *SAD* expression in *O. sphegodes*. GTE and WRKY candidate genes have been cloned and will allow the exploration of their DNA binding sites by DAP-Seq. Ultimately, our results will contribute to understanding the genetic bases of floral scent biosynthesis and specificity of pollinator attraction in *Ophrys* orchids.

P.0447 A novel, fast, efficient, and stable transformation method for Gorteria diffusa

Xiao Yu Wang[1], Udhaya Ponraj[1], Beverley J. Glover[1]

1 Department of Plant Sciences, University of Cambridge, UK.

Gorteria diffusa has emerged as a model species for studying plant evolution, flower development and insect pollination behaviour. Multiple distinct populations ("morphotypes") have evolved in a recent radiation, with remarkable diversity of floral morphology between populations, allowing studies of incipient speciation. Some populations attract pollinators through sexually deception, producing fly-mimicking complex petal spots. These structures present exciting opportunities to explore development of novel traits, and recent studies have shed light on likely genetic pathways which may have evolved through co-option of genetic elements involved in other developmental pathways. However, inability to manipulate gene expression within the species has so far limited functional analyses. In this study, we conducted Agrobacterium tumefaciens - mediated somatic embryogenesis (SE) transformations on G. diffusa, targeting the Springbok and Naries morphotypes. SE initiation was induced using 2,4-D on explants. Various growth regulators at different concentrations were tested across different growth stages for both morphotypes. Interestingly, cytokines and auxins elicited distinct responses in each *morphotype. Moreover, both morphotypes demonstrated modulation by multiple growth regulators, influencing SE and shoot promotion. This novel discovery highlights the critical roles played by multiple growth regulators in plant regeneration across developmental stages. Stable transformation was confirmed in the T1 generation through crosses between T0 transgenic plants and wild-type (WT). The differential responses of various morphotypes to different growth regulators are discussed in detail. This work pioneers a research method for studying gene function in G. diffusa and holds significant importance in understanding the evolution of complex petal morphologies.*

P.0448 The convergent evolution of re-differentiated perianth in Caryophyllineae

Yi Zhao[1], Sam F. Brockington[1], Beverley J. Glover[1]

1 Department of Plant Sciences, University of Cambridge, UK.

The perianth is one of the unique features of angiosperms, yet it is not conserved and has been lost and regained multiple times during angiosperm evolution. The perianth consists of whorls of modified sterile leaves that cover the fertile leaves (i.e., stamens and carpels) in angiosperm flowers, and which can be showy or protective. A plant can acquire whorl(s) of perianth by either sterilising the stamens from above or modifying vegetative leaves from below. The Caryophyllineae is a good clade for studying the re-differentiated perianth—the ancestor of the clade only had one whorl of protective perianth, while the descendants independently re-differentiated the perianth multiple times in various different ways, yet the details of which remain unclear. To better understand perianth evolution in Caryophyllineae and to provide foundations for future genetic studies on their perianth, I used scanning electron microscopy to study general floral morphology, inflorescence structures and floral developmental series of five representative species with undifferentiated or re-differentiated perianth across Caryophyllineae. Based on the results, I inferred some general perianth evolution models in the Caryophyllineae—When the showy perianth are from sterile stamens, the plant can either abort the anthers and elongate the filaments, or keep and expand the thecae of the anthers and shrink the filament. When the showy perianth are derived from bracts immediately below the stamens, the hyaline margins are often well expanded and coloured. When the protective perianth are derived from bracts below the bracts immediately below the stamens, the inflorescence structures are extensively modified, so that prophylls (i.e., a type of bract) that once belong to the central flower or other flowers in the inflorescence now become part of the perianth. This study provides a basis for future studies considering which developmental genetic changes may be involved in differentiating the perianth in the Caryophyllineae.

S.056. EVOLUTION OF KEY INNOVATIONS IN LAND PLANTS REVEALED THROUGH THE LENS OF EVODEVO

P.0450 Mechanical conflicts emerging at the inflorescence stem in Arabidopsis thaliana

Mariko Asaoka[1,2], Eric Badel[3], Olivier Hamant[2], Kazuhiko Nishitani[1]

1 Department of Biological Sciences, Faculty of Science, Kanagawa University, Yokohama, Japan. 2 Laboratoire de Reproduction et Développement des Plantes, Université de Lyon, ENS de Lyon, Lyon, France. 3 Université Clermont Auvergne, Clermont-Ferrand, France.

In plants, mechanical integrity of organs requires coordinated growth because cells remain contiguous through their walls. Recently, we demonstrated that stem integrity in *Arabidopsis thaliana* relies on three additive mechanical components: the epidermis that resists inner cell growth, cell proliferation in inner tissues, and growth heterogeneity associated with vascular bundle distribution in deep tissues. More specifically, we find that the unbalanced growth of stem organ in the *clavata3 de-etiolated3* mutant stretched epidermal cells, ultimately generating cracks in stems (**Maeda et al. 2014, Asaoka et al. 2021**). We also find another regulator of stem integrity, the transcription factor *INDETERMINATE DOMAIN9* (*IDD9*), which triggers stem cracking when expressed as a dominant repressor version (**Asaoka et al. 2023**). This work reveals how multifactorial stem integrity is. Yet, we are still lacking for a comprehensive understanding of this research field. Here, we present a new mutant line that displays stem cracking. Unlike the other lines mentioned above, this mutant showed no obvious defects on inner stem arrangement, except for thicker stem. We report the results of the analyses of mechanical properties and cell wall components of this line. **References: Maeda et al. 2014.** *Plant Cell Physiol.* **55**:1994-2007; **Asaoka et al. 2021** *Development* **148**: dev198028; **Asaoka et al. 2023** *Development* **150:** dev201156.

P.0451 Homeolog-aware genetic e Conservation and vulnerability of seagrass communities on the coast of the Gulf of Mexico.

Margarita E. Gallegos Martìnez[1], Sergio A. Fuentes Agueda[1], Gabriela Márquez Labastida[1], Francisco J. Ordoñez Gasca[1], Iliana Pérez Espinosa[2]

1 Universidad Autónoma Metropolitana-Iztapalapa México City, Mexico. 2 Comisión Nacional para el Conocimiento y Uso de la Biodiversidad México City, Mexico.

Seagrass communities are relevant for protecting the coastline and are important carbon sinks. Nowadays, they are experiencing a strong decline globally, due to global warming and anthropogenic changes. However, the current state and ecosystem services they provide in both tropical and temperate zones are unknown. The objective was to analyze the vulnerability of seagrasses with biotic and abiotic variables in the Gulf of Mexico. In 7 areas along 63 stations of The Gulf of Mexico, with an ecosounder BioSonics model DT-X, the relative coverage of Submerged Aquatic Vegetation was registered. Also, environmental parameters (temperature pH, depth, dissolved oxygen, salinity, nutrients in the water column, interstitial water, type of sediment, and organic carbon) and biotic parameters (Distribution and abundance (g/m2) of Submerged Aquatic Vegetation, phytoplankton, and epiphyte biomass) were registered at each site, the years 2016 and 2019 for each of the four months. The areas have significant differences in depth, salinity, and dissolved oxygen, which are related to the composition and abundance of the SAV. Area 4 (Dzilam de Bravo) has the highest biomass in SAV and the lowest is Area 2 (Champotón). Phytoplankton biomass was higher in Area 1 (Laguna de Terminos) and epiphyte biomass was higher in Area 2. Vulnerable seagrass communities are the ones that are less protected and have high anthropogenic activities like Area 2. The most abundant are communities in Area 3 (Petenes) and 4, which are related to conserved areas and have less anthropogenic impacts.

P.0452 The origin and early evolution of water transport in land plants

Alexander M. C. Bowles1

1 Department of Biology, University of Oxford, Oxford, UK.

Around 500 million years ago, the first plants moved from aquatic environments onto land, transforming the atmosphere and promoting the evolution of animals and fungi. The transport of water is a key innovation that enables plants to thrive in terrestrial habitats. Water availability is one of the most limiting factors to plant growth, with important implications for crop production and food security. Thus, understanding the evolutionary development of water transport tissues will not only inform us about the past, by revealing how the first land plants conquered terrestrial environments, but it will also aid us in the future, by shedding light on plant development and water transport mechanisms. A key unresolved question is whether water transport tissues in land plants evolved once, or on multiple occasions. I will address this question through a suite of interdisciplinary and complementary analyses of fossil collections, living taxa and omics data. Here, I present my fellowship research objectives and initial insights into the evolution of water conducting and vascular tissues in land plants. This work will transform our understanding of the morphological and genetic changes associated with the origin and early evolution of water transport in plants. Deciphering the origin and evolution of water transport will have profound implications for our understanding of the first land plants and their influence on the biosphere. Furthermore, greater insight into the evolutionary development of water transport will improve our understanding of adaptations to yield-limiting stressors (e.g., drought tolerance) in the descendants of the first land plants (e.g., crops).

P.0453 A fifth origin of dissected and pseudo-compound leaves in monocots: the remarkable leaf development of the genus Eriospermum

Samuel F. Brockington[1]

[1] Department of Plant Science, University of Cambridge, Cambridge, UK.

The leaves of monocots are typically simple and entire, and relative to eudicots, the occurrence of dissected to compound leaves is extremely rare. The classical perspective is that dissected leaves have arisen convergently four times in four orders, the Alismatales, Pandanales, Dioscoreales and Arecales. Independent evolutionary origins of leaf dissection are indicated by phylogenetic analyses and are reflected in the diversity of mechanisms employed during leaf development including blastozone fractionation, abscission-like leaflet separation and cell-death mediated perforation. Here we describe a fifth origin of pseudo-dissection and peudo-compound leaf development in the monocot geophyte genus Eriospermum, that has radiated within semi-arid areas in the Western Cape of South Africa. In contrast to previously described mechanisms in other origins, apparent leaf dissection in Eriospermum arises through the emergence of ectopic meristematic activity on the adaxial surface of the leaf to generate leaflets. In extreme cases the true leaf is reduced almost to a vestigial organ, and the leaflet enations then form the bulk of the photosynthetic lamina giving the appearance of a dissected leaf. In at least two species within Eriospermum, the enations have further fused to give the impression of a central rachis supporting leaflet like enations that strongly resemble a compound leaf (pseudo-compund). We will present the phylogenetic evidence for the evolution of this unusual leaf morphology coupled with developmental data that evidence ectopic adaxial blastozome activity and fusion as a novel developmental mechanism leading to the development of pseudo-compund leaves in monocots. We further explore the adaptive significance of this unusual evolutionary developmental trajectory for Eriospermum species in semi-arid habitats.

P.0454 The expression of KN1 orthologue in the shoot apical meristem of Commelina erecta L. (Commelinaceae)

Arthur K. Chan[1,*], Gladys F. A. Melo-de-Pinna[1]

*[1] São Paulo University, São Paulo, Brazil. *arthurchan@usp.br*

KNOX are a well-conserved family of genes expressed in the shoot apical meristem through angiosperms, regulating its indetermination and the formation of leaves. In addition, homologues of Class 1 *KNOX* genes also affect the shape of leaf margins in some eudicots, while in monocots, there have been evidences of its expression determining its fusion in sheathes. However, there haven't been studies focusing on its effect on families with closed sheath margins. One of them, Commelinaceae, is described as herbaceous monocotyledonous plants, with simple leaves with smooth margins, alternate phyllotaxy, no ligules and closed tube-like sheathes. As it's still unknown how these genes are expressed in the meristems of this family, the present study investigated the expression of orthologs of *KN1* genes at the leaf sheaths within *Commelina erecta* L. Samples of apical meristems from specimens of *C. erecta* were subjected to *in situ* hybridization in order to verify the expression of *KNOX* within its leaves, with the probe sequence established by degenerate RT-PCR based on conserved regions of *KN1* in species closer to *Commelina*. The sections of *C. erecta* reveal no expression of *KN1* at the region of the fused sheath margins, being only expressed at the apical and axillary meristems extending into the first internodes, but with a clear absence at the ring-shaped region of the disk of insertion from leaves. This result is therefore expected as the usual expression of the *KNOX* family is concerned. It contrast, however, with the current model for sheath fusion in Poaceae, where it is assumed that *KN1* orthologues are correlated with the lower sheath margins separation. The expression of *KN1* has been evaluated and described for *C. erecta*, being the first investigation of this gene within this family.

P.0456 Unearthing the diversity and evolution of phloem in ferns

Zishan Fu[1], Alexander J. Hetherington[1]

1 Institute of Molecular Plant Sciences, University of Edinburgh, United Kingdom.

Phloem is vital for vascular plants because of its fundamental role in transporting photosynthate and comprehensive roles in signalling. Despite its importance, the evolution of phloem remains poorly understood. This is because phloem structure is usually poorly preserved in fossils and little attention has been paid to characterising phloem structure across the full diversity of vascular plants including major groups such as ferns. This limits our ability to characterise the evolution of phloem over long periods of geological time. Therefore, my research aims to reconstruct the evolution of key phloem traits in ferns. Sieve elements (SEs), the conducting cells in the phloem, are central to this investigation. Utilizing histology and advanced microscopy techniques, I am examining the phloem structure in various extant and extinct fern species, allowing for the quantification of critical phloem traits, including SE size. Initial findings reveal notable intraspecific and interspecific variations in SE radius, with the latter displaying greater differences. A significant correlation between SE radius and petiole radius in extant ferns has been identified. Ancestral state reconstruction is applied to outline the trait evolution and to predict phloem structure in the common ancestor of ferns. Fossil data are then used to validate these predictions. By integrating information from both extant and extinct ferns, this research aims to quantify the evolutionary changes in key phloem traits over geological time and contribute valuable insights into the evolution of phloem in land plants.

P.0457 The genetic basis for natural variation in plant trichome density

Yumali Hewage[1], Andrew Hudson[1]

1 Institute of Molecular Plant Sciences, University of Edinburgh, Edinburgh, UK.

Most plant species have trichomes: epidermal hairs with diverse structures and roles in resistance to pests, UV radiation, or possibly drought. The genus *Antirrhinum* (snapdragons) provides a useful research system in which to identify and study the genetic basis of natural variation of trichomes because of its species differ for trichome morphology and possibility to cross and produce hybrids in which the genes underlying the differences can be mapped. The pattern of trichome distribution in the genus reflects activity of the trichome-suppressing *Hairy* gene. However, one species, *A. siculum*, appears to have a low density of leaf and stem trichomes because of variation in a second gene or genes. Near-isogenic lines have been obtained by back-crossing *A. siculum* x Hairy hybrids to either *A. siculum* or the hairy parent. Self-pollinated near-isogenic lines, segregated 1 densely hairy: 2 intermediate hairy: 1 bald plant, suggesting that baldness of *A. siculum* is determined by a single locus (*Bald*) with semi-dominant alleles. A duplication of chromosome 5 in the back-cross to *A. siculum* in both bald and hairy segregants prevented the accurate mapping of the bald gene. However, chromosome counts in the back-cross to the hairy parent, suggests no chromosome duplication in this line. Therefore, the *Bald* gene will be identified by resequencing pools of densely hairy or bald plants segregating for the *A. siculum* bald allele and the allele from the hairy parent. Its identity and function as a trichome promoter or repressor will be confirmed by reducing its expression with virus-induced gene silencing (ViGS). It will then be possible to find out whether mutations in the bald gene are responsible for differences in trichome density in other *Antirrhinum* species.

P.0458 The role of climate variation and genetic analysis in shaping sensitivity to vernalization

Masoumeh Khodaverdi[1], Jill Preston[1]

1 Department of Plant Biology, University of Vermont, Burlington, USA.

Flowering earlier in response to cold temperatures is referred to as vernalization. This trait has evolved several times independently across angiosperms to adapt the reproduction process of plants to relatively colder temperatures of temperate habitats in comparison to tropical regions, where many Pooideae (Poaceae) have originated from. Based on the previous studies, this process has evolved in the early divergent tribes of Pooideae, implying that vernalization is required for Meliaceae species. However, there is not enough data to conclude whether the underlying mechanisms for vernalization-induced flowering are different or similar at narrower levels (e.g., species-level) in Meliaceae species. To test the hypothesis that vernalization responsiveness has evolved in the early divergent tribes of Pooideae and test the genetic mechanisms of their early acquisition of cold, we conducted a series of experiments on 15 species from Melica L. (Meliceae) collected from broad climatic regions to study how flowering time changes in connection to a gradient of temperatures. In these experiments, we carefully measured the flowering time of different groups of plants that were exposed to various lengths of cold periods as an indication of their sensitivity to vernalization against the control group that experienced no cold period. We then quantified the association between their vernalization sensitivity and several environmental factors including latitude and bioclimatic variables. Our results demonstrated that vernalization-induced flowering time shows variability across Melica species and populations and that local adaptation plays an important role in this trait. Moreover, we studied the genetic basis of variation in vernalization sensitivity by choosing one sensitive population and one non-sensitive population to perform a comparative transcriptome analysis between three thermal conditions: after eight hours (cold shock), four weeks, and nine weeks of cold treatment at 6°C. Based on this analysis we found that differential gene expressions in the sensitive population are mostly distinct from those in the non-sensitive one, though there also existed a decent overlap.

P.0459 Size matters: revealing the genes controlling shot apical meristem gigantism in the Mexican cactus Mammillaria san-angelensis

Brenda A. López-Ruiz[1], Michael D. Purugganan[2], Ulises Rosas[1]

1 Jardín Botánico, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, México. 2 Center for Genomics and Systems Biology, Department of Biology, New York University, New York, USA.

The Cactaceae family has larger shoot apical meristems (SAMs) than other seed plants, such as *Arabidopsis thaliana*. Mechanisms involved in regulating SAM size in cacti may be similar to those found in model plants. Yet, larger SAM may be achieved by reconfiguring existing genetic elements, leading to novelties found in cacti. The *Mammillaria* genus is a good model system for studying SAM development due to its short life cycle, high diversity and ease of reproduction. We identified five developmental stages of *M. san-angelensis* plantlets and compared SAM size with adult plants using histological and microscopic electronic analysis. We also *de novo* sequenced the whole genome of *M. san-angelensis* using the PacBio long-read sequencing platform and identified two putative gene homologues that control SAM size: *WUSCHEL (WUS)* and *SHOOT MERISTEMLESS (STM)*. The *MsWUS* gene consists of 2409 nucleotides with three exons, two introns, and a putative protein of 273 amino acids. We found a high level of conservation at the nucleotide and amino acid level of the homeodomain, WUS-box, and EAR-like domains compared to *A. thaliana*. However, the acidic region showed less conservation as compared to the *A. thaliana* sequence but was highly conserved among several members of the Caryophyllales. Furthermore, bioinformatic analysis predicted an *MsSTM* gene double the size of the *A. thaliana* gene, with larger introns but high conservation of the KNOX1/2, homeodomains, and ELK domains. We are currently validating the coding sequence by sequencing these genes and performing expression analysis in the established developmental stages.

P.0460 Living xylem cells are origins of vascular sap peptide precursors

Min R. Lu[1†], Chia-Chun Tung[2], Chia-En Huang[3], Chang-Hung Chen[3,4], Pin-Chien Liou[3,4], Chan-Yi Ivy Lin[1], Jhong-He Yu[3], Ying-Lan Chen[4*], Ying-Chung Jimmy Lin[2,3], Isheng Jason Tsai[1]

1 Biodiversity Research Center, Academia Sinica, Taipei, Taiwan. 2 Department of Life Sciences, College of Life Science, National Taiwan University, Taipei, Taiwan. 3 Institute of Plant Biology, College of Life Science, National Taiwan University, Taipei, Taiwan. 4 Department of Biotechnology and Bio-industry Sciences, College of Bioscience and Bio-

technology, National Cheng Kung University, Tainan, Taiwan.

Signaling peptides have been considered as a type of plant hormone due to their crucial roles in regulating various developmental processes and physiological changes responding to environmental cues. Based on the traveling distance, the signaling peptides can be categorized into two groups: short-distance migrating peptides for cell-cell communications and long-distance migrating peptides for inter-organ/tissue signaling. Extensive knowledge has been revealed in the former, highlighting their roles in both apical and lateral plant growth. However, the origins and potential functions of long-distance migrating peptides remain to be fully elucidated. To investigate the origin of the long-distance migrating peptides, we carried out peptidomic analyses using LC-MS/MS on the vascular sap of Populus trichocarpa. Inference of ortho group with 14 representative species, we designated a total of 4,804 orthologs as sap peptide precursor genes. The transcriptome across multiple tissues showed that sap peptide precursor gene expression was higher in xylem-associated tissues compared to other tissues. This pattern was also observed in Eucalyptus grandis, Cinnamomum kanehirae, and Arabidopsis thaliana, pointing to the crucial role of the sap peptide precursor gene in plant vascular biology and evolution. By employing laser-capture microdissection, we further partitioned the xylem transcriptome across five developmental stages: one primary growth, two transition, and two secondary growth stages. The sap peptide precursor genes exhibited the highest gene expression in the first transition stage, contributing 41.05% of the entire transcriptome. A consistent pattern was also found inE. grandis, suggesting that the sap signaling peptides originated from sap precursor genes in the early stages of xylem development. Our study has revealed that the living xylem cells express sap peptide precursors, suggesting they act as command centres for coordinating communication across the plant.

P.0461 Complete organelle genomes of hemiparasitic genus Cymbaria (Orobanchaceae)

Yang Ma[1], Jordi López-Pujol[2,3], Dongqing Yan[1], Zhen Zhou[1], Zekun Deng[1], WenjianSong[1], HaoZeng[1], Jianming Niu[1, 4, 5]

1 School of Ecology and Environment, Inner Mongolia University, Hohhot, China. 2 Botanic Institute of Barcelona, CSIC-CMCNB, Barcelona, Spain. 3 Escuela de Ciencias Ambientales, Universidad Espíritu Santo, Samborondón, Ecuador. 4 Ministry of Education Key Laboratory of Ecology and Resource Use of the Mongolian Plateau, Hohhot, China. 5 Inner Mongolia Key Laboratory of Grassland Ecology and the Candidate State Key Laboratory of Ministry of Science and Technology, Hohhot, China.

The Orobanchaceae family is widely recognized as an exemplary model system for examining the evolutionary dynamics of parasitic plants. However, reports on the complete organelle genome of the hemiparasitic genus *Cymbaria* L. are currently lacking. In addition, the traditional Mongolian medicine, *C. daurica* L., namely “Xinba” in Chinese and “Kanba-Arong” in Mongolian, is frequently subjected to adulteration because of minor morphological differences with *C. mongolica* Maxim. In this study, we sequenced the organelle genomes of two ecologically and medicinally important *Cymbaria* species and performed comprehensive comparisons with the other Orobanchaceae species. We found that the *Cymbaria* chloroplast genomes were characterized by pseudogenization or loss of stress-relevant genes (*ndh*), genome size (150,488 bp on average) similar to autotrophs, and typical quadripartite structure with a unique inversion in the LSC region. In contrast, their mitochondrial genomes were characterized by gene content typical of flowering plants, larger genome size (1,558,151 bp on average), and pentacyclic structure. Further analyses of repetitive sequence, codon usage preference, RNA editing site, and selective pressure were conducted for both organelle genomes. Phylogenetic analyses yielded a well-supported phylogenetic tree for Orobanchaceae, where in two hemiparasitic *Cymbaria* species formed an independent sister clade to the remaining parasitic lineages. The diversification of this monophyletic genus occurred during the late Miocene (6.72 Mya) in the Mongol-Chinese steppe regions. Furthermore, there were minimal evidence of intracellular gene transfers (IGTs) and horizontal gene transfers (HGTs) although the mitochondrial plastid sequences (MTPTs) were identified in these mitogenomes. Notely, four pairs of specific DNA barcodes were developed and validated to distinguish the herb from its adulterants. Our findings provide valuable genetic resources for studying the phylogeny and evolution of Orobanchaceae and plant parasitism, and genetic tools to validate the authenticity of the traditional Mongolian medicine.

P.0462 Convergent evolution of plant prickles is driven by repeated gene co-option over deep time

James W. Satterlee[1,2], David Alonso[3], Pietro Gramazio[3], Katharine M. Jenike[4,5], Jia He[1,2], Andrea Arrones[3], Gloria Villanueva[3], Mariola Plazas[3], Srividya Ramakrishnan[4,5], Matthias Benoit[6], Iacopo Gentile[7], Anat Hendelman[1,2], Hagai Shohat[1], Blaine Fitzgerald[1,2], Gina M. Robitaille[1,2], Yumi Green[8], Kerry Swartwood[8], Michael J. Passalacqua[7], Edeline Gagnon[9,10], Rebecca Hilgenhof[10], Trevis D. Huggins[11], Georgia C. Eizenga[11], Amit Gur[12], Twan Rutten[13], Nils Stein[13,14], Shengrui Yao[15,16], Clement Bellot[17], Mohammed Bendahmane[17], Amy Frary[18], Sandra Knapp[19], Tiina Särkinen[10], Jesse Gillis[1,20], Joyce Van Eck[8,21], Michael C. Schatz[4,5], Yuval Eshed[22], Jaime Prohens[3], Santiago Vilanova[3], Zachary B. Lippman[1,2,7]

1 Cold Spring Harbor Laboratory, Cold Spring Harbor, USA. 2 Howard Hughes Medical Institute, Cold Spring Harbor Laboratory, Cold Spring Harbor, USA. 3 Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Valencia, Spain. 4 Department of Computer Science, Johns Hopkins University, Baltimore, USA. 5 Department of Genetic Medicine, Johns Hopkins University, Baltimore, USA. 6 French National Institute for Agriculture, Food, and Environment, Laboratory of Plant-Microbe Interactions, Toulouse, France. 7 School of Biological Sciences, Cold Spring Harbor Laboratory, Cold Spring Harbor, USA. 8 Boyce Thompson Institute, Ithaca, New York, USA. 9 Department of Integrative Biology, University of Guelph, Ontario, Canada. 10 Royal Botanic Garden Edinburgh, Edinburgh, UK. 11 USDA-ARS, Dale Bumpers National Rice Research Center, Stuttgart, USA. 12 Department of Vegetable Sciences, Agricultural Research Organization, Newe Ya'ar Research Center, Ramat Yishay, Israel. 13 Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany. 14 Crop Plant Genetics, Martin Luther University of Halle-Wittenberg, Halle (Saale), Germany. 15 Department of Plant and Environmental Sciences, New Mexico State University, Las Cruces, USA. 16 Sustainable Agriculture Sciences Center, New Mexico State University, Alcalde, USA. 17 Laboratoire Reproduction et Developpement des Plantes, INRAE, CNRS, Universite Lyon, Lyon, France. 18 Department of Biological Sciences, Mount Holyoke College, South Hadley, USA. 19 Natural History Museum, London, UK. 20 Physiology Department and Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto, Canada. 21 Plant Breeding and Genetics Section, Cornell University, Ithaca, USA. 22 Department of Plant and Environmental Sciences, The Weizmann Institute of Science, Rehovot, Israel.

An enduring question in evolutionary biology concerns the degree to which episodes of convergent trait evolution depend on the same genetic programs, particularly over long timescales. Here we genetically dissected repeated origins and losses of prickles, sharp epidermal projections, that convergently evolved in numerous plant lineages. Mutations in a cytokinin hormone biosynthetic gene caused at least 16 independent losses of prickles in eggplants and wild relatives in the genus *Solanum*. Strikingly, homologs promote prickle formation across angiosperms that collectively diverged over 150 million years ago. By developing new *Solanum* genetic systems, we leveraged this discovery to eliminate prickles in a wild species and an indigenously foraged berry. Our findings implicate a shared hormone-activation genetic program underlying evolutionarily widespread and recurrent instances of plant morphological innovation.

S.057. EVOLUTION OF PLANT SEXUAL REPRODUCTION

P.0463 Assessing fire regime effects on floral resources in Brazilian highland grasslands (Campo Rupestre)

Gudryan J. Baronio[1,2]; Vânia R. Pivello[1]

1 Departamento de Ecologia, Instituto de Biociências, Universidade de São Paulo (IB-USP), São Paulo, Brazil. 2 Evolutionary Fire Ecology Lab, Centro de Investigaciones sobre Desertificación (CSIC), Valencia, Spain.

Understanding the impacts of fire on floral resources is crucial for effective ecosystems' conservation and management. Our study aimed to assess the effects of fire on the quantity of floral resources in a Brazilian *Campo Rupestre* (Minas Gerais state) according to different burning regimes. We hypothesized that fire and post-fire vegetation regrowth would affect phenological patterns among plant communities, leading to increased floral resource availability in post-fire flowering events. From August 2021 to July 2022, we quantified bi-monthly the numbers of open flowers per plant and flowering individuals of twelve plant species, in plots burned in both the early and late dry seasons (respectively in May and September of 2019). These flowers provide a source of income for locals, who use them in handicrafts. We found significant variations in floral resource availability across different burning regimes, with late-fire plots showing higher post-fire floral resource abundance. In October 2021, *Vellozia* flowers were more abundant in late-burned plots compared to the early-burned ones, while *Comanthera aciphylla* showed higher flower abundance in late-burned areas in February 2022, indicating enhanced vegetation regrowth. Responses to fire varied among the studied species: *Xyris* species showed variable effects across species and months, *Vellozia* species exhibited different responses between burned and unburned plots, and the number of *Comanthera* species individuals correlated with burn timing. Overall, the late burning regime showed a positive effect on individual abundance across the studied plant genera, while the main effect of fire treatment (burned vs. unburned) was not significant. Establishing a late fire regime could mitigate reductions in floral resources and enhance plant reproductive success in the *Campo Rupestre*. This highlights the importance of carefully managing fire regimes to maintain ecosystem resilience.

P.0464 Plastid phylogenomic insights into the evolution of floral oil-producing species among Tigridieae (Iridaceae: Iridoideae)

Timothée Bastide[1], Xavier Aubriot[1] Olivier Chauveau[1]

1 Université Paris-Saclay, CNRS, AgroParisTech, IDEEV, Écologie Systématique et Évolution, Gif sur Yvette, France.

Floral oils are the third type of reward collected by pollinators in Iridaceae, besides pollen and nectar. Among species of Tigridieae (Iridoideae), this uncommon pollination resource is secreted by trichomal glandular structures, called elaiophores. Previous studies suggested that elaiophores may have played a significant role in the diversification of Iridaceae, especially in the American tribe of Tigridieae where they evolved several times independently. Phylogenies of Tigridieae published to date have shown that three major Tigridieae genera (i.e., *Calydorea*, *Cypella*, *Herbertia*) are probably not monophyletic, but various crucial nodes were weakly supported. Therefore, the current study aimed to provide a deeper comprehensive understanding of the phylogenetic relationships in this clade and the resulting framework was used to infer the evolutionary history of elaiophores. Mainly based on new genomic data, we performed the first comprehensive phylogenomic analysis of *Cypella* and closely allied genera from an expanded set of specimens. The phylogenetic analyses were conducted with maximum likelihood and Bayesian inference methods. Ancestral states inference methods were applied to trace the evolutionary history of floral secretory structures. With strongly supported nodes, the phylogeny obtained is consistent with previous studies and confirmed that the three genera *Cypella*, *Calydorea* and *Herbertia* are clearly not monophyletic. This result suggested that the floral characters used so far to define genera of Tigridieae are probably homoplastic. Then, a taxonomical revision of *Cypella* and closely allied genera is necessary. The reconstruction of the evolutionary history of floral glandular structures in this robust phylogenetic context has also shed light on how they evolved within this clade of Tigridieae.

P.0465 Floral ontogeny of a cryptically dioecious Protium heptaphyllum (Burseraceae)

Silva, Débora C.[1], Paulino, Juliana V.[2], Sakuragui, Cássia M.[2]

1 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Universidade Federal do Rio Janeiro, Rio de Janeiro, Brazil.

Protium heptaphyllum (Aubl.) Marchand, commonly known as “breu branco” or “amescla,” occurs in the Amazon and Atlantic Forest biomes in Brazil. The genus *Protium* exhibits intriguing floral characteristics, such as merism lability and cryptic dioecy, with non-functional organs ranging from reduced to vestigial. In this context, *P. heptaphyllum* stands out with nectariferous, honey-bearing, tetramerous, cryptically dioecious, and yellow flowers. The pistillate flowers have staminodes below the height of the pistil, while the staminate flowers exhibit the pistillode below the height of the stamens. Hence, the objective of this study is to elucidate floral development, with a particular focus on the ontogenetic pathways leading to staminate flower development in *P. heptaphyllum*. For that, flowers and floral buds at various developmental stages were collected and fixed in FAA70 and prepared for observation under scanning electron microscopy (SEM). The inflorescence emerges from the axil of a bract. The whorls develop in acropetal order in the floral meristem, following this sequence: primordia of sepals, petals, antesepalous stamens, antepetalous stamens, and the carpel primordia at the center of the floral apex. During the intermediate developmental stage, the petals elongate, surpassing the sepals, assuming the role of protective whorl for the reproductive organs. Papillae are formed in the petals' apical region of the petals, intertwining to aid in corolla closure. Following anther differentiation, the filaments of antesepalous stamens elongate, followed by the elongation of antepetalous ones. With the elongation, the androecium surpasses the pistillode in height, which remains with the carpel clefts open, showing little differentiation of style and stigma. These preliminary findings are significant, and further exploration promises a more comprehensive understanding of complex floral structures, including dioecy, which can influence pollination processes within the group. Advancements in research outcomes will facilitate robust ontogenetic inferences, enriching our understanding of floral evolution in the genus *Protium*.

P.0466 Unravelling evolutionary history of Cypella and closely allied genera of Tigridieae (Iridaceae: Iridoideae) with a focus on floral resources

Julia Gabriele Dani[1], Verônica Thode[1], Olivier Chauveau[2], Tatiana Teixeira de Souza Chies[1]

1 Programa de Pós-Graduação em Botânica da Universidade Federal do Rio Grande do Sul. Brazil. 2 Unité Écologie, Systématique et Évolution Université Paris-Saclay, Gif-sur-Yvette, France.

Floral resources play an important role in the diversification of the family Iridaceae. Predominantly composed of South American species, the genus *Cypella* and closely allied genera of the tribe Tigridieae offer diverse floral resources, including floral oil. Floral oil, a specialized reward, typically secreted by glandular trichomes known as elaiophores. This attribute, present in various genera, may have had a significant effect on evolutionary processes. We aim to test elaiophore presence's link to diversification rate shifts among lineages. To achieve this aim, we reconstructed a well-sampled dated phylogenetic tree and diversification analyses were undertaken. Nine DNA sequence regions, three nuclear (ITS, *rpb2* and *At*103) and six plastidial (*trn*H-*psb*A, *trn*Q-*rps*16, *mat*K, *rbc*L, *rps*4 and *rps4-trn-S*), were used. Sampling includes new sequences for 32 species and 29 other sequences were obtained from NCBI representing 61 taxa (seven outgroups). Alignments were in MAFFT 7 with manual adjustments. To estimate divergence times, a relaxed Bayesian clock with secondary calibrations was used. For phylogenetic inference and divergence time estimation we used BEAST 2.6 with the stationarity checked in Tracer 1.7. Analysis of diversification is still in progress. Our preliminary results showed a well-supported dating tree (branches value (1)) with six main clades. High levels of species diversity are related to recent origin (Pliocene–Pleistocene). During the Miocene, floral-oil taxa grouped into two clades, one exclusively with such taxa and another including species lacking oil-flowers. In other clades, most taxa lack floral oil, with isolated cases suggesting evolutionary reversions throughout the group's history. Biogeographic patterns were observed, with groupings of South American species. Some genera, like *Calydorea*, were not monophyletic even with the comprehensive sampling used. This result aligns with previous studies and suggests that *Cypella* and closely allied genera require taxonomic revision.

P.0467 Phylogenetic position and sex expression of the first known Neotropical Monimiaceae paradioecious species

Elton J. de Lírio [1,3], Heloisa Alves de Lima [2], Ariane Luna Peixoto [3], Marc Pignal [4], Vitor Hugo dos Santos Gomes Maia [5], Gabriel Silva Santos [6], Cassia Mônica Sakuragui [2,3]

1 Universidade de São Paulo, São Paulo, Brazil. 2 Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil. 3 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 4 Muséum national d'Histoire naturelle, Paris, France. 5 Pontifícia Universidade Católica, Rio de Janeiro, Brazil. 6 Instituto Nacional da Mata Atlântica, Espírito Santo, Brazil.

Monimiaceae encompasses three subfamilies: the first diverging lineage, Monimioideae (dioecious spp.), is the sister group of Hortonioideae (hermaphrodite) and Mollinedioieae (dioecious, monoecious, and gynodioecious spp.). Mollinedia (tribe Mollinedieae, Mollinedioieae) is a Neotropical genus with ca. 60 dioecious species. Although, some specimens of *Mollinedia sphaerantha* Perkins from the Espírito Santo state, Brazil, caught our attention due to the presence of pistillate and staminate flowers in the same individual (cosexuality). This rarity led us to investigate its frequency in fieldwork during three flowering seasons (n= 58). We also positioned the species in a phylogenetic tree using ITS1 + 5.8S + ITS2, *psbA-trnH*, *trnL* intron, and *trnL-trnF* through Bayesian Inference (BI) and Maximum Likelihood (ML) analyses. The ingroup included 13 species of the Neotropical Mollinedieae clade, and the outgroup was based on Renner et al. (2010). The studied subpopulation revealed 21% of cosexuality, even within a single flowering season. Across the three seasons, 46.5% presented only staminate flowers, 22.4% only pistillate, and 17.2% were exclusively cosexual. During the three observed blooms, *M. sphaerantha* presented 62 unisexual events and 16 cosexual events leading to its categorization as paradioecious due to sex inconstancy. In the BI, *M. sphaerantha* was recovered among other Neotropical Mollinedieae species in a polytomy with *Mollinedia uleana* Perkins and *Mollinedia glabra* (Spreng.) Perkins, both from Brazil. In ML, the species is the sister group of *Mollinedia uleana* Perkins, and this clade is a sister group of M. glabra. The present study raises new questions about the sexual system pathways in Monimiaceae.

References: Renner SS, Strijk JS, Strasberg D, Thébaud C. 2010. Biogeography of the Monimiaceae (Laurales): A role for East Gondwana and long distance dispersal, but not West Gondwana. Journal of Biogeography 37: 1227–1238.

P.0468 Influence of the herkogamy in the breeding system in two subspecies of Centaurium quadrifolium (L.) G.López & C.E.Jarvis

Zoila Díaz Lifante[1], Vania Jiménez Lobato[2], Cristina Andrés Camacho[1], Alejandra de Castro[1], Marta Franco[1], Juan Arroyo[1]

1 University of Seville, Seville, Spain. 2 Autonomous University of Guerrero, Guerrero, Mexico.

The reproductive biology of the Iberian endemic *Centaurium quadrifolium* (Gentianaceae) is investigated for subsp. *quadrifolium* and subsp. *barrelieri*. The effect of the pollen kind, self or cross pollen, on the degree of fertilization was analyzed through experimental crosses in plants collected in natural populations, grown in a greenhouse. A very low seed set was found after self-pollinations, pointing out a self-incompatible breeding system. The degree of floral herkogamy and its evolution throughout the flower life-span was analyzed through a morphometric analysis of several morphological traits (corolla, androecium and style-stigma set) in the natural populations, finding traits of high diagnostic value. Likewise, the analysis of the difference in floral traits between the two groups of plants, pre-assigned in the field as morphotypes "with herkogamy" and "without herkogamy", demonstrated that herkogamy is stronger in subsp. *barrelieri* than in subsp. *quadrifolium*, whereas in this last scarce morphological differentiation was found between both morphotypes. The analysis of the effect of herkogamy on the degree of fertilization in the natural environment in both subspecies indicates that open cross-pollination is more effective when there is herkogamy. The subsp. *quadrifolium* achieved higher fertilization rates than subsp. *barrelieri*. On the other hand, the high variation found in fruiting within individuals in both subspecies seems to indicate that the influence of herkogamy on pollen limitation, the reproductive guarantee and the pollinator failure are not very relevant. The results obtained in natural conditions confirm those obtained in the greenhouse in terms of the rates obtained for each fertilization treatment, as well as the existence of a strong degree of self-incompatibility and the need for an animal pollinator vector for sexual reproduction. There are clear differences between both subspecies, being found in subsp. *barrelieri* a greater dependence on the pollinator for fertilization than in subsp. *quadrifolium*.

P.0469 Different post-pollination response to heterospecific pollen among populations and the contribution of female and male functions

Yusuke Hoshino[1], Sachiko Horie[1], Masayuki Maki[1], Ikumi Dohzono[2]

1 Botanical Gardens, Tohoku University, Sendai, Japan. 2 Department of Environmental Sciences, Tokyo Gakugei University, Tokyo, Japan.

Heterospecific pollen (HP) deposition can negatively affect plant reproduction by usurping ovules and interfering with conspecific pollen (CP) germination and CP tube growth. It has been reported that a history of coexistence with congeners may favor selection for high tolerance to negative HP effects. However, it is not well understood whether male gametophyte (pollen) or female sporophyte (stigma and pistil) plays a critical role in mitigating the negative effects of HP. Hence, we tested whether *Oxalis corniculata* (Oxalidaceae), a native weed in Japan in sympatric population with the alien *O. dillenii*, limits the effects of HP on conspecific mating. Conspecific and heterospecific pollinations were performed on *O. corniculata* from two population types (sympatric and allopatric populations), and the result revealed consistently lower seed production in heterospecific pollination across population types. However, the significant interaction effect between pollination treatment and population type indicates that female function more in sympatric populations than in allopatric populations to effectively suppressed hybrid seed formation. Mixed pollination using both conspecific and heterospecific pollen grains was also performed to assess the effects of HP on conspecific seed production. Contrary to our hypothesis, conspecific seed production decreased in the mixed pollination compared to the conspecific pollination in two of the three sympatric populations; on the contrary, HP did not affect the conspecific seed production in allopatric populations. These trends were consistent even in another mixed pollination experiments using the CP source of a population type different from the maternal origin. Thus, individuals in allopatric populations are tolerant to HP, and female function may play a crucial role in this HP tolerance. We are currently conducting experiments on pollen tube elongation to investigate how HP affects conspecific mating and investigating the ecological significance of reduced conspecific seed production by HP in sympatric populations compared to allopatric population.

P.0470 Evolution and diversification of the NADPH oxidase family in plants

Julian Ingelfinger[1], Lisa Zander[2], Finja A. Bohle[1,2], Andreas J. Meyer[2], Stefanie J. Müller-Schüssele[1]

1 Department of Biology, Molecular Botany, TU Kaiserslautern, Kaiserslautern, Germany. 2 INRES - Chemical Signalling, Faculty of Agriculture, University of Bonn, Bonn, Germany.

Reactive oxygen species (ROS) and redox signalling are evolutionary old and likely predated the origin of land plants. To specifically produce superoxide, plants possess enzymes of the NADPH-oxidase family, the respiratory burst oxidase homologs (RBOH). RBOHs are transmembrane enzymes that transfer electrons from NADPH across the plasma membrane to oxygen, producing superoxide in the apoplast. Apoplastic ROS are important for plant development, sexual reproduction as well as stress responses. During land plant evolution the RBOH family evolved several isoforms with neo- and sub-functionalisation. However, it is yet unknown which RBOH-dependent ROS functions are ancestral. We investigate the role of the four RBOH isoforms of the model moss *Physcomitrium patens*. To monitor the balance between ROS generation and detoxification *in vivo*, we use redox sensitive GFP-based biosensors (roGFP2).

P.0471 Herkogamy, a key factor in mating system of Centaurium (Gentianaceae) species

Vania Jiménez Lobato[1], Marcial Escudero[2], Alejandra de Castro[2], Zoila Díaz Lifante[2], Cristina Andrés Camacho[2], Alegría Montero Ramírez[2], Juan Arroyo[2]

1 Autonomous University of Guerrero-LANASE-CONAHCYT, Guerrero, Mexico. 2 University of Seville, Seville, Spain.

In plants, mating system can vary within and among populations and species. Herkogamy, the separation between anthers and stigma within flowers, is one of the factors that may affect mating system preventing or promoting the capacity of self-fertilization of individuals and interfering the outcrossing capacity. Higher herkogamy is expected to be selected in those places where a proper pollinator activity for plant reproduction occurs. Hence, herkogamy is generally associated with high outcrossing rates, while its absence may generate high selfing rates of individuals. In heterogeneous pollinator environments, herkogamous and non-herkogamous individuals may coexist and be selected in different years, generating mixed mating systems in populations. We investigated if these patterns occur within natural populations of three species of *Centaurium*, a genus presenting lateral herkogamy that decrease at the end of the flower´s lifespan. We characterized 15 herkogamous and 15 non-herkogamous individuals within one population of each species and associated them with outcrossing rates obtained by microsatellite markers. Further, we registered pollinator visitation rates in each group of individuals. We find that in *C. triphyllum*, natural selection has not favored any level of herkogamy within the population, which was associated, as expected, with high selfing rates and poor pollinator visitors. In contrast, in *C. barrelieri and C. boissieri*, both with variation in herkogamy levels, show variable and high outcrossing rates associated with high pollinators visits. These results suggest that herkogamy play a key factor in determining mating system in all three species of *Centaurium,* mainly in *C. barrelieri and C. boissieri* during the first days of flower life, when pollinators can promote cross pollination and outcrossing. However, when pollinators are abundant, it seems that the role of herkogamy is not so relevant as other traits associated to attraction to pollinators could be more critical.

P.0472 Chronological transcriptome reveals the common program for gynoecium development in eudicots

Doudou Kong[1], Le-Han Nguyen[1], Annette Becker[1]

1 Institute of Botany, Justus-Liebig-Universität Gießen, Gießen, Germany.

The growth and development of gynoecium are crucial components of the reproductive process in flowering plants. The diversity of gynoecium and floral architecture among different plant species is a significant aspect of plant evolution. Although many of the regulatory genes involved in gynoecium have been characterized, we know little about the changes in GRNs that are involved in the dynamic development of gynoecium at high resolution. California poppy (*Eschscholzia californica*), a member of Ranunculales, which is a sister lineage to all other eudicots. Here, we present high-resolution profiles of a range of expression dynamics from the floral meristem (FM) to the gynoecium in California poppy obtained by laser microdissection and analyzed a large set of regulatory factors by gene co-expression clustering. This includes, but is not limited to, YABBYs, MADS transcription factors, and ARFs that are differentially expressed at early and late stages of morphogenesis, and some of them have been shown to play important roles in floral meristem determinacy, such as EscaLFY. We further compared the dynamic transcriptome clustering of gynoecium in California poppy (dried dehiscent fruits) with Arabidopsis (dried dehiscent fruits) and tomato (fleshy fruits). We characterized the expression trends of a range of homeotic genes during gynoecium development and described the conservation of GRNs in fruit morphogenesis after 127 Mya of independent evolution.

P.0473 Trade-offs in sex allocation revealed by transitions between combined and separate sexes under experimental evolution

Ehouarn Le Faou[1], John R. Pannell[1]

1 Department of Ecology and Evolution, University of Lausanne, Switzerland.

Theory for the evolution of sex allocation predicts the conditions under which sexual systems are stable or subject to change. This theory is based on the fundamental assumption of antagonistic expression of male and female functions (a trade-off) and the heritability of sex allocation. However, quantifying the phenotypic or genetic trade-offs between male and female functions has proved difficult. Here, we outline our strategy for analysing the evolution of sex allocation by the plant *Mercurialis annua* under strong selection for a transition from dioecy to monoecy. Our results demonstrate a clear linear trade-off between male and female functions, the shape of which is constant from one generation to the next, so that it is possible estimate sex allocation by calibration one sex on the the other. We highlight the utility of a quantitative genetic approach to expose (1) the antagonism of sexual functions through their strong negative additive genetic correlation and (2) the high heritability of sex allocation in the *M. annua* population studied. Our study paves the way for an analysis of the link between allocation and reproductive success - the key link required to test predictions of theories of sex allocation.

P.0474 Implication of the population epigenomic diversity on the adaptation of a plant clonal species

Le Veve Audrey[1], Sammarco Iris[1], Lafon-Placette Clément[1]

1 Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic.

Climate change poses a significant threat to plant species, potentially pushing them beyond their adaptive capacities. Epigenetic modifications, such as DNA methylation, have emerged as a key mechanism enabling plants to quickly adapt to environmental changes by generating locally adapted phenotypes. These phenotypic changes can be even inherited across multiple generations, thus potentially becoming targets of natural selection. However, whether natural selection can act on these epialleles has hardly been tested directly. Addressing this knowledge gap is crucial as population survival may heavily rely on DNA methylation, especially in populations with restricted genetic diversity, such as within clonal plant species. We compared the genomic and epigenomic diversity from seven natural populations of four individuals of the clonal species woodland strawberry (*Fragaria vesca*). We distinguised the epigenomse on the three methylation contexts (CG, CHG, CHH). Specifically, we investigated the effect of the wide altitudinal range on the diversity of these epigenomes and of the genome. Moreover, we studied the heritability of the epigenetic diversity across clonal generation in new environment in low altitude. Our analyses found a wide intra- and interpopulation epigenetic diversity despite a considerably low genetic diversity. We identified heritable epialleles exhibiting signs of positive selection associated with altitude in the CG, CHG and CHH contexts. Interestingly, some of these epialleles were independent of genetic variation, suggesting they may have arisen stochastically or in response to environmental variation. These findings hint at the role of epigenetic variation in facilitating rapid adaptation to varying environment in the face of reduced genetic diversity, as in clonal species.

P.0475 The genetic basis of the evolution of self-compatibility in wild Petunia axillaris

Hiromu Nakao[1], Syo Ikeyatsu[1], Kazuho Isono[1], Yu Okamura[1], Ken-Ichi Kubo[2], Sota Fujii[3], Kenta Shirasawa[4], Hitoshi Watanabe[5], Koichi Uehara[6], Takashi Tsuchimatsu[1]

1 School of Science, The University of Tokyo, Tokyo, Japan. 2 Nagahama Institute of Bio-Science and Technology, Shiga, Japan. 3 School of Agricultural and Life Science, The University of Tokyo, Tokyo, Japan. 4 Kazusa DNA Research Institute, Chiba, Japan. 5 Center for Environment, Health and Field Sciences, Chiba University, Chiba Japan. 6 College of Liberal Arts and Science, Chiba University, Chiba, Japan.

The evolutionary transitions from obligate outcrossing to predominant selfing through the loss of self-incompatibility (SI) have been considered one of the most prevalent events in angiosperms. Although selfing often leads to inbreeding depression, selfing can also be advantageous due to the inherent transmission advantage and reproductive assurance. The genetic basis of loss of SI and the evolution of selfing have been a major focus of plant evolutionary biology for decades. The S-RNase-based gametophytic SI system is widely reported across angiosperms, including Solanaceae, Rosaceae, and Rubiaceae. This system consists of the female specificity gene encoding the S-ribonuclease (S-RNase) and tandemly duplicated multiple male specificity *S-locus F-box* genes (*SLF*s), which are tightly linked at the *S*-locus. In the SI system of Solanaceae, the 'collaborative non-self-recognition' model has been proposed, which postulates that SLFs are involved in specific recognitions and degradations of non-self S-RNase protein leading to successful outcrossing. To investigate how predominant selfing evolved under this SI system, we focused on wild strains of *Petunia axillaris*, where both self-compatible (SC) and self-incompatible (SI) populations have been reported. We have identified notable genetic changes between SC and SI strains through the integration of population genomics, crossing experiments and whole genome sequencing analyses, and discuss how selfing populations originated.

P.0476 The maintenance of females, males and hermaphrodites in metapopulations

Mai Thu Nguyen[1], John R. Pannell[1]

1 Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland.

The co-existence of females, males and hermaphroditism (trioecy) is rare in both plants and animals, and the few cases that do exist are poorly understood. A previous model showed that trioecy can be stable following the invasion of a cytoplasmic male sterility (CMS) mutation in a large population of males and hermaphrodites, but only under restricted conditions. Here, I present the results of stochastic computer simulations to ask whether the additional selective forces in a metapopulation in which colonization balances extinction (the advantage of colonization to self-fertile hermaphrodites and frequency-dependent selection on sex allocation within populations) can further help to explain the maintenance of trioecy. Results indicate that the conditions for the maintenance of trioecy are further restricted by population turnover in a metapopulation, but they depend on several acting parameters, particularly the number of founders. I will discuss the results of the model with reference to what is known about trioecy in a well-studied plant metapopulation.

P.0477 Reproductive interference between a periodical mass-flowering plant and an annual-flowering plant of Strobilanthes

Sachiko Nishida[1], Akiyo Naiki[2], Satoshi Kakishima[3]

1 Nagoya University, Nagoya, Japan. 2 University of the Ryukyu, Yaeyama, Japan. 3 Showa University, Fujiyoshida, Japan.

Reproductive interference, an interspecific interaction associated with mating systems that adversely affects the fitness of the recipient species, has an aspect of positive frequency dependence and exerts stronger effects when the recipient is in the minority. To clarify how this aspect is involved in a mass-flowering phenomenon, we studied the interaction between two species of *Strobilanthes*. *Strobilanthes flexicaulis* is a monocarpic perennial plant with mass-flowering on Okinawa Island, Japan, whereas in other regions it is polycarpic or monocarpic with no mass-flowering. A closely related species, *S. tashiroi*, is a polycarpic perennial with annual-flowering and co-occurs with *S. flexicaulis* only on Okinawa Island. We hypothesized that mass-flowering would increase the frequency of *S. flexicaulis* flowers and reduce the negative effects of reproductive interference from *S. tashiroi.* To test this hypothesis, we carried out artificial pollination between the two species and examined the negative effect of counterpart species pollen on the seed set of the focal species. The results showed that the negative effect of counterpart species pollen was sometimes recognized in *S. flexicaulis*, depending on the population and year, whereas it was always recognized in *S. tashiroi.* These results suggest that reproductive interference is bidirectional, but stronger from *S. flexicaulis* to *S. tashiroi* than vice versa. It is likely that reproductive interference from *S. tashiroi* is only partly responsible for the mass-flowering of *S. flexicaulis*, whereas reproductive interference from *S. flexicaulis* was enhanced by the mass-flowering phenomenon and reduced *S. tashiroi* offspring in the regions where the two species were co-occurring.

P.0478 Evolutionary trends in Croton flowers: reduced petals become colleters in Croton splendidus (Euphorbiaceae)

Narah C. Vitarelli[1], Anna Luiza P. Lima[1], Mariana de O. Miquilini[1], Maria Eduarda G. Heleno[1], José Danizete B. Miranda[2], Renata M. S. A. Meira[2], Ricarda Riina[3]

1 Instituto Federal de Educação, Ciência e Tecnologia do Sudeste de Minas Gerais, Departamento de Educação e Ciências, Núcleo de Biologia, Campus Juiz de Fora, Juiz de Fora, Brazil. 2 Universidade Federal de Viçosa, Departamento de Biologia Vegetal, Laboratório de Anatomia Vegetal, Campus Universitário, Viçosa, Brazil. 3 Real Jardín Botánico, CSIC, Madrid, Spain.

The presence of petals is generally an uncommon character in the Euphorbiaceae. *Croton* (~1,300 spp.) bears unisexual flowers, with staminate flowers having a complete whorl and most pistillate flowers lacking or having reduced petals. Understanding petal development in *Croton* pistillate flowers is still an open question. The genus is rich in secretory structures, but these have mostly been studied in vegetative organs. Here we present an anatomical study of *Croton splendidus*, a species with reduced petals in pistillate flowers, by analyzing floral buds in different stages of development and anthesis. We use light and scanning electron microscopy. We provide a detailed anatomical description of pistillate flowers and highlight that this species presents 5 reduced and unequal petals, showing strong different morphologies. At least 2 petals are even more reduced and developed as specialized secretory structures, presenting a colleter in the apex. Standard colleters type remain functional from flower to unripe fruit. The secretion is produced by the palisade epidermal cells and excreted into the subcuticular space culminating in the rupture of the cuticle and subsequent of the exudation. Previous studies have used the term filamentous structure to name such colleters, which has led to misinterpretations. We suggest avoiding this term and giving a useful name to this floral whorl. In the case of *C. splendidus* it corresponds to a reduced petal with an apical colleter. We hypothesize that *C. splendidus* petals have a tepalar origin, since the flower bud bracts, sepals and petals show a very similar anatomical structure. This similarity is maintained in petals and bracts of pistillate flowers until anthesis, while sepals become more conspicuous during development and during anthesis showing an anatomical structure that resembles the leaf anatomy.

P.0479 A genetic basis of Baker's law: lessons from self-compatible Lycium sandwicense (Solanaceae) in Japanese oceanic islands

Hidenori Sassa [1], Kota Ikebe[1], Koichiro Ushijima[2], Mai Minamikawa[1, 3]

1 Graduate School of Horticulture, Chiba University, Matsudo, Japan. 2 Graduate School of Environmental and Life Science, Okayama University, Okayama, Japan. 3 Institute for Advanced Academic Research, Chiba University, Chiba, Japan.

Diversity in reproductive strategies, such as selfing or out-crossing, is associated with the evolutionary history of the species. Environmental changes promote the shifting of mating systems. Diploid species of *Lycium* (Solanaceae) are generally self-incompatible (SI) while *L. sandwicense*, which is distributed in oceanic islands and is thought to be colonized after long-distance dispersal from mainland America, exhibits self-compatibility (SC). This is in agreement with Baker's law which suggests that successful colonization after long-distance dispersal is often associated with uniparental reproduction, however, little is known about the genetic mechanisms underlying the shift from out-crossing to selfing. We analyzed the cause of SC of *L. sandwicense* in Japanese oceanic islands; Ogasawara Islands, Kitadaito Island and Minamidaito Island. Full length cDNAs for the *S-RNases* were isolated by RACE. Sequence analysis suggested that they encode functional S-RNase proteins, and all the analyzed plants exhibit almost the same *S* genotype except for a SNP. Further genetic and genomic analyses showed that mutation of the *S* locus that would affect the pollen-part SI function would be the cause of SC of *L. sandwicense*, representing a genetic basis of Baker's law.

P.0480 Establishing CRISPR-Cas9-mediated mutagenesis for Ceratopteris richardii to investigate the role of MADS-box genes in ferns

Robin Schulz[1], Günter Theißen[1]

1 Matthias Schleiden Institute of Genetics, Bioinformatics and Molecular Botany, Friedrich Schiller University Jena, Jena, Germany.

The origin of the seed habit is one of the major events in plant evolution as it allowed sexual reproduction in the absence of external free water. Hence, seeds allow plants to colonize habitats that are not accessible for plants reproducing by spores. The genetic basis for the origin of the seed, however, is largely unknown. Recently, there have been great technological advances and newly sparked scientific interests in the developmental genetics of the closest relatives of seed plants, ferns and their allies. This has led to the publication of multiple fully sequenced genomes of ferns, including *Ceratopteris richardii*, and the development of transformation protocols. This will potentially allow comparison of the genetic programs of spore development in ferns and seed development in seed plants to elucidate the genetic basis for the origin of the seed habit. Here, we show the establishment of a transgenic line of *C. richardii* that expresses the endonuclease Cas9. Cas9 is expressed under a strong constitutive promoter. This line can further be transformed with vectors expressing a single guide RNA for CRISPR-Cas9-mediated mutagenesis of *C. richardii*. The first application would be to characterize knock-out plants of close relatives of those MIKC^{C}-type MADS-box genes which are known to control seed development in flowering plants to reveal more about their function in non-seed plants. Our line allows easy-to-use, flexible, and fast gene editing of *C. richardii* for future experiments, whether it would be single mutation or multiplexing.

P.0481 Elucidation of the reproductive isolation mechanism of bryophytes through the artificial fertilization experiments

Masaki Shimamura[1], Yuka Ishii[1]

1 Graduate School of Integrated Sciences for Life, Hiroshima University, Hiroshima, Japan.

Although closely related species of bryophytes often grow sympatrically and have overlapping periods of sexual reproduction season, there is no detailed cell biological information on the mechanisms of reproductive isolation between these species. In order to elucidate the basic mechanism of reproductive isolation that exists between the different species of bryophytes, we conducted artificial crossing experiments between the closely related dioecious liverworts, *Marchantia polymorpha* and *M. paleacea*. Although hybrid sporophytes were not formed between these species, it was clarified that the sperms are also attracted to archegonia of another species and enter the interior of archegonia. The crossing experiments between *M. polymorpha* males and *M. paleacea* females even showed sperm penetration into the egg cell. However, karyogamy between sperm and egg nuclei occurred only between the same species. These findings suggest that there is no strong pre-fertilization isolation mechanism between the two species and post-fertilization isolation, which causes abnormalities in karyogamy and sporophyte development, plays an important role in reproductive isolation.

P.0482 The allelic diversity of the self-incompatibility gene across natural populations of Petunia

Takashi Tsuchimatsu[1], Kazuho Isono[1], Taiga Maenosono[1], Takanori Kuronuma[2], Miho Hatai[1], Kaori Chimura[1], Ken-ichi Kubo[3], Hitoshi Watanabe[2], Koichi Uehara[4]

1 Department of Biological Sciences, Graduate School of Science, The University of Tokyo, Tokyo, Japan. 2 Center for Environment, Health and Field Sciences, Chiba University, Chiba, Japan. 3 Nagahama Institute of Bio-Science and Technology, *Nagahama, Japan. 4 College of Liberal Arts and Sciences, Chiba University, Chiba, Japan.*

In flowering plants, diverse molecular mechanisms of self-incompatibility (SI) systems evolved multiple times to avoid inbreeding (selfing) and promote outcrossing. SI systems generally consist of male and female specificity genes at the *S*-locus and other genes involved in signalling pathways. The male and female specificity genes are usually linked tightly at the *S*-locus, in which dozens of *S*-alleles are segregating. The S-RNase-based gametophytic SI system is widely reported in flowering plants, including Solanaceae and Rosaceae. This system consists of the female specificity gene encoding the S-ribonuclease (S-RNase) and tandemly duplicated multiple male specificity *S-locus F-box* genes (*SLFs*). In the SI system of Solanaceae, the 'collaborative non-self-recognition' model has been proposed, postulating that SLFs are involved in specific recognitions and degradations of non-self S-RNase protein, resulting in successful outcrossing. To comprehensively understand the pattern of polymorphism at the *S*-locus in wild populations, we focused on self-incompatible *Petunia* species. An RNA-seq-based large-scale genotyping of *S-RNase* using the long-read sequencer revealed the allelic diversity of *S*-alleles, shared polymorphism between populations as well as species, and signatures of positive selection at hypervariable regions of S-RNase. We discuss how *S*-allele specificities are differentiated in the presence of an extensive population structure.

P.0483 Revealing the mixed-mating mechanism in the wild: modulation of selfing rates by the duration of stamen-pistil contact.

Shizuka Tsuneki[1], Nene Yamauchi[1], Motoharu Hayase[1], Makoto Nino[1]
Shunsuke Serizawa[2]

1 Natural Science Department, Aichi University of Education, Japan. 2 Aichi Green Association, Japan.

Self-fertilization in angiosperm ensure reproductive success, but may lead to inbreeding depression, while outcrossing can enhance offspring quality but comes with the cost of uncertainty regarding reproductive success. Therefore, a mixed-mating system ensures more certain generation turnover, serving as a crucial reproductive strategy. Several studies have reported populations where the self-fertilization rate fluctuates in response to pollinator visit frequency, but the mechanism by which populations adjust this rate remains unclear. *Veronica undulata,* a native of Japan, is an emergent aquatic plant found in rivers, waterways, and paddy fields, often visited by hoverflies. It frequently coexists with *Veronica anagallis-aquatica*, which originates from Europe to Asia, grows larger, and hybridizes with it, raising concerns about ecological competition and genetic disruption. In this study, we focus on environmental factors such as pollinator visitation frequency and alien species presence. We examine how floral phenology changes with selfing rates by quantifying stamen-pistil contact time, average seed number per fruit, and seed number variability. As a result, in populations with high pollinator visitation frequencies, stamen-pistil contact time was shorter, leading to larger seed number variability per fruit and decreased average seed number. Conversely, in populations with low visitation frequencies, contact time was slightly longer, with smaller seed number variability and slightly higher average seed number compared to high visitation populations. However, in populations coexisting with alien species, stamen-pistil contact persisted throughout flowering, resulting in smaller seed number variability per fruit and the highest average seed number among the three populations. From the above findings, populations with lower visitation frequencies and those coexisting with alien species show longer stamen-pistil contact times and higher self-fertilization rates. This suggests that natural selection may influence the selfing rate by affecting stamen-pistil contact duration.

P.0484 Always on the safe side: integrated flower roles in Fritillaria persica inflorescences

Katarzyna Roguz[1], Barbara Płaskonka[1], Paweł Pstrokoński[2], Justyna Ryniewicz[1], Emilia Stasiak[1], Yuval Sapir[3], Magdalena Chmur[4], Andrzej Bajguz[4], Marcin Zych[1]

1 Botanic Garden, Faculty of Biology, University of Warsaw, Warsaw, Poland. 2 Department of Animal Breeding, Institute of Animal Sciences, Warsaw University of Life Sciences, Warsaw, Poland. 3 The Botanical Garden, School of Plant Sciences and Food Security, Faculty of Life Science, Tel Aviv University, Tel Aviv, Israel. 4 Department of Biology and Ecology of Plants, Faculty of Biology, University of Bialystok, Bialystok, Poland.

Flowers are specialized organs, linking several features that work together for the plant reproductive success. This integration may be extended to the level of the inflorescence, where flowers serve distinct roles and increase reproductive success in changing environments. In our study, we explored the variability of flowers and their roles within the inflorescence of *Fritillaria persica* L. (Liliaceae), a geophyte native to the East Mediterranean region. Moreover, to better understand the role played by spontaneous pollen deposition we tracked pollen grain movements within one inflorescence using quantum dots. Our findings reveal that in *F. persica*, flower features and the arrangement of reproductive parts within the inflorescence may demonstrate integrated roles at the inflorescence level, with bottom flowers primarily serving the female reproductive function, middle flowers functioning as a reassurance mechanism that facilitates spontaneous self-pollination, and top flowers performing the male reproductive role. Spontaneous pollen deposition on the stigma in *F. persica* may play a dual role. It not only facilitates autogamy but also potentially aids in cross-pollination, increasing male function gain due to efficient pollen removal.

S.058. EVOLUTIONARY ECOLOGY OF PLANTS.

P.0485 Floral key innovation or environmental isolation? Drivers of speciation in a pair of Mediterranean sister species of Linaria

Alejandro Alonso[1], Sergio Bustamante[1], Xun Tang[1], Roxana Ghergheluca[2], David Monjas[2], Concepción Ornosa[3], Eduardo Moreno[1], María Leo Montes[2], Erin Cullen[4], Alberto J. Coello[1,2], Virginia Valcárcel[1], Nagore G. Medina[1], Beverley J. Glover[4], Mario Fernández-Mazuecos[1,2,4]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Real Jardín Botánico, CSIC, Madrid, Spain. 3 Universidad Complutense de Madrid, Madrid, Spain. 4 University of Cambridge, Cambridge, UK.

The Mediterranean Basin is a biodiversity hotspot harbouring numerous plant lineages that have undergone rapid *in situ* diversification. The Baetic Mountains, in the western Mediterranean, are a particularly rich centre of plant diversification associated with high topographic, climatic and edaphic heterogeneity. A plant lineage that has radiated in this region is the tribe Antirrhineae (Plantaginaceae), and particularly the genus *Linaria*. Interestingly, this genus displays a floral key innovation potentially driving diversification, the nectar spur. The pair of recently-diverged sister species formed by *L. becerrae* and *L. clementei*, endemic to neighbouring areas of the Baetic Mountains (Málaga, Spain), is an ideal system to investigate the interplay of factors driving plant speciation. These species occur on calcareous substrates and display a striking difference in spur length. They interbreed under nursery conditions, but this does not seem to happen in nature, most likely because of ecological isolating factors, potentially including biotic interactions and small-scale differences in climate and soil. To disentangle the factors driving speciation and population differentiation in this species pair, we generated genotyping-by-sequencing (GBS) data and investigated climatic and edaphic variables, accompanying plant communities and pollinator interactions. The GBS analyses revealed strong genetic isolation between species despite their geographical proximity (<5 km for the closest population pair). According to pollinator censuses and discriminant analyses of ecological variables, pollination interactions or climatic differences alone do not seem to explain this genetic pattern. Remarkably, both species inhabit edaphic islands on distinct calcareous lithologies: calcarenite for *L. becerrae* and marble for *L. clementei*. We propose that these edaphic differences have been a primary driver of speciation in these species, possibly in combination with climatic and biotic factors. These results are congruent with a major role of the edaphic factor as driver of plant diversification in the western Mediterranean biodiversity hotspot.

P.0486 Block then sting: the two-step evolution of defensive cage architectures in herbivore-driven ecosystems

Artémis Anest[1,2,3], Yanis Bouchenak-Khelladi[4], Tristan Charles-Dominique[3,5], Félix Forest[6], Yves Caraglio[3], Gareth P. Hempson[7], Olivier Maurin[6], Kyle W. Tomlinson[1,8]

1 Center for Integrative Conservation & Yunnan Key Laboratory for Conservation of Tropical Rainforests and Asian Elephants, Xishuangbanna Tropical Botanical Garden, Yunnan, China. 2 University of Chinese Academy of Sciences, Beijing, China. 3 AMAP, Univ Montpellier, CIRAD, CNRS, INRAE, IRD, Montpellier, France. 4 Agroécologie, Univ. Bourgogne, Univ. Bourgogne Franche-Comté, INRAE, Institut Agro, Dijon, France. 5 Centre National de la Recherche Scientifique, Sorbonne University, Paris, France. 4 Place Jussieu, Paris, France. 6 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 7 Ecology & Environmental Change, School of Biodiversity, One Health & Veterinary Medicine, University of Glasgow, Glasgow, UK. 8 Center of Conservation Biology, Core Botanical Gardens, Yunnan, China.

Environmental factors vary across biomes worldwide, shaping different vegetation types. In response to the varied effects of these factors, plants have evolved contrasted architectures adapted to the most constraining factors for growth and survival. While the influence of plant structure on ecological performance is recognised, its role in plant evolution remains relatively unexplored. Plant architecture, an integrative approach to describing plant structure, contains valuable information for understanding the evolution of plant forms shaped by main environmental factors over time. My research aims to enhance our understanding of the relationship between plant form and environmental factors throughout the plant evolutionary history by investigating the evolution of plant architecture under diverse climatic constraints and disturbances. Here, I will present a framework that categorises plant traits into distinct evolutionary groups. These groups include: 1) developmental constraints, comprising traits that are useful for taxonomy; 2) convergences, focusing on traits related to ecology; and 3) key confluences, which involve traits that are valuable for studying evolutionary ecology. Using this framework through two examples, I will illustrate how plants have developed contrasted architectures in response to different environmental constraints: Climatic constraints, particularly drought and frost, have selected for specific morphologies in the large genus Euphorbia. Conversely, in stable tropical climates, the ecologically dominant family Combretaceae exemplifies how specific structural traits have evolved to defend against large mammal herbivores.

P.0487 Influence of warming rate on thermal resistance and acclimation/adaptation response in freshwater phytoplankton

Elena Bañares-España[1], Raquel Sánchez de Pedro[1], Ignacio José Melero Jiménez[1,2], Andreas Reul[3], María Ángeles Viruel[4], Antonio Flores-Moya[1], María Jesús García-Sánchez[1]

1 Universidad de Málaga, Andalucía Tech, Departamento de Botánica y Fisiología Vegetal, Málaga, Spain. 2 Centro de Biotecnología y Genómica de Plantas UPM–INIA, Madrid, Spain. 3 Universidad de Málaga, Andalucía Tech, Departamento de Ecología y Geología, Málaga, Spain. 4 Instituto de Hortofruticultura Subtropical y Mediterránea La Mayora, UMA-CSIC, Algarrobo-Costa, Spain.

Global warming is affecting the composition of freshwater phytoplankton communities because of the varying capacities of species to adapt to increasing temperatures. Eco-evolutionary theory proposes that the rate of environmental degradation influences the probability of evolutionary responses to selective pressures (Ferrière et al. 2004). Thus, might different warming rates elicit distinct responses, including both adaptive and acclimation processes, as well as an increase of the thermal resistance limits in freshwater phytoplankton? We compared the growth response of one strain of the colony forming green microalga *Chlorella chlorelloides* (Naumann) C.Bock, L.Krienitz & T.Pröschold and the flagellated one *Chlamydomonas reinhardtii* P. A. Dang under two different warming scenarios. A ratchet protocol was used to test if different warming rates (slow, +2 °C, and rapid, +4 °C) affect the ability of both species to survive over their initial limit of thermal resistance (LTR). After 5 months (128 generations for both species), one of the four populations of *C. chlorelloides* exposed to slow warming was able to exceed its initial LTR (33 °C) after 46 generations, being able to grow at 35 °C, but showing a lower photosynthetic performance than its ancestral populations at control conditions (25°C). However, at rapid warming, none of the *C. chlorelloides* populations surpassed the initial LTR, as observed in *C. reinhardtii* regardless of warming rate. Nevertheless, the derived populations of *C. reinhardtii* showed higher photosynthetic capacity at their initial LTR (37 °C) compared to the ancestral populations. A subsequent experiment suggested that, although the LTR was not exceeded, some adaptive mechanisms are present in this population. Meanwhile, survival under slow warming at their LTR was related to acclimation processes. Long-term evolution experiments could shed some light on the issues raised by these results.

References: Ferrière R, Dieckmann U & Couvet D (eds). 2004. Evolutionary conservation biology. Cambridge, UK: Cambridge University Press.

P.0488 Evolutionary history and ecological divergence of the Oncocyclus irises species complex in the Southern Levant

Yamit Bar-Lev[1], Sissi Lozada-Gobilard[1,2], Aleena Xavier[3], Lior Glick[1], Itay Mayrose[1], Yuval Sapir[1]

1 Tel Aviv University, Tel Aviv, Israel. 2 Lund University, Lund, Sweden. 3 Indian Institute of Science, Education and Research, Bhopal, India.

Understanding how populations evolve and diverge into species is of essential importance to evolutionary biology. Speciation is a continuous process and species can be found at different stages of divergence. Although speciation has long been the focus of evolutionary research, it was rarely studied in species in the course of speciation, which may provide a more informative picture of divergence evolution. In this study, we focus on eight Israeli *Oncocyclus Iris* species, The Royal Irises, which are proposed to be in an ongoing speciation process. These species are endemic or sub-endemic to Israel, in which the populations are highly fragmented, and persist along varied ecological environments. Our goal was to find the role of geographical distribution and ecological divergence in the speciation process of this evolutionary-young group. We used restriction-site associated DNA sequencing (RADseq) to reconstruct the phylogeographic history of the Royal Irises, and to decipher the spatial and ecological evolutionary relationships among populations of these species.Overall we found concordance between the phylogeny and the accepted taxonomy. All analyses showed a clear divergence of *I. bismarckiana* and all other *Oncocyclus* species. In most analyses *I. atropurpurea* and *I. mariae* also formed a discrete group from other species. Several other species, defined previously by their morphology and distribution, are not distinguishable genetically. We show that both geographical distance, as well as ecological parameters, are significantly associated with the genetic relatedness, suggesting that both geographical distribution and local adaptation play a role in driving intraspecific divergence in these irises.

P.0489 Assessing the adaptive role of plasticity to temperature to cope with climate change in Lemna minor

Mario Blanco-Sánchez[1], Koen J. F. Verhoeven[1]

1 Department of Terrestrial Ecology, Netherlands Institute of Ecology, Wageningen, The Netherlands.

Climate change is altering the patterns of temperature and precipitation worldwide, which compromises the long-term persistence of plant populations. Under a climate change scenario, phenotypic plasticity has been proposed as a crucial mechanism to cope with the higher climatic variability and unpredictability. However, understanding whether plasticity can mitigate the negative effects of climate change is far from resolved. Using the clonal duckweed species *Lemna minor*, this project will use a multidisciplinary approach to shed light on the adaptive value of within- and transgenerational plasticity under conditions that simulate the changes in temperature patterns led by climate change. Specifically, ~40 *L. minor* clonal lines will be grown under two contrasting and realistic temperatures. Using RNA-seq, we will quantify gene expression in each line and temperature, and identify differentially expressed genes. Additionally, we will measure relevant ecophysiological and fitness traits, such as frond chemical composition and pigments, frond and root areas, and photosynthetic traits. We will assess the adaptive value of plasticity in gene expression and traits using phenotypic selection analyses. To empirically confirm whether plasticity is adaptive, we will use experimental evolution assays in which populations with highly- and lowly-plastic lines will evolve under different ecologically-meaningful temperature regimes. We expect a higher abundance of high-plasticity lines under heterogeneous temperature regimes, confirming the adaptive value of plasticity. Finally, we will evaluate the role of DNA methylation and transgenerational plasticity by exposing a single clone to two contrasting temperatures for several months. Acclimated lineages will be reciprocally grown in these temperatures, and we will assess DNA methylation, gene expression, and performance with and without suppressing DNA methylation with zebularine. Overall, our project will enhance our understanding of the importance of intra- and transgenerational plasticity to cope with the increased temperature heterogeneity of climate change.

P.0490 Plant structural diversity, dispersal modes and ecological history: the study case of the family Thymelaeaceae

Hugo Bonnaudet-Anest1,2, Yves Caraglio1, Artémis Anest1

1 AMAP, Univ Montpellier, Montpellier, France. 2 University of Montpellier, Montpellier, France.

Plant structure is acknowledged to reflect key traits related to plant ecological performances, as well as holding critical information regarding clades' evolutionary history. The whole plant structure can indeed be interpreted as a syndrome of traits selected by the major constraints in the habitat in which species have evolved. By using the architectural analysis of plants (sensu Hallé et al., 1978), it is possible to describe the arrangement of plant organs, stable at the species level, in the whole plant structure across space, and over time during the major steps of plant ontogeny. While architectural analysis methods hold many keys to understanding plant structural evolution in relation to major ecological changes throughout deep-time history, only few studies have attempted to characterise plant architectural evolution, especially with regard to the environment, and to other functional traits such as flowering and dispersal modes. Here, we performed the first attempt to use the architectural analysis to understand the evolutionary history of Thymelaeaceae, a worldwide distributed plant clade. This family is a well-suited candidate for this purpose given its relatively modest size, which allows a satisfactory coverage of species. It expresses a large diversity of growth forms and is distributed in a variety of biome types from arctic climates to tropics, allowing us to test the effect of various environmental factors on plant structural evolution. We expose the first results on the relation between plant architectural diversity and dispersal types, biotic and abiotic factors, and use this information to discuss the family Thymelaeaceae's history.

P.0491 Analysing plant functional trait data

Neil Brummitt[1], Ana Claudia Araújo[1], Ben Scott[1], Tim Harris[1,2,3], Sinan Gürlek[1,4], Laurel Constanti Crosby[1,5], Cui Qianyuan[1,4], Bai Peiwei[1,4], Liu Xinyu[1,4], Xiao Zhang[1,4], Adriana De Palma[1], Claire Harris[6,7]

1 Natural History Museum, Cromwell Road, South Kensington, London, UK. 2 Geography Department, King's College London, London, UK. 3 Institute of Botany, The Czech Academy of Sciences, Třeboň, Czech Republic. 4 Imperial College London, Exhibition Road, South Kensington, London, UK. 5 Centre for Biodiversity and Environmental Research, Department of Genetics, Evolution and Environment, University College London, Gower Street, London, UK. 6 Boyd Orr Centre for Population and Ecosystem Health, University of Glasgow, Glasgow, UK. 7 Biomathematics and Statistics Scotland, James Clerk Maxwell Building, Peter Guthrie Tait Road, The King's Buildings, Edinburgh, UK.

Functional traits mediate interactions between plants and their environment, and also other species. They help determine species' climatic niches and the size of their distributions. Analyses of functional trait data across thousands of species suggest that trade-offs between key traits shape the overall morphology of plants and the life forms that they adapt to. Many trait-based analyses are limited by lineage or geography, and by the availability of data on plant functional traits. The largest compendia of trait data contain information for tens of thousands of species, but this includes only <15% of plant species and the information is not comprehensive in every case. A rich but under-utilised source of potential data on plant functional traits is the species and higher-level descriptions published in taxonomic literature over the past hundreds of years. Limitations in utilising this source of information include its scattered and piecemeal nature – published for hundreds of thousands of plant species in thousands of issues of hundreds of journals – and the bewildering variety of botanical terminology, with separate taxonomic traditions for individual lineages sometimes using the same term in a unique way, or a unique term for the same feature. Overcoming access to taxonomic trait data requires: firstly, that taxonomic literature is readily available and easily searchable; secondly, that common terminology be applied across species groups to standardise the great variety of botanical terms; and thirdly, that data can be extracted automatically by machine learning algorithms rather than compiled by hand. We present recent research developments that demonstrate exactly this, illustrating its utility with application to: determining spatial patterns of plant functional diversity; in highlighting potentially threatened species; revealing the functional composition of biogeographic regions; identifying possible invasive species; predicting plant pollination syndromes; reducing the number of Data Deficient plant species; and in large-scale biodiversity modelling.

P.0492 Japanese knotweed invasion genomics: what we know and future directions

Bethany Burns[1], Malika Ainouche[5], Elena Barni[11], Jingwen Bi[2], Peipei Cao[2], Armand Cavé-Radet[3,5], Stacy Endriss[6], Elisa Giaccone[11], Ramona E. Irimia[3], Ruiting Ju[2], Sophie Karrenberg[12], Kyle Keefer[1], Zhiyong Liao[4], Madalin Parepa[3], Armel Salmon[5], Marc W. Schmid[13], Nicole Sebesta[11], Isolde van Riemsdijk[3,10], Shengyu Wang[2], Jihua Wu[2], Ji Yang[2], Wei Yuan[7], Lei Zhang[2], Weihan Zhao[2,8], Yujie Zhao[2], Xin Zhuang[2], Bo Li[2,9], Oliver Bossdorf[3], Christina L. Richards[1,3]

1 University of South Florida, Tampa, USA. 2 Fudan University, Shanghai, China. 3 University of Tübingen, Tübingen, Germany. 4 Xishuangbanna Tropical Botanical Garden, Xishuangbanna, China. 5 University of Rennes, Rennes, France. 6 University of North Carolina Wilmington, Wilmington, USA. 7 Max Planck Institute, Tübingen, Germany. 8 University of Konstanz, Konstanz, Germany. 9 Yunnan University, Kunming, China. 10 Lund University, Lund, Sweden. 11 University of Turin, Turin, Italy. 12 Uppsala University, Uppsala, Sweden. 13 MWSchmid GmbH, Glarus, Switzerland.

Japanese knotweed is a robust plant invading many habitats across North America and Europe. Originally from East Asia, it was introduced and rapidly colonized many areas becoming one of the most invasive species in the world. Knotweeds provide a compelling example of the invasive species paradox: they have colonized new habitats and become dramatic invaders with very little genetic diversity. We present the results of a range of genomics approaches that have clarified the evolutionary history of this complex, revealing its introduction history from Japan to China and beyond. We also provide evidence of evolution of increased clonality and local adaptation in the introduced range. To do so, we integrate 15 years of data across common gardens and field surveys in the native and introduced ranges. This work is the product of an ongoing research collaborative comprised of experts across three continents that investigates how genetic, epigenetic, and phenotypic variation mediate variation in performance of this species across its global distribution. Ongoing and future studies will integrate plant genomics and microbiome studies with assessments of eco-evolutionary feedback along latitudinal gradients in the native and introduced ranges to answer questions about the functional importance of intra- and interspecific biodiversity in the process of invasion.

P.0493 Correlated evolution between plant life forms and floral traits in a Neotropical legume lineage

Bruna C. Barbosa[1], Tamiris D. D. Lima[1], Luana S. Prochazka[1,2], Amanda Vieira da Silva[1], Juliana Gastaldello Rando[3], Anselmo Nogueira[1]

1 Universidade Federal do ABC, São Bernardo do Campo, Brazil. 2 Instituto de Pesquisas Ambientais, São Paulo, Brazil. 3 Universidade Federal do Oeste da Bahia, Barreiras, Brazil.

Pollination mutualism is a pivotal factor driving the diversification of plant life forms. The understanding that perennial plant species frequently have large flowers dependent on cross-fertilization is well-established, whereas annuals often exhibit tiny flowers with high self-fertilization rates. This study investigated the correlated evolution of plant life forms and floral traits within the Neotropical legume lineage of the genus *Chamaecrista*. We aim to unravel the nuanced dynamics shaping the evolution of plant reproductive strategies. To assess the evolution of life forms, we first classified 31 species in the phylogeny into three distinct life forms based on the literature: (i) annuals, (ii) resprouting perennials, and (iii) non-resprouting perennials. For floral traits, we sampled 2 to 3 flowers from different specimens, measuring the size of each floral whorl, including sepals, petals, androecium, and gynoecium. We finally used different comparative phylogenetic methods to investigate the evolutionary correlation between plant life forms and their floral traits. Among evolutionary models, the OUM model best fit all flower traits analyzed, indicating that plant life forms evolved towards different floral trait adaptative peaks. Annual plant species evolved the smallest optimum for petal, androecium, and gynoecium sizes. Resprouting perennials evolved intermediate sizes of petals and androecium, but not gynoecium, which achieved the largest size. Finally, the non-resprouting perennials evolved the largest optimum values for petals and androecium sizes, but not gynoecium with intermediate size. Our study clarifies the evolutionary link between life forms and floral traits, emphasizing different floral phenotype' optima for annuals, resprouting, and non-resprouting perennials. The disparities in optima between the two types of perennial plants may result in distinct reproductive strategies in plants with a longer life cycle.

P.0494 Integrative demographic modelling reduces uncertainty in estimated rates of species' historical range shifts

Antonio R. Castilla[1], Alissa Brown[2], Adam B. Smith[3], Andria Dawson[4], Sean Hoban[5], Everett A. Abhainn[6], Jeanne Romero-Severson[7], John R Tipton[8], Allan Strand[9], John D. Robinson[10]

1 Department of Plant Biology, Ecology, and Evolution, Oklahoma State University, Stillwater, USA. 2 Center for Tree Science, The Morton Arboretum, Lisle, USA. 3 Center for Conservation and Sustainable Development, Missouri Botanical Garden, Saint Louis, USA. 4 Department of Biology, Mount Royal University, Calgary, Canada. 5 Center for Tree Science, The Morton Arboretum, Lisle, USA. 6 Department of Biological Sciences, University of Notre Dame, South Bend, USA. 7 Department of Biological Sciences, University of Notre Dame, South Bend, USA. 8 Department of Mathematical Sciences, University of Arkansas, Fayetteville, USA. 9 Department of Biology, College of Charleston, Charleston, USA. 10 Department of Fisheries and Wildlife, Michigan State University, East Lansing, USA.

Reconstructions of species' biogeographic histories commonly rely on disparate types of data and analyses: occurrence data modeled with species distribution models (SDMs), pollen relative abundance models informed by fossil pollen records, and genetic data analyzed with scenario-based models. Using green ash (*Fraxinus pennsylvanica*) in eastern North America as a case study, we analyze the consistency of inference between the three data types and the most commonly used method associated with each data type. Genetic data were modeled using Approximate Bayesian Computation and a spatially-explicit forward-time demographic model coupled with coalescent simulations. Relative abundance of tree pollen, including ash pollen, across space and through time was estimated using a Bayesian hierarchical spatio-temporal model, and climatically suitable habitat was modeled using SDMs with multiple algorithms. We integrated pollen data and SDMs with genomic data through Approximate Bayesian Computation. We then compare estimates of the pace of range movement (biotic velocity) through time from these three datasets and corresponding approaches. Overall, biotic velocities estimated using fossil pollen were higher than those using either genomic data or SDMs. We also found a temporal mismatch between methods detecting peaks in biotic velocity. Both integrated ABC-SDM and ABC-pollen analyses reduced the uncertainty of biotic velocity estimates. Our results demonstrate the need for quantitative comparison of the results from different biogeographic reconstruction methods and suggest that integration of these multiple lines of evidence in a unified framework may result in improved biogeographic inference.

P.0495 Local adaptation and mating system variation in Viola pubescens

Caroline Edwards[1], Leonie Moyle[1]

1 Indiana University, Bloomington, USA.

Local adaptation can shape many important processes, including the distribution of genetic variation within species, the likelihood of range expansion, and the transition to ecologically-mediated speciation. While many studies have found local adaptation in plants, few have identified the specific environmental drivers of local adaptation, the traits responding to differential selection across the species' range, and the factors that maintain locally fit genotypes despite the potentially homogenizing effects of gene flow. We have been examining these factors in the North American wildflower species, *Viola pubescens*, focusing particularly on the role of its distinctive mixed mating system on patterns of local adaptation. This species exhibits seasonal cleistogamy, in which individuals produce primarily outcrossing chasmogamous (CH) flowers in the spring, and then produce selfing, cleistogamous (CL) flowers in late spring and summer. The timing of the switch between floral types has been hypothesized to be in response to an environmental cue, specifically light quantity or pollinator abundance. Variation among populations in growing season length and/or pollinator abundance may therefore influence the proportion of offspring produced by outcrossing versus selfing, with potentially important consequences for patterns of genetic diversity, gene flow, and local adaptation. Here, we present data from the first two seasons of a reciprocal transplant experiment in *Viola pubescens* to evaluate evidence for local adaptation to environmental and geographic variation, and investigate the selective agents potentially responsible. We also quantify patterns of mating system variation in order, ultimately, to test the contribution that variation in CL and CH flowers might make to shaping these patterns among populations.

P.0496 Phylogenetic structure along a topographic gradient in the understorey of a Neotropical plant community

Luciana A. Botacim[1], Renan K. Hollunder[2], Karina Ferreira-Santos[2], Écio S. Diniz[3], Tatiana T. Carrijo[4], Mário L. Garbin[1,4]

1 Universidade Estadual do Norte Fluminense, Campos dos Goytacazes, Brasil. 2 Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brasil. 3 Autonomous University of Barcelona (CREAF), Barcelona, Spain. 4 Universidade Federal do Espírito Santo, Alegre, Brasil.

Topography is a well-known driver of changes in plant community organization in the tropics. However, we have a limited understanding of how the evolutionary history of the component species shapes the organization of Neotropical plant communities along topographic gradients. In this study, we investigated how the phylogenetic structure of an understorey plant community changes along a topographic gradient in a fragment of Neotropical forest in southeastern Brazil using metrics of phylogenetic diversity and structure. Twenty plots (10m x 10m) were surveyed along a topographic gradient, distributed across four topographic habitats: valley, SW slope, NW slope, and ridge. In every plot, we calculated the phylogenetic diversity (PD), the mean pairwise distance (MPD), the mean nearest taxon distance (MNTD), and SES (standardized effect sizes). We found 1.695 individuals belonging to 70 species, 53 genera, and 24 families. The richest families were Fabaceae, Rubiaceae, and Myrtaceae. Overall, the studied community exhibited a non-random phylogenetic structure: valley habitat presented a phylogenetic clustering and ridges exhibited phylogenetic overdispersion. Environmental filtering imposed by the topographic gradient possibly acted on convergent clades, thus assembling overdispersed communities. The valley was characterized by the presence of Rubiaceae, Piperaceae, Myrtaceae, and Lauraceae, while representatives of Lecythidaceae, Bignoniaceae, and Salicaceae were more present in the ridge. Our findings suggest that environmental filtering is more likely to play a stronger role in the understorey organization of this tropical community with closer related species occupying the valleys and distantly related species living in the ridges. Acknowledgments: CAPES, CNPq, FAPES

P.0497 How clustering promotes biodiversity: A solution to the plankton paradox

Karen K. Huruntz1, Lilit E. Ghukasyan[1], Gor A. Gevorgyan[2]

1 Research Institute of Biology, Yerevan State University, Yerevan, Armenia. 2 Scientific Center of Zoology and Hydroecology, National Academy of Sciences of RA, Yerevan, Armenia.

The plankton paradox, a term coined by Hutchinson in 1961, refers to the enormous diversity of phytoplankton species observed virtually in all aquatic ecosystems, while a straightforward understanding of the principle of competitive exclusion, the core tenet of theoretical ecology, teaches that in competitive equilibrium a number of species competing for fewer number of resources cannot coexist. Hutchinson saw the solution to the problem in that varying environmental conditions prevent the formation of competitive equilibrium in a phytoplankton community. Over the past six decades, other solutions to the problem have been discussed in the literature, with an equally remarkable diversity of proposed mechanisms. While most allow the coexistence of a few more competitors in addition to what is allowed by competitive exclusion, only a few highly idealized theories allow for the coexistence of hundreds of species limited by a small number of resources. In the absence of a generally accepted solution to the problem, we outline here another conceptual solution that, however, fits well within the framework of competitive exclusion, rather than specifying how species-rich communities can defer the competitive exclusion. It is known that a species-saturated ecological community driven by competitive Lotka-Volterra equations, following a path of competitive exclusion, lingers in a long-term state with species congregated in niche space into well-separated clusters. Characterizing the topology of the niche structure of this state as a hierarchical one, we put forward a generalization of the Lotka-Volterra multi-resource competition model, which recognizes this topology at the basis of its own network structure of interrelated differential equations. This kind of generalization significantly reduces the competitive constraints on species coexistence, offering promising potential for a conceptual resolution of the plankton paradox.

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P.0498 Different selective forces shaped the evolution of leaf anatomy in crops

Alicia Gómez-Fernández[1], Rafael Villar[2], Rubén Milla[1]

1 ECOEVO Research Group, Departamento de Biología y Geología, Física y Química Inorgánica, Instituto de Investigación en Cambio Global, Universidad Rey Juan Carlos, Móstoles, Spain. 2 Departamento de Botánica, Ecología y Fisiología Vegetal, Universidad de Córdoba, Campus de Rabanales, Córdoba, Spain.

Variation in SLA is closely related to C fixation rates and resource use, both at the plant and ecosystem level (Wright *et al. 2004*). In crops and their wild progenitors, SLA is generally high, but varies substantially depending on the origin and history of crops (Gómez-Fernández et al. 2023). Variation in SLA can be explained by leaf thickness and/or leaf density, both of which are influenced by anatomical traits of the leaf (John et al. 2017). Compared to woody species, the study of the anatomical components underlying SLA variation has been overlooked in herbs. Our aim is to explain the anatomical basis of SLA at the upper end of its spectrum and to explore the role of distinct crop origins and domestication histories in the evolution of leaf anatomical traits. We conducted a common-garden experiment with wild progenitor and domesticated accessions of 28 herbaceous crops, and analysed morpho-anatomical traits at leaf, tissue and cell level by means of cross sections. Our results show that crops tend to have a higher proportion of mesophyll and a lower proportion of bundle sheaths than their wild progenitors and no general trend for the remaining traits. As well as for SLA, climate, plant organ under human selection and evolutionary history contributed to explain some of the effects of domestication on anatomical traits. In this contribution, we will show how diversity in domestication histories and origins have influenced the evolution of SLA and its anatomical components in crops.

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P.0499 Advances in the study of carrying capacity of extensive livestock systems through natural analog ecosystems

González L[1], Serrano-Zulueta R[1], Pardo G[1], del Prado A[1,2]Manzano P[1,2,3,4]

1 Basque Centre for Climate Change (BC3), 48940 Leioa, Spain. 2 Ikerbasque — Basque Foundation for Science, Bilbao, Spain. 3 Global Change and Conservation Lab, Organismal and Evolutionary Biology Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki, *Finland. 4 Faculty of Biological and Environmental Sciences, Helsinki Institute of Sustainability Science, University of Helsinki, Helsinki, Finland.*

During the Eocene, records indicate the emergence of forests, leading to mosaic landscapes comprising wooded areas between grasslands. The diversification in vegetation structure, driven by declining temperatures, atmospheric CO_2 concentration reduction and the advent of megaherbivores, fostered ecosystem opening. Subsequently, angiosperms evolved simultaneously with the pressure exerted by these animals, giving rise to both chemical and physical defense strategies. These modifications combined with the emergence of C4 plants in grasslands and savannas, increased the flammability of vegetative masses, giving rise to fires. The ecosystems evolution is conditioned by synergies between herbivore evolution and natural fires, being both primary vegetation *consumers* in temperate zones. However, during the Pleistocene and in a climate change context, relevant extinctions of megaherbivores occurred in Eurasia influenced by hunting and domestication. Extensive livestock replaced many ecosystem services provided by megafauna and wild herbivores, highlighting the essential role of extensive livestock, especially the grazers herbivores, in maintaining open ecosystems. However, extensive livestock is often criticized for high emissions rates, extensive land occupation, and water consumption. This is largely because environmental analyses overlook the inevitable effects from a wild state of the land used for extensive livestock (e.g.: methane emissions). To estimate this, attempts are made to assess the natural levels of herbivory in protected natural areas, although this proves complex due to animal migratory barriers, incomplete trophic dynamics, supplementation, or resource competition with domestic herbivores. For this study, a database of European protected areas is established, containing data of grazing herbivores biomass, both domestic and wild, predators, grass productivity, aiming to identify patterns or trends in wild herbivory densities under various ecosystem scenarios with different vegetation types. Targeting to estimate what portion of the carbon footprint of extensive systems is anthropogenic and what part can be deemed inevitable, as linked to ecological cycles of vegetation consumption.

P.0500 Challenges to understand adaptive importance of red light responses of phytochrome B

Hajime Ikeda[1]

1 Department of Multidisciplinary Sciences, Graduate School of Arts and Sciences, The University of Tokyo, Tokyo, Japan.

Phytochromes play a central role in mediating adaptive responses to light and temperature throughout plant life cycles. Despite evidence for adaptive importance of natural variation in phytochromes, little information is known about molecular mechanisms that modulate physiological responses of phytochromes in nature. I will show our previous findings of evolutionary divergence in physiological responses relevant to thermal stability of a physiologically active form of phytochrome (Pfr) between two sister species of Brassicaceae (*Cardamine bellidifolia* and *Cardamine nipponica*) growing at different latitudes. In addition, I will present further challenges of molecular evolutionary analyses on phytochrome genes from multiple species and of physiological experiments exploring ecological roles of the divergence in light responses.

P.0501 Comparative analysis of diversification rates in clonal and non-clonal plants

Sonia Kadyan[1], Jan Smyčka [2], Tomas Herben [1]

1 Department of Botany, Charles University, Czech Republic. 2 Center of Theoretical Studies, Charles University, Czech Republic.

Clonality is present in about half of the plant species. Many plant species are clonal, meaning they can reproduce vegetatively by placing stems horizontally and using adventive roots or roots that bear buds that can produce stems. Clonality in plants influences various factors such as effective population size, meiosis frequency, and genet lifetime, all of which can significantly shape the diversification rates. However, the role of clonality in influencing species diversity has been largely overlooked. Here, we aim to investigate the potential impact of clonality on rates of diversification and whether the patterns of diversification in clades where clonal species predominate differ from those with non-clonal species. In order to do this, a wide range of taxonomic groups with different proportions of species capable of clonal growth were sampled. Worldwide clonality data was sourced from the CLOPLA database and linked with existing phylogenetic information on these species, namely the Smith & Brown (2018) Angiosperm phylogeny. Our approach involves a variety of phylogenetic methodologies, each characterized by specific assumptions. We employ hypothesis-free tip rate estimations using different methods, like DR metrics, BAMM, and ClaDS, to assess diversification rates. Statistical analysis involves regressing tip diversification rates against the clonal status of plants, employing phylogenetic linear models. The study has the potential to clarify the role that clonality plays in measuring observed variation in diversification metrics.

P.0502 In situ evaluation of assisted evolution tools for the advancement of flowering onset in Lupinus angustifolius L. (Fabaceae)

Sacristán-Bajo, S.[1], García-Fernández, A.[1], Lara-Romero, C.[1], Poyatos, C.[1], Rubio Teso, M.L.[1], Morente-López, J.[2], Prieto-Benítez, S.[3], Torres, E.[4], Iriondo, J.M.[1]

1 Universidad Rey Juan Carlos, Móstoles, Spain. 2 Island Ecology and Evolution Research Group, Instituto de Productos Naturales y Agrobiología, CSIC, Tenerife, Spain. 3 Centro de Investigaciones Energéticas, Medioambientales y Tecnológicas, Madrid, Spain. 4 Universidad Politécnica de Madrid, Madrid, Spain.

Current climate change is threatening the survival of many species. Artificial selection and assisted gene flow have recently arisen as useful tools to better manage and protect biodiversity and to increase the adaptive potential of species. Considering that flowering time is a key trait for plant responses to global warming, the objective of our study was to test the potential risks and benefits of artificial selection and assisted gene flow for enhancing the evolutionary potential *of Lupinus angustifolius* L. populations through the advancement of flowering onset. We collected seeds from four populations in Spain at two latitudes (north and south), and grew them in a common garden experiment. For the artificial selection experiment, two early flowering selection lines were created for each of the populations, using both self-crosses and outcrosses. For the assisted gene flow experiment, we established an F1 generation by pollinating plants from northern populations with pollen from southern individuals. The F1 was self-pollinated to produce an F2 self-pollination line in the following season. All lines were maintained through self-pollination for a third season. In autumn 2020, seeds obtained (F3) from the two experiments from the northern populations were sown in a common garden under natural conditions, close to the original wild populations' locations. In spring 2021, we measured the flowering onset and other different plant traits. None of the measured traits showed differences between the control and the artificial selection lines, contrary to the results obtained in previous works under controlled conditions. On the contrary, plants derived from the assisted gene flow lines, flowered significantly earlier and showed lower shoot growth than the control line, in line with results obtained under controlled conditions in earlier works. These results show that assisted gene flow was more efficient than artificial selection in modifying flowering initiation under natural conditions.

P.0503 Phylogenomic reconstruction of Fagaceae using transcriptomes to explore phylogenetic signal and adaptive evolution of traits

Min-Xin Luo[1], Chien-Ti Chao[1], Jui-Tse Chang[1], Pei-Chun Liao[1]

1 School of Life Science, National Taiwan Normal University, Taipei, Taiwan.

Fagaceae species, prevalent across diverse Northern Hemisphere habitats, play vital roles in ecosystems and economies. Their morphological and genetic diversity, essential for adapting to environmental stress, makes them ideal for trait evolution studies. Previous research encountered conflicts among gene trees at the genus level, impacting phylogenetic inferences. This study investigates the source of phylogenetic discordance within Fagaceae, focusing on six genera (*Fagus*, *Lithocarpus*, *Quercus*, *Castanea*, *Castanopsis*, and *Notholithocarpus*). Transcriptome data is utilized to reconstruct phylogenetic relationships and explore causes of inconsistencies. Gene conflicts primarily occur between *Lithocarpus* and *Quercus* due to incomplete lineage sorting, not gene flow. *Castanopsis* and *Castanea* show common selection related to environmental factors or pathogens, likely stemming from a shared ancestor's experience during the Paleocene-Eocene Thermal Maximum. Trait evolution analysis indicates that evergreen/deciduous traits are influenced by precipitation seasonality and mean diurnal range. Late embryosis abundant genes, associated with water deficiency response, are under selection, linked to deciduous traits and seed desiccation in *Quercus*. This study provides a comprehensive exploration of Fagaceae diversity, revealing associations between functional genes and traits, enhancing our understanding of trait evolution and environmental adaptation.

P.0504 Effects of aromatic dwarf-shrubs on community richness and composition in coastal harsh habitats in Sardinia (Italy)

Silvia Macis [1], Erika Bazzato [1], Alfredo Maccioni [2,*], Michela Marignani [1], Emmanuele Farris [2]

*1 University of Cagliari, Cagliari, Italy. 2 University of Sassari, Sassari, Italy. * amaccioni@uniss.it*

Numerous processes influence plant species richness and community composition. Plants establishment and survival are highly sensitive to micro-habitat structure and conditions, especially in harsh habitats. To verify if the richness and composition of plant communities in a mosaic of coastal Mediterranean herb and garrigue habitats was conditioned by the presence of aromatic dwarf-shrub canopies, we selected three model species and studied each of them at three sites in North-Western Sardinia. At each combination species × site, 10 individuals were randomly sampled between April and July 2023. The selected model species were: *Helichrysum italicum* subsp. *tyrrhenicum*, *Teucrium capitatum* subsp. *capitatum*, and *Salvia rosmarinus*. At each individual, we assessed the presence/absence of vascular plants beneath the plant canopies and in adjacent open areas, using point transects. Statistical analyses showed significant differences in community composition between under and outside canopies for each of the three model species. The presence of canopies did not influence species richness but affected beta dispersion for all model species, and the mean composition for *H. italicum tyrrhenicum* and *T. capitatum capitatum*. Preliminary data suggest that the presence of these canopies caused significant differences in species composition among areas under the canopies of dwarf-shrubs and those outside them, indicating that conditions under the canopies affected diversity compared to adjacent open areas. Furthermore, our results evidenced significant difference in species richness, mean composition and beta dispersion among the model species under the canopies, highlighting the influence of the dominant species on plant diversity. We argue that these preliminary results, which provide an understanding of the biocoenosis dynamics and plant-plant interactions in harsh Mediterranean environments, could be affected more by the phytochemistry of secondary metabolites at both soil litter and fresh leaves of aromatic dwarf-shrubs, than simply the exclusion of direct sun light under their canopies.

P.0505 Altitudinal and climatic adaptation in flowering initiation phenology in Linum bienne

Macarena Marín-Rodulfo[1], Jose R. Grande-Allende[1], Isabel Martín-Girela[1], Eduardo de la Peña[2], Rocio Pérez Barrales[1]

1 Departamento de Botánica, Facultad de Ciencias, Universidad de Granada, Granada, Spain. 2 Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora (IHSM-UMA-CSIC), Estación Experimental "La Mayora", Málaga, Spain.

There is increasing evidence that global warming significantly alters flowering phenology, primarily advancing the onset of flowering. Studying the shifts in flowering in this context is important because flowering is a trait under genetic regulation and dependent on environmental cues. In addition, the onset and the phenology of flowering strongly influences plant growth and fitness. However, it still remains poorly investigated whether the shift in flowering onset correspond with a plastic response to changing local environmental cues, or to adaptive response to climate change. In the present study, we investigate how the genetic variation in the onset of flowering of *Linum bienne* Mill. responds to environmental variation along an altitudinal gradient, and the consequences for plant fitness. *Linum bienne* is an annual, biennial, or perennial herb, distributed in the Mediterranean Region, Atlantic Europe, and the British Isles. It is a grassland species growing from sea level up to 1200m. The flowers are homostylous, self-compatible and commonly experience self-pollination upon flower opening. In the present study, we sampled seeds from 16 populations (21 to 11 families per population) at different altitudes (range 50-1200 m a.s.l) in the south of the Iberian Peninsula, and exposed them at three different altitudes (86, 738, 1980 m a.s.l) in provenance trials and under the control conditions of the greenhouse. In these experiments, we measured growth rate, plant size at flowering, days to flowering onset, flower production, days to fruiting and fruit production. These data were used to investigate phenotypic plasticity, but also to study if populations coming from environments similar to that in the experimental site experience higher performance and fitness. Our results underscore the adaptive value of traits that allow species to shift their distribution along altitudinal gradients, and how they adapt to new environments.

P.0506 Analysis of exposure and slope gradient impact on tree layer profile of Moerolakop vegetation in Nylsvley Nature Reserve

T Mavhila[1], M.P Tshisikhawe[1], K Magwede[1]

1 Department of Biological Sciences, University of Venda, Thohoyandou, South Africa.

Plant ecologists have been eager to consider slope aspect related issues in vegetation communities in the 1850s. The effects are more noticeable in the mountainous regions, of which are set apart by steeper slope. The aspect of slope is very much important when it relates to diversity and distribution of plants. This study was be conducted in Nylsvley Nature Reserve Point centered method was used to achieve the aim of this study which is to analyze and compare the vegetation structure of the north-facing slope against the south-facing slope and the objectives being to determine density and frequency of tree layer species dominance against opposite slopes directions, to determine importance value indices of tree layer species against opposite slope directions and gradients, to determine the vegetation structure against slope gradient. The biological parameters that were checked was the stem circumference, height, and canopy diameter. Diversity was measured using Shannon-Weiner diversity index, Simpson diversity index and Evenness index. Shannon diversity index for North facing Downslope 2.20, Midslope 1,97, Uplsope 1.77 and South facing downslope 1.74, Midslope 1,64. The average Simpson diversity index for the North facing slope was 0.82 and South facing slope 0.77. Average Evenness index for the North facing slope was 0.93 and, on the South facing slope was 0.81. Which indicated that on the North facing slope there's high species diversity and species evenness which is not affected much by the slope gradient as it shows from downslope to upslope diversity decreases, on this part of the slope diversity was high on the downslope. On the South facing slope it was shown that there's is low diversity and evenness since the Shannon-Weiners and Simpson diversity was low, and on this part of the slope high diversity and evenness was high on the upslope.

P.0507 Zygomorphic flowers last longer: the evolution of floral symmetry and floral longevity

Ruby E. Stephens[1,2,3], Rachael V. Gallagher[1,4], Marcos Méndez[5], Hervé Sauquet[2]

1 School of Natural Sciences, Macquarie University, Ryde, Australia. 2 Royal Botanic Gardens and Domain Trust, Sydney, Australia. 3 Ecology & Evolution Research Centre, University of New South Wales, Sydney, Australia. 4 Hawkesbury Institute for the Environment, University of Western Sydney, Richmond, Australia. 5 Area of Biodiversity and Conservation, Universidad Rey Juan Carlos, Madrid, Spain.

Floral symmetry has long been considered a key trait in floral evolution. Although zygomorphic (bilaterally symmetric) flowers typically receive fewer floral visitors, it is yet to be determined whether this translates to a slower rate of pollination. Floral longevity, the time from flower anthesis to senescence, is an evolved trait which balances floral costs against the rate at which flowers are pollinated. Using newly collected field data combined with data compiled from the literature we assess whether floral longevity varies with floral symmetry. Phylogenetic regressions show that zygomorphic flowers last longer than actinomorphic flowers, though there is considerable variation in longevity in both groups. Zygomorphic flowers opened on average for 4.7 days, whereas actinomorphic flowers typically lasted 3.6 days. Our results provide further evidence of the costs of zygomorphy for flowers. Despite these costs, zygomorphy has evolved numerous times throughout angiosperm history, and the reward of more targeted pollination, and lower pollen interference must be worth having to keep your flowers open for longer.

P.0508 Shattering no more: experimental evolution of non-shattering fruits in crop domestication

Rubén Milla[1], Beatriz Pablo-Carmona[1], Sergio Nuñez-Castillo[1]

1 Departamento de Biología, Geología, Física y Química Inorgánica. Universidad Rey Juan Carlos, Madrid, Spain.

Agricultural crops have played a pivotal role in human culture and evolution. The transition from wild plants to fully domesticated crops has been marked by the development of unique traits. One such critical trait is the non-shattering of fruits, where fruits either do not disarticulate or remain enclosed at maturity. This evolutionary shift towards non-shattering was a critical step, allowing early farmers to maximize their seed harvest before substantial losses to the ground occurred. Non-shattering is prevalent in the domestication history of major crops and serves as a distinct marker differentiating wild and domesticated plant remains at archaeological sites. However, the specific selective pressures that led to the fixation of this crucial trait have remained elusive. To address this knowledge gap, we conducted an experimental evolution study on populations of Arabidopsis thaliana composed of a mixture of shattering and non-shattering genotypes. In our study we mimicked various harvesting techniques employed by early agriculturalists, such as sickle harvesting – hypothesized to encourage domestication – and methods like beating into baskets – hypothesized to deter domestication –. In this contribution, we will share the results of our investigation, revealing how silique shattering evolved across 18 replicate populations over three generations of experimental evolution under distinct harvesting scenarios. This research sheds light on the driving forces behind the emergence of non-shattering in agricultural crops and provides valuable insights into the early stages of crop domestication.

P.0509 Unraveling interaction assembly rules at global scales: trait-matching between frugivores and fruits

Morán-López Teresa[1,2], García Daniel[1], Campagna María Sofía[2], Schleuning Matthias[3], Morales Juan Manuel[2,4]

1 Departamento de Biología de Organismos y Sistemas, Universidad de Oviedo and Instituto Mixto de Investigación en Biodiversidad (Universidad de Oviedo-CSIC-Principado de Asturias), Oviedo y Mieres, Asturias, España. 2 Grupo de Ecología Cuantitativa, INIBIOMA-CONICET, Universidad Nacional del Comahue, Bariloche, Río Negro, Argentina. 3 Senckenberg Biodiversity and Climate Research Centre, Frankfurt am Main, Germany. 4 School of Biodiversity, One Health & Veterinary Medicine, University of Glasgow, Glasgow, UK.

Predicting plant-frugivore interaction rearrangement after human-driven disturbances is a priority and challenging task in the current Global Change Crisis. Recruitment in many plant populations depends on frugivory, which often maintains seed rain diversity. There are three commonly accepted rules in plant-frugivore interactions—(i) abundant species tend to interact more often, (ii) fruit size cannot largely surpass beak width and (iii) lipidic fruits tend to attract more insectivorous birds. Yet, their degree of generalization across communities and bird and plant lineages remains uncertain. We gathered a dataset of 65 plant-frugivore networks from contrasting latitudes (from 0.2 to 53 degrees), belonging to mainland and island systems. We designed a Hierarchical Modeling of Species Communities Model (HMSC) to quantify arrangement rules affecting 7417 interactions between 799 plants and 733 bird species belonging to 84 and 76 different families. We evaluated (a) the degree of generalization of trait-matching across the globe, (b) the effects of the biogeographical context on its strength and (c) its consequences on species complementarity within plant communities. Despite the contrasting environments analyzed (e.g., temperate and tropical forests), in almost all networks we could detect the fingerprint of the above-mentioned interaction rules with plants attracting a subset of frugivores according to their morphological and nutritional characteristics. However, the strength of trait-matching varied with latitude and insularity with higher intimacy of interactions in temperate mainland than in tropical areas. In the tropics, the prevalence of highly frugivorous birds mixing diverse fruits in their diets softened trait-matching resulting in generalized interactions. In temperate areas, strong trait-matching lead to a high complementarity among frugivores and plants. Overall, our results show that interaction assembly between plants and their frugivores is governed by common rules throughout the globe, but modified by the biogeographical context affecting the intimacy of such interactions and frugivore complementarity within plant communities.

P.0510 Reproductive isolation between two sister Cnidoscolus species in sympatry

Miguel A. Munguía-Rosas[1], Víctor Parra-Tabla[2], José M. Rodríguez-Domínguez[3]

1 Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (Cinvestav). Mérida, México. 2 Universidad Autónoma de Yucatán, Mérida, México. 3 Centro de Investigación y Asistencia en Tecnología y Diseño del Estado de Jalisco, Guadalajara, México.

Reproductive isolation is conferred by several barriers that occur at different stages of reproduction. Comprehensive reviews on the topic have identified that barriers occurring prior to zygote formation are often stronger than those that occur afterward. However, the over-representation of temperate perennial herbs in the current literature precludes any generalization of this pattern to plants that present other life forms and patterns of distribution. Here, we assessed reproductive isolation barriers and their absolute contribution to reproductive isolation and asymmetry in *Cnidoscolusa conitifolius* and *C. souzae*, two closely related tropical shrub species that co-occur on the Yucatan peninsula. The reproductive barriers assessed were phenological mismatch, pollinator differentiation, pollen-pistil incompatibility (three pre-zygotic barriers), fruit set failure, and seed unviability (post-zygotic barriers). Reproductive isolation between the study species was found to be complete in the direction *C. aconitifolius* to *C. souzae*, but only partial in the opposite direction. One post-zygotic barrier was the strongest example. Most barriers, particularly the pre-zygotic examples, were asymmetrical and predicted the direction of heterospecific pollen flow and hybrid formation from *C. souzae* to *C. aconitifolius*. Both parental species, as well as the hybrids, were diploid and had a chromosome number 2n=36.

P.0511 The naturalization of almond (Prunus dulcis (Mill.) D.A.Webb.) is mediated by cyanogenic processes

Francisco J. Ocaña-Calahorro[1], Andrés Barea Márquez[1], Miguel G. Ximenez-Embun[1], Rocio Pérez Barrales[1], Rafael Rubio de Casas[1]

1 University of Granada, Granada, Spain.

The seeds of Prunus spp. species are known for their toxicity, caused by a high content of cyanogenic compounds. One emblematic exception is almond (*Prunus dulcis* (Mill.) D.A. Webb) which is cultivated for its edible, non-cyanogenic (i.e., sweet) seeds. Seed cyanogenesis in almond is a Mendelian trait, the 'sweet' allele being dominant, and the recessive, toxic allele can be found in heterozygotic cultigens. Previous work has shown rapid evolution of cyanogenesis during the feralization (de-domestication) of this crop. Feral populations have a much higher rate of toxic seeds than their cultivated ancestors. However, the causes and consequences of this increase in cyanogenesis remain to be elucidated. Understanding cyanogenesis requires to account for its role across organs and life stages. Toxicity might influence various ecological interactions, both with mutualists and antagonists, and the synthesis and accumulation of N-rich cyanogenic compounds may affect plant physiology. Here we present the results of combined field, common garden and growth chamber experiments investigating how cyanogenesis influences almond feralization by estimating its effects across the reproductive cycle, including pollination, seed dispersal and predation and seedling survival. Our findings suggest a complex pattern of selection on cyanogenesis. In flowers, cyanogenic compounds reduce the number of pollinator visits. Additionally, seed dispersers showed a significant preference for "sweet" almonds. However, this also correlated with an increase in seed predation, and cyanogenic seedlings were also more likely to survive stressful events caused by cold, drought or herbivory. We conclude that while cyanogenesis appears to be positively selected during almond feralization overall, this net result is the outcome of complex and maybe conflicting adaptive dynamics.

P.0513 Desiccation in Mediterranean oak acorns: does morphology influence germination rate?

David A. Oropesa-Olmedo[1], Lucía Cano[1], Enrique Andivia[1], Raúl Bonal[1]

1 Department of Biodiversity, Ecology and Evolution, Complutense University of Madrid, Madrid, Spain.

The relationship between weight and size of the acorns can be an important factor in the loss of moisture and therefore affect the germination rate of *Quercus* acorns. The acorns of Mediterranean oaks are considered to be recalcitrant seeds, so biological and climatic processes are important to maintain a constant moisture content in the seeds, as a drop in moisture content of up to 25-30% can affect their viability. This study hypothesises that the more elongated and narrower seeds lose moisture more easily and are therefore more sensitive to germination rate during periods of desiccation. The aim of this study is to find out whether the morphological traits of the acorns, mainly width and length are variables that might influence seed desiccation and thus limit the germination rate. For this purpose, seeds of different shape and size from different *Quercus* species (*Q. ilex*, *Q. pyrenaica*, *Q. faginea*, *Q. suber*, and *Q. coccifera*) are exposed to different drying times and subsequently germinated under constant humidity conditions. In this way, the amount of moisture lost by the acorns as a function of time exposed to dryness, their length and width are recorded and related to germination capacity.

P.0514 Harmony in diversity: decoding plant-microbian dynamics in Mediterranean ecosystems

Leyre Pedros-Pla[1], Amanda Mármol-Salvador[1], Miguel Verdú del Campo[1], Daniel Rodríguez-Ginart, Santiago Donat-Caerols[1], Marta Goberna[1], Alba Navarro-Montagud [1], Clara Gracia Mas[1], Patricio García-Fayos[1], Francesco de Bello[1]

1 Centro de Investigaciones sobre Desertificación, Valencia, Spain.

While interactions between plants and soil microbiota play a pivotal role in driving biodiversity and ecosystem functioning, the extent to which changes in plant composition influence the microbiota and reciprocally remain elusive. Addressing the fundamental question of whether diversity primarily associates with specific traits of dominant species or results from the complementarity of species traits, this study investigates intricate ecosystem interactions among plant, fungal, and bacterial diversity across 59 permanent plots in diverse natural parks of the Valencian Community. Furthermore, we examine the contributions of factors such as micro and macroclimatic variables, coupled with plot heterogeneity parameters, to elucidate these interactions. Preliminary findings indicate that, despite a vegetation-induced shift in microbial composition, the preservation of overall biodiversity necessitates considerations beyond habitat diversity alone, contingent on multiple factors. This research establishes a foundation for conservation strategies that holistically incorporate both biotic and abiotic determinants.

P.0515 Do warming and competition interactions with drought change selection and plasticity patterns in a Mediterranean shrub?

Marina Ramos-Muñoz[1], Mario Blanco-Sánchez[1], Beatriz Pías[2], José Alberto Ramírez-Valiente[3,4], Raquel Benavides[5,6], Adrián Escudero[1], Silvia Matesanz[1]

1 Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, Móstoles, Spain. 2 Departamento de Biodiversidad, Ecología y Evolución. Universidad Complutense de Madrid, Madrid, Spain. 3 Department of Forest Ecology & Genetics, Forest Research Center (INIA, CSIC), Madrid, Spain. 4 Centre for Ecological Research and Forestry Applications, Bellaterra, Spain. 5 Dep. Sistemas Y Recursos Naturales, E.T.S. Ingeniería de Montes, Forestales y del Medio Natural, Madrid, Spain.

Evaluating the adaptive potential of plant populations is key to understand their future evolutionary responses and to predict their vulnerability in a climate change context. Drought is the main selective pressure in the Mediterranean region, but, in natural conditions, Mediterranean plant populations experience a complex combination of abiotic and biotic conditions. Adaptive trait evolution under new conditions requires phenotypic selection and genetically based phenotypic variation within populations. Although both the patterns of selection (i.e., the traits and trait values affecting individual fitness) and the expression of genetic variation are environmentally dependent, little is known about how they vary under realistic, multivariate environmental conditions. Using an experimental approach based on multivariate common gardens, we quantified the potential response to selection to water stress and whether it is modified by warming and intraspecific competition. We sampled a total of 42 maternal families from two populations of the gypsum shrub *Helianthemum squamatum* that represent the extremes of the geographical and climatic distribution of the species. Experimental treatments simulated the stress gradient experienced in natural conditions, resulting from the combination of drought, warming and intraspecific competition. In each experimental individual, we measured a wide set of eco-physiological traits and quantified their reproductive fitness. Using phenotypic selection analyses, we identified adaptive traits, i.e., those influencing individual fitness, in each experimental treatment. We also quantified the presence of genetic variation under each experimental condition, and how the phenotypic expression varied across conditions. We hypothesize that the presence of coocurring stresses will alter the adaptive value of traits (i.e., the patterns of selection) and reduce the presence of genetic variation, since harsher environments usually constraint the expression of genetic variation across genotypes and populations. Our study will further our understanding on the future adaptive responses to drought of gypsophile populations under more realistic environmental conditions.

P.0516 Extrafloral nectar is more costly and less inducible in shaded plants

Lucas J. R. Bartsch[1], Anselmo Nogueira[1], Laura C. Leal[2]

1 Universidade Federal do ABC – UFABC, São Bernardo do Campo, Brazil. 2 Universidade Federal de São Paulo – UNIFESP, Diadema, Brazil.

Plants exhibit many anti-herbivore defenses. Maintaining these defenses can reduce the carbon available for allocation to other plant functions. Therefore, any factor compromising a plant's carbon assimilation is expected to increase the relative cost of defense and its inducible nature. Extrafloral nectar is a carbon-based indirect anti-herbivory defense commonly inducible under herbivory events. However, the relative cost of this indirect defense under variable conditions, including situations of carbon limitation, is unclear. In this study, we investigated how photosynthetic restriction due to shading influences leaf traits, plant biomass, and the carbon investment and inducibility of extrafloral nectar in *Chamaecrista nictitans* (L.) Moench (Fabaceae). We cultivated 30 plants randomly separated in three levels of shading (0%, 30%, and 50%) and quantified leaf functional traits, plant biomass, and sugar mass of the extrafloral nectar before and after herbivory. Increasing shading causes an increase in leaf area and a decrease in leaf thickness, concomitantly with an increase in the aboveground plant biomass in contrast with a reduction in the belowground biomass. However, the carbon allocated to extrafloral nectar and the induced response to herbivory were lower as the shading level was higher. The shading constrained the plant investment in extrafloral nectar secretion due to an increase in the relative cost of extrafloral nectar secretion under low carbon assimilation conditions, preventing the plant from being able to respond to herbivory events by increasing sugar in nectar for protective ants. The decrease in carbon investment in this defense implies that defensive function may not be a plant priority under shaded conditions. In contrast, the maintenance of biomass accumulation throughout plant development remains crucial. Our study shed new light on the cost of the extrafloral nectar mediating ant-plant protection mutualisms and opened new avenues of investigation about the responses of these defenses to changes in habitat conditions.

P.0517 Leaf trait variation, phylogenetic signal and ecological strategies in the Italian endemic forest plants: preliminary evidence

Federico Selvi[1], Andrea Coppi[2], Roberto Canullo[3], Elisa Carrari[1], Cristina Gasperini[1], Emmanuele Farris[4], Leonardo Rosati[5], Camilla Wellstein[6]

1 University of Florence, Department of Agriculture, Food, Environment and Forestry, Florence, Italy. 2 University of Florence, Department of Biology, Florence, Italy. 3 University of Camerino, School of Biosciences and Veterinary Medicine, Camerino, Italy. 4 University of Sassari, Department of Chemical, Physical, Mathematical and Natural Sciences, Sassari, Italy. 5 University of Basilicata, Scuola di Scienze Agrarie, Forestali, Alimentari ed Ambientali, Potenza, Italy. 6 Free University of Bolzano, Faculty of Agricultural, Environmental and Food Sciences, Bolzano, Italy.

Endemic plant species represent the most valuable component of the flora of a given region, due to their restricted distribution and, often, vulnerability to habitat changes. The Italian flora includes ca. 1600 endemic species and subspecies, of which ca. 130 live in forest habitats, especially in the understory of the southern regions and islands. Overall, the biological, ecological and functional characteristics of these taxa are poorly known, making it difficult to predict their responses to forest management and disturbances. In the framework of a national project on this topic, we focused on the functional dimension, analysing six leaf traits associated with different resource-use strategies and ecosystem processes. Leaf area, fresh mass, dry mass, dry matter content, specific leaf area and nitrogen content were measured in ca. 30 Italian endemic taxa (one population per species) from different forest types and seed plant clades, as well as in selected non-endemic sister taxa. Our aims are: i) estimating the range and patterns of variation for each trait across our taxon sample, ii) exploring the relationships with major geographic and environmental characteristics of the population sampling sites, iii) determining Grime ecological strategies and comparing endemic vs. non endemic sister, and iv) evaluating the role of evolutionary constraints on each trait and determining their phylogenetic signal. Preliminary results point to broad interspecific variation and significant covariation between some traits. Grime strategies were also widely variable in terms of C, S and R percentages, with divergence in some endemic-non endemic species pairs. Blomberg K statistics suggests trait evolution to be largely independent of phylogeny, but some traits showed a significant signal when including non-endemic sister species in the analysis. Dependency of trait variation on environmental variables is still under study and more results will come once more species will be sampled.

P.0518 Do plant functional traits contribute to the maintenance of a flower colour hybrid zone?

Rosina Soler[1], Sean Stankowski[1,2], Parvathy Surendranadh[1], David Field[3], Nick Barton[1]

1 Institue of Science and Technology Austria, Klosterneuburg, Austria. 2 University of Sussex, Brighton, UK. 3 Macquarie University, Sydney, Australia.

Spatial variation in natural selection shapes phenotypic variation in wild populations and drives their evolution. Functional traits of plants influence growth, reproduction, and survival, and are therefore important components of fitness. In the *Antirrhinum majus* hybrid zone, a sharp transmission from yellow to magenta flowers implies that strong selection acts on flower colour. However, the agents of selection acting on colour variation remain unclear. Furthermore, the influence of other traits aside from flower colour on the eco-evolutionary dynamics within the zone also lacks clarity. We assessed functional trait variation according to phenotypic category (flower colour) over time, within an *A. majus* population in a hybrid zone of the Pyrenean mountains in north Spain. We used a multi-year dataset (2014-2020) including >20,000 sampled individuals to analyze variation in the following plant traits: number of flowering stems, plant height, survival past the first year, and node: height ratio. Plant traits varied greatly between years, but there was no obvious difference between floral colour categories. We found that plants that survive the first year are larger (on average twice as large) and produce more flowering stems (on average 3 times more) than first-year plants, likely contributing to higher reproductive success. However, the probability of finding old plants was significantly lower for hybrid individuals only during 2014 and 2018, which does not represent a clear reproductive barrier. We also discuss the effect of possible interactions between traits and year, and the influence of plant location by comparing the focal plant with its neighbour as a control. Our preliminary analysis highlights the importance of considering both temporal and phenotypic dimensions in understanding the evolutionary dynamics of plant fitness.

P.0519 The study on phylogenetic position of some Stephania spp. in Thailand

Thanakit Suparat[1], Thaya Jenjittikul[1], Saroj Ruchisansakun[1], Nicha Thawara[1]

1 Department of Plant Science, Mahidol University, Bangkok, Thailand.

The genus *Stephania* (Menispermaceae) consists of approximately 70 species distributed in the old-world tropics and subtropics, some of which are used as medicinal and ornamental plants. The Flora of Thailand project has recorded about 15 species of *Stephania* found in Thailand. Later, the research in 2020 reported a new species; *Stephania kaweesakii*. However, there has been no previous molecular research on this genus in Thailand, and some species are still lack DNA data. That is the reason for this research to study more molecular data on *Stephania* in Thailand. The silica gel dried leaves of 8 species have extracted DNA and sequenced on the nuclear region (Internal transcribed spacer (ITS) and chloroplast region (*psbA-trnH*). The new sequence dataset was combines with another *Stephania* species in Genbank. The phylogenetic tree is reconstructed using two methods: (1) Bayesian inference and (2) Maximum Likelihood. The study also examines some dominant morphological character to construct the ancestral state by Mesquite. Our result show that the phylogenetic position of *Stephania* included new species found in Thailand, and some character evolution can analyze the ancestral state, related to understand evolution of morphological parts of *Stephania*.

P.0520 Using the evolutionary history of conifers to establish conservation priorities in Northeast Mexico

Katia Treviño-Cuellar[1], Susana Favela-Lara[2], Catherine Kidner[1,3], Kyle Dexter[3], Hannah Wilson[1]

1 Royal Botanic Garden Edinburgh, Edinburgh, UK. 2 Universidad Autónoma de Nuevo Leon, Nuevo Leon, Mexico 3 The University of Edinburgh, Edinburgh, UK.

Conifers worldwide are in decline with climate change modelling predicting reduced ranges of suitable climatic conditions for their establishment as well as exacerbating other threats such as increased frequency and intensity of wildfires, pests, and pathogen outbreaks. Of the world's 615 conifer species, 34% is currently listed by the International Union for Conservation of Nature (IUCN) as being threatened. In Mexico climate projections for year 2050 show an increase in the desertification of the northeast region where 30 species of conifers inhabit, mostly restricted in the Sierra Madre Oriental Mountain range. As temperate zones become extinct, changes in the structure of the northeastern forests of Mexico will begin to become more and more evident. With the world climatic conditions making rapid and drastic changes in ecosystems, genetic diversity is now more than ever crucial for species adaptation and is a component of biodiversity that should not be overlooked when stablishing conservation priorities. We believe that genetic diversity within and across species must be understood and protected to give populations the chance to adapt and evolve into more resilient communities. Species are not fixed entities, but a cluster of dynamic populations going through microevolutionary processes of their own and in order to conserve species, we must respect and protect the evolutionary processes that lay underneath the species concepts, which depend strictly on genetic diversity. National conservation actions are urgently needed to ensure that most of our forest's biodiversity is preserved, but with limited financial resources and time, what species and areas matter most? The main objective of this project is to explore the genetic variation of conifer species in NE Mexico and use an integrative approach using GIS, population structure analyses, and phylogenetics to understand the distribution of genetic resources across the landscape and inform conservation actions.

P.0521 Aquatic, amphibious and terrestrial Isoetes (Lycopodiopsida): ecological and evolutionary aspects

Angelo Troia[1], Daniel F. Brunton[2]

1 University of Palermo, Palermo, Italy. 2 Canadian Museum of Nature, Ottawa, Ontario, Canada.

The nearly cosmopolitan genus *Isoetes* is the only representative of one of the three currently living evolutionary lines within Lycophytes. It is important as witness to and relic of the first solutions adopted by vascular plants to colonize the terrestrial subaerial environment of the planet. According to recent estimates, there are more than 200 living species. They colonize a wide range of habitats, from the bottom of permanent lakes to seasonally saturated meadows and ephemeral bedrock pools. Considering the few morphological characters useful for characterizing species, ecology can be an important factor in differentiating and characterizing taxa. Moreover, the presence of species adapted to live permanently underwater and at least seasonally exposed species living in the air (with intermediates between the two extremes) can be interpreted from an evolutionary point of view. Unfortunately, being rare plants often overlooked due to their unobtrusive habit and their uncommon habitats, makes gathering *Isoetes* data and observations difficult on a global scale. We adopted the old ecological subdivision in aquatic, amphibious, and terrestrial species, as re-defined from Troia & Greuter (2015). We tried to assign each of the currently recognized species to one of these 3 categories; this was not easy or possible in some cases, both for the lack of information on some species and the apparently variation between one category and another in others. Preliminary results suggest that aquatic species are ca. 52%, amphibious ca. 42%, and terrestrial just the (ca.) 6%. In addition, we have tried to investigate the distribution of the three ecological categories along the evolutionary history of the whole genus or of single clades, with interesting observations.

References: Troia A. & Greuter W. (2015) A conspectus of and key to Greek *Isoetes* (Isoetaceae), based on a reassessment of Haussknecht's gatherings of 1885. Willdenowia 45: 391-403.

P.0522 The role of biotic interaction and temperature in the elevational distribution of two Stewartia species.

Shuntaro Watanabe[1]

1 Department of Biology, Kagoshima University, Kagoshima, Japan.

Many species' range limits occur across continuous environmental gradients without obvious barriers imposing them. Such species distribution results from a complex suite of abiotic and biotic processes including adaptation, ecological interactions and reproductive dynamics but disentangling these factors in present distribution is still challenging. To address this problem, we focused on the elevational distribution in which two closely related and reproductively isolated plant species. We surveyed elevational distribution of two *Stewartia* species (*S. monadelpha* and *S. pseudocamellia*) in 10 mountains in while collecting in situ temperature and precipitation data in southwest Japan. We first tested the hypothesis that temperature limits elevational distribution by comparing the degree of overlap in the vertical distribution of the two species and temperature. Second, we tested whether negative interspecific interaction (e.g., competition) limits elevational distribution by searching for distributional evidence of competition between sympatric congeners and for evidence of competitive release when the congener was absent. We found that when two species coexist in same mountain, lower elevation area tends to be dominated by *S. monadelpha*, whereas two species tend to coexist at higher elevation area suggest habitat segregation along elevation are often imperfect. We also found that *S. pseudocamellia* tends to expand their range to lower and warmer area when *S. monadelpha* was absent, suggesting competitive release. These results suggest that negative interspecific interaction results in coexistence of closely related species in unsuitable environment (e.g., high elevation area) and interspecific interaction among closely related species could be important factor for structure the species warm range limit.

P.0523 A Benford's law based model for determining the boundaries of a floristic community

Justin K Williams[1]

1 Sam Houston State University, Huntsville, USA.

Communities are interacting populations of various individuals of different species common to a specific location. Despite having a clear definition for community, there is not a clear understanding of where the boundary of a community should be defined. Most often communities are understood on a fine scale in terms of local processes or symbiotic relationships, such as the interaction between a flower and its pollinator, or a predator and its prey. However, this view of a local community has been criticized for not incorporating the full scale and complexity of a community. Ricklefs (2008) argues that it is more useful to think of communities on a regional scale, while conceding that at present there is *no model/system for determining regional size*. This study proposes a model for determining the size of a community at the regional scale by utilizing adherence to Benford's Law. By analyzing floras at various scales and their adherence to Benford's Law, the model was able to determine a breakpoint at which vegetative communities no longer comply to Benford's Law. This break from Benford's Law represents the boundary of a floristic community at the regional scale. This model is preliminary and has only been tested on twenty-three different floras, but the results appear promising and as further data accumulates, it is predict the model will remain sound.

S.059. EVOLUTIONARY HISTORY OF ARID FLORAS AND THEIR UNDERLYING BIOLOGICAL SURVIVAL MECHANISMS

P.0524 Metabolite evolution in desert plants: defenses and adaptations

Arora S.[1], Barupal M.[1]

1 Department of Botany, JNV University, Jodhpur, Rajasthan, India.

Desert plants have evolved intricate defense mechanisms to combat biotic stresses and adapt to climatic fluctuations. Metabolites play crucial roles in mediating these adaptive responses, yet their evolutionary trajectories in desert plants remain poorly understood. This literature survey investigates the evolution of metabolites in desert plants, with a focus on their involvement in defense systems and climatic adaptations. Through an extensive review of existing studies across various species and ecological contexts, specific metabolites associated with defense responses against biotic stresses and facilitation of climatic adaptations are identified. Key metabolic pathways contributing to plant resilience in arid environments are synthesized, emphasizing the importance of metabolic plasticity in extreme conditions. Desert plants have evolved efficient photosynthetic strategies, such as Crassulacean acid metabolism (CAM) and C_4 pathways instead of solely relying on the C_3 pathway, further enhancing their adaptive capabilities. Plants in arid regions harbor unique chemicals that aid in adaptation to the prevailing harsh conditions. The water stress experienced by these plants triggers the production of high quantities of reactive oxygen species (ROS), which, through a series of pathways, ultimately leads to increased production of specific secondary compounds. This review provides valuable insights into the evolutionary dynamics of metabolites in desert plants.

P.0525 Climatic drivers in Strombocarpa strombulifera: Evidence of spring physiological traits on flower production

Felipe S. Carevic[1,2], Roberto Contreras[2,3], Erico Carmona[3], Ermindo Barrientos[4].

1 Laboratorio de Ecología Vegetal, Facultad de Recursos Naturales Renovables, Universidad Arturo Prat, Iquique, Chile. 2 Millennium Nucleus on Applied Historical Ecology for Arid Forests, Santiago, Chile. 3 Centro Regional de Investigación y Desarrollo Sustentable de Atacama, Universidad de Atacama, Copiapó, Chile. 4 Laboratorio de Bionanomateriales, Facultad de Recursos Naturales Renovables, Universidad Arturo Prat, Iquique, Chile. 5 Engineering Agriculture Department, Natural Sciences and Agriculture Faculty, Universidad Técnica de Oruro, Oruro, Bolivia.

Strombocarpa strombuliferais a widely distributed woody species distributed along arid ecosystems in America. The interannual evolution of ecophysiological parameters and their effects on fruit production and flower sprouting in Strombocarpa strombulifera were studied for three years in a natural population distributed in the Atacama Desert. Xylem water column tension, pressure–volume curves, specific leaf area (SLA), and chlorophyll fluorescence parameters were assessed. Flower sprouting was assessed in different weeks using tagged flowers. To assess fruit production, four small containers were placed under twenty-five individuals, allowing the estimation of total annual production and individual production. We found considerable variability between years and between individuals. Positive relationships were found between plant water parameters, SLA, and chlorophyll variables measured in spring at flower sprouting and during fruit production. A negative correlation was found between the mean of the minimum temperatures in spring and flower sprouting. These results suggest that spring ecophysiological parameters strongly affect the reproductive status of S. strombulifera. The results also reflect the potential of this species to adapt to a hyperarid climate by preserving a high relative water content before flower sprouting.

P.0526 Chloroplast genome of three species from Mexican arid zones of the genus Acacia s.l. (Leguminosae: Caesalpinioideae)

Ember Hidalgo Franco[1], Anahí Canedo Texón[2], Gabriela Castellanos Morales[2], Sandra Gómez Acevedo[1]

1 Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México. Estado de México, Mexico. 2 El Colegio de la Frontera Sur, Unidad Tabasco, Tabasco, Mexico.

The Tehuacán-Cuicatlán Valley is located in the Southeast of the state of Puebla and in the Northeast of the state of Oaxaca, Mexico. This area is of particular interest for understanding the evolutionary dynamics of arid and semi-arid zones, since it is one of the main reservoirs of biological diversity in America. The main components of this type of vegetation include species of Acacia s.l., a genus that is currently divided into 5 genera, of which two (Vachellia and Senegalia) are found in arid Mexican areas. Vachellia constricta is a tetraploid species whose distribution extends from Mexico to the United States, while diploid species Vachellia bilimekii and Senegalia acatlensis are endemic to arid Mexican areas. These three species are key elements of the Tehuacán-Cuicatlán valley and in the best of cases the taxonomic description is available, with important characteristics such as the size and organization of the chloroplast genome unknown. Due to this, in this work the characteristics of the chloroplast genome for three species of "acacias" are presented for the first time, allowing us to show the comparison between a species with a wide distribution against two with a restricted distribution, as well as the contrast between genomes of two genera that were previously united. The results obtained provide relevant information on the evolution of the genus Acacia s.l. in Mexico.

P.0527 Plant clonality along the gradient of aridity: Lamiaceae in Iranian Plateau

Chonour Mahmoudi[1], Tomáš Herben[1], Jitka Klimešová[1]

1 Department of Botany, Charles University, Czech Republic.

Clonal growth, a widespread growth form in plants, can play a crucial role in their survival and persistence, while we already know that their occurrence changes along environmental gradients, there is very limited data on their distribution in arid and subtropical regions. We aim to address a broader question how clonal growth strategies occur along climatic gradients with special focus on dry conditions. We thus broaden our scope, shifting our focus to Iran and the Middle East as our study region, beyond the previously explored territories. Iran's unique climate gradients, spanning from high mountains to lowland deserts, provide an ideal region for understanding the adaptive role of clonality, particularly in extending the range of the water availability gradient well beyond what has been studied. We study the Lamiaceae family, which is an excellent candidate for studying the relationship between clonality and environmental factors due to its diverse clonal growth forms and high species diversity. We analyzed the diversity of clonal growth traits across Lamiaceae species and linked them to species distribution patterns. We explore whether gradients in environmental conditions, namely drought, correlate with shifts in the frequency and types of clonality. Further, we use phylogenetic data to determine individual clonal growth organs in the family. This will help to identify how ecological conditions have influenced evolution of clonality as an unexplored component of the plant form response to the environment.

P.0528 The Brazilian semi-arid is becoming arid: insights from historical collections on aridification threats to plant biodiversity

Reyjane P. Oliveira[1], Grênivel M. Costa[2], Domingos B.O.S. Cardoso[3,4], Evandro N. Silva[1], Luciano P. de Queiroz[1], Marcos C. Dórea[1], Ligia S. Funch[1], Daniela S. Carneiro-Torres[1], Ana M. Giulietti-Harley[1]

1 Universidade Estadual de Feira de Santana, Bahia, Brazil. 2 Universidade Federal do Recôncavo da Bahia, Bahia, Brazil. 3 Universidade Federal da Bahia, Bahia, Brazil. 4 Instituto Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil-

The Brazilian semi-arid (BSA) region is the largest and most biodiverse nucleus of the neotropical seasonally dry tropical forest and woodland (SDTFW) biome. A recent report from Brazilian spatial and on natural disasters agencies (INPE and CEMADEN, respectively) identified a previous semi-arid area measuring 5,700 km^2 experiencing an arid climate in northern Bahia state, by comparing its aridity indexes over seven decades. Three municipalities are enclosed in this newly discovered arid region (Abaré, Chorrochó, and Macururé), and three are only partially enclosed (Juazeiro, Curaçá, and Rodelas). By examining a taxonomically verified database of virtual collections from national and regional herbaria, we show how rich the region's flora undergoing aridification is. We found 388 specimen records, with more than 95% coming from the PPBIO program, an extensive network of biodiversity inventories in the BSA. Abaré has the most records (245 samples), followed by Chorrochó (126) and Macururé (17). A total of 149 plant species were found in 54 families and 115 genera, most of which were from Angiosperms. The most diverse families repeat the floristic pattern of the Brazilian Caatinga (SDTFW): Fabaceae (26 species), Euphorbiaceae (14), Malvaceae (13), and Cactaceae (7), from which 23 species are Caatinga endemic. *Cenostigma pyramidale* (Fabaceae) was recorded in the three municipalities, while more than 80% of the species were recorded in only one municipality. *Gossypium mustelinum* (Malvaceae), collected in 1988 (a population of 20 individuals), is listed as endangered on the IUCN Red List, and the collection point is now a pasture. Many species recorded in the arid area have not been collected since 1950. Aridification has caused agricultural land degradation and environmental deforestation to establish new crop fields or pastures, threatening rare species. Further investigation must shed light on the possible influence of aridification on the decline or local extinction of their populations.

P.0529 South American cacti shed light on plant diversification of arid and semiarid regions in the Neotropics

Monique Romeiro-Brito[1], Milena C. Telhe[1], Flávia M. Lanna[2], Bryan C. Carstens[2], Matias Kohler[1], Luciano A. Digiampietri[3], Daniela C. Zappi[4], Nigel P. Taylor[5], Fernando F. Franco[1], Evandro M. Moraes[1]

1 Departamento de Biologia, Centro de Ciências Humanas e Biológicas, Universidade Federal de São Carlos, Sorocaba, Brazil. 2 Museum of Biological Diversity & Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, USA. 3 Escola de Artes, Ciências e Humanidades, Universidade de São Paulo, São Paulo, Brazil. 4 Instituto de Ciências Biológicas Universidade de Brasília, Brasília, Brazil. 5 University of Gibraltar, Gibraltar Botanic Gardens Campus, Gibraltar.

The global expansion of arid environments during Miocene is the frequently associated with the diversification of succulent lineages. In addition to this event, various life history and reproductive traits in succulents have been proposed as the key traits which promote diversification of lineages in the Neotropics. Here we focused on the tribe Cereeae (Cactaceae) to explore the role of biotic and abiotic traits in the diversification of succulent lineages in South America. We estimated a calibrated tree to infer major biogeographic events and ancestral geographic ranges in this group. We also explored the contribution of biotic and abiotic traits in the diversification of this tribe using traditional diversification analysis and machine learning models. The Cereeae diverged in the late Miocene, forming a widespread region from Central and Southern Andes through Espinhaço Mountain Range in eastern Brazil. A series of vicariant events isolated major lineages geographically in the Peruvian Andes, Southern Andes, and in the Espinhaço Mountain Range. The recolonization of eastern Brazil occurred through long-distance dispersal events in the late Miocene and Pliocene. Biotic traits, such as globose growth form and hummingbird pollination, were the most important traits associated with high speciation rates in Cereeae. Our findings reveal a continuous distribution of Cereeae across the west-to-east region of South America during the late Miocene period. Following this, the vicariance events that led to the segregation of east and west lineages occurred concurrently with marine transgressions and the assembly of Cerrado domain during the same period. Furthermore, they suggest that morphological and ecological traits exert a stronger influence on the diversification within the Cereeae lineages than abiotic traits. The results of this study emphasize the role of the Southern Andes region as a source of pre-existing dry-adapted plant lineages capable of colonizing new xeric environments during the Miocene period.

P.0530 Correlations between biome shifts, speciation, and trait evolution in genera from Cereinae tribe (Cactaceae)

M. C. Telhe[1], M. Romeiro-Brito[2], F. F. Franco[1], E. M. Moraes[1], T. N. C. Vasconcelos[3]

1. Biology Department, Federal University of São Carlos, Sorocaba, Brazil. 2. Natural History Department, Florida Museum of Natural History, Gainesville, USA. 3. Ecology and Evolutionary Biology Department, University of Michigan, Ann Arbor, USA.

The Neotropical region is well known for its species richness, although how this species richness was established and maintained is still subject to discussion. Plant lineages undergoing biome shifts have been identified in large numbers in the Neotropical region, indicating a key role of this process in assembling regional communities. However, the role of biome shifts between dry and open environments in changing diversification rates in plant lineages is poorly understood. Although the studies investigating biome shifts yield critical evolutionary insights into the Neotropics, evolutionary changes allowing lineages to transcend biome boundaries, such as niche evolution, are rarely considered. With the advancement of ecological niche modeling methods and niche evolution inferences, it is now possible to combine niche evolution with precise quantification of lineage responses to climate, allowing accurate inferences of biome shifts. Here, we investigated how biome shifts between Seasonally Dry Tropical Forest and Savanna biomes and past climate oscillations may have affected the distribution and diversification of cacti, contributing to the understanding of the role of these events in the diversification of the tribe Cereeae. To reach this goal, over 500 orthologous loci developed with Cactaceae591 probe-set, biogeography, phylogenetic niche modeling, and diversification rates estimation were integrated to answer when and where biome shifts occurred in the evolutionary history of cacti lineages and how they contribute to its species richness.

S.060. EVOLUTIONARY TRENDS IN SKYISLANDS: NEW INSIGHTS IN THE SEARCH OF MAJOR BIOGEOGRAPHIC AND PHYLOGEOGRAPHIC PATTERNS

P.0531 Speciation on sky islands: The diversification of Cirsium (Carduoideae: Compositae) on mountaintops in western North America

Carolina M. Siniscalchi[1], Jennifer R. Ackerfield[2], Ryan A. Folk[1]

1 Department of Biology, Mississippi State University, USA. 2 Denver Botanic Gardens, USA.

Alpine ecosystems of western North America are comprised of a series of archipelago-like ‘sky islands’ consisting of high-elevation habitat surrounded by a matrix of low-elevation environments. These disjunct sky islands formed when the continuous alpine communities present during the last glacial maximum fragmented and were forced to retreat upslope in response to warming temperature, providing refugia for formerly widely distributed organisms.

Cirsium ("thistles") consists of approximately 100 species in North America, 12 of which are exclusive to alpine ecosystems. *Cirsium* is also hypothesized to have undergone a geologically recent, rapid, continent-wide radiation. Therefore, reconstructing the biogeographic history of mountaintop-dwelling *Cirsium* would provide insight into the origin of the alpine flora during Pleistocene glacial cycles. The resulting biogeographic and diversification analyses found that North American alpine species of *Cirsium* originated from at least four lowland progenitors. The integrated effects of niche conservatism and glacial-interglacial cycles played a critical role in shaping current distributional patterns in alpine mountain systems as well as adjacent low-elevation canyons of the Colorado Plateau. The Colorado Plateau is a high-elevation mesa bounded by mountain ranges and deeply cut by the Colorado River canyon system. One of the most unique habitats of the Colorado Plateau is that of hanging gardens, which form a patchwork of low-elevation "islands" along this canyon system. Three instances of sister-species pairs comprised of species restricted to hanging gardens and species in alpine habitats were also recovered. These results are consistent with ecological vicariance involving fragmentation of a once more widespread common ancestor. Therefore, current alpine and hanging garden populations of *Cirsium* are hypothesized to be the result of Pleistocene population fragmentation in conjunction with glacial-interglacial cycles, with these two markedly different habitats offering refugia for *Cirsium*. Isolation and subsequent diversification resulted in the genetically distinct, yet superficially similar alpine species present today.

P.0532 The role of Pleistocene dispersal in shaping species richness of sky-island wintergreens from the Himalaya-Hengduan Mountains

Xiao-Juan Cheng[1], Peter W. Fritsch[2], Yan-Jun Lin[1], Ming-Ying Zhang[3], Lu Lu[1]

1 School of Pharmaceutical Sciences and Yunnan Key Laboratory of Pharmacology for Natural Products, Kunming Medical University, Kunming, China. 2 Botanical Research Institute of Texas, University Drive, Fort Worth, USA. 3 College of Pharmacy, Shanxi University of Chinese Medicine, Xi'an, China.

In addition to topography and climate, biogeographic dispersal has been considered to potentially influence plant diversity in the Himalaya-Hengduan Mountains (HHM). Yet, the mode and tempo of sky-island dispersal and its influence on species richness has been still little explored. In this study, we test the hypothesis that dispersal has affected current local species richness, by *Gaultheria* ser. *Trichophyllae*, a sky-island alpine clade within the HHM. We then inferred the biogeographic dispersal dynamics in geographic distributions, and performed a few correlation tests on dispersal (i.e., direction, distance and occurrence time) and regional species richness. We found that *G.* ser. *Trichophyllae* originated at the end of the Miocene and mostly evolved toward higher longitudes (eastward), with the eastward short-distance dispersals and westward long-distance dispersals frequently occurred. We discovered a prevalence of eastward short-distance dispersals in either glacial periods or interglacials, which may be facilitated by the reorganization of paleo-drainages and monsoon intensification through time. We suggested the dispersal occurrence time (glacial period) and distance (short-distance), rather than frequency (times) significantly influence the pattern of species richness of *G.* ser. *Trichophyllae*. This study facilitates a more comprehensive understanding of biodiversity in the sky islands within the HHM.

P.0533 Edaphic ecology in sky island-like systems—a case study in the Heuchera parviflora complex

Dexcem Pantinople[1], Nicholas Engle-Wrye[1], Ryan Folk[1]

1 College of Arts & Sciences, Mississippi State University, Mississippi State, USA.

Inherently discontinuous habitat requirements, whether montane, edaphic, or otherwise, generate island-like, geographically discontinuous distribution patterns in continental landscapes, with distinct implications for population-level processes and speciation mechanisms. Yet, the implications of distinct niche and organismal traits for understanding broader biogeographical patterns remain poorly implemented in current paradigms. From the applied point of view, especially in plants, the geographic complexity and lack of study in taxa distributed in ecological islands is likely also to result in cryptic species-level diversity and gaps in conservation effort. Here, I investigate the unique phylogeographic and speciation processes in terrestrial island-like systems using the *Heuchera parviflora* group (subsect. *Villosae*, Saxifragaceae). The group, as wide-ranging specialists of rockhouses (shallow caves and cliff undercuts) with diverse edaphic ecology, a highly disjunct distribution, and a relatively established phylogenetic framework, makes an ideal model system for studying island-like continental distribution patterns. To discover phylogeographic structure and test the current hypothesis of relationships in the group, I ran phylogenetic analyses on a target capture dataset comprising 277 loci and dense population-level sampling, using concatenation in RAxML and coalescent methods in ASTRAL-III. To discover significant predictors explaining species distributions and test whether any phylogeographic structure is mediated by refugial or edaphic mechanisms, I applied a demographic modeling approach using GATK4 and DIYABC, implementing a series of phylogeographic hypotheses based on recognized refugial areas and gridded soil datasets from SoilGrids. Preliminary results identify north-south phylogeographic differentiation between each of the taxa recognized currently in the group, in addition to the phylogenetically deeper west-to-east pattern already known. Initial ASTRAL analyses demonstrate a strong phylogenetic backbone and phylogeographic resolution within several subclades. My work has also generated surprises including a new species and the inclusion of *H. villosa* within a paraphyletic *H. parviflora* group, suggesting the need for further investigations on obscure, fragmented habitats.

S.061. FERN AND LYCOPHYTE EVOLUTION: A PHYLOGENOMIC PERSPECTIVE.

P.0534 The third opinion on fern phylogenetics with novel insights into their mitogenome evolution

Glenda G. Cárdenas[1], Samuli Lehtonen[1]

1 Biodiversity Unit, University of Turku, Turku, Finland.

The current understanding of fern phylogeny is primarily based on plastid and nuclear sequences, but the third genome—the mitogenome—has remained practically unstudied. We inferred the first broad scale fern phylogeny based on mitogenomic data, obtained from the One Thousand Plant Transcriptomes Initiative project, and compared it with the plastid phylogeny. The trees were mostly congruent and corresponded to the current understanding of the fern phylogeny, but we observed different evolutionary patterns between the two genomes. Protein-coding markers located in the plastome had, on average, over two times higher substitution rate than the markers from the mitogenome. The similar rate variation pattern between the genomes in different fern lineages supports the idea that a common mechanism, like life history traits, drives the rates of molecular evolution. The few conflicting nodes we observed have also been difficult to resolve in other studies, suggesting that even genomic data may not suffice to resolve them.

P.0535 Taxonomic complexes and the evolution of niche specificity in tropical American plants: the case of Trichomanes (Hymenophyllaceae)

Laura Kragh Frederiksen[1], Wolf Eiserhardt[1,2], Hanna Tuomisto[1,3]

1 Aarhus University, Aarhus, Denmark. 2 Royal Botanic Gardens, Kew, UK. 3 University of Turku, Turku, Finland.

Correct species identification is crucial in ecological and evolutionary research and for conservation planning, but is often difficult to achieve for tropical plants. Our field observations of Amazonian ferns have revealed that many well-known widespread species are actually species complexes, where the constituent (often previously unnamed) species have smaller distributional ranges than the complex as a whole. Different species of such complexes may be geographically isolated, but they may also be found sympatrically in forests that differ in soil properties. In some cases, species identification remains elusive, which might reflect either incipient/incomplete lineage divergence or hybridization. Combining phylogenetic information with distributional and environmental information can help to elucidate to what degree lineage diversification has been driven by geographical isolation vs. adaptive radiation. The fern genus *Trichomanes* (Hymenophyllaceae) is common and species-rich in the wet forests of tropical America and provides an interesting group for studying these questions. Our study combines morphological and genetic analyses to reconstruct the evolutionary history and resolve the taxonomy of these ferns. We take advantage of systematic field observations from ecological inventories to address niche specificity and niche evolution, which enhances our understanding of the drivers of plant evolution both in this specific case and in general.

P.0536 Unravelling the diploid-tetraploid complex in Cheilanthes mollis, a desert coastal inhabitant from Chile

Rosa Ramirez-Castillo[1], Amanda L. Grusz[2,3], Claudio Palma-Rojas[1], Cristian Araya-Jaime [1,4], Pedro Jara -Seguel[5], Hugo A. Benítez[6,7], Andrea Loayza[4,8]

1 Departamento de Biología, Universidad de La Serena, La Serena, Chile. 2 University of Minnesota Duluth, USA. 3 National Museum of Natural History, Smithsonian Institution, Washington, USA. 4 Instituto de Investigación Multidisciplinario de Investigación y postgrado, Universidad de La Serena, La Serena, Chile. 5 Facultad de Recursos Naturales, Universidad Católica de Temuco, Temuco, Chile. 6 Centro de Investigación de Estudios Avanzados del Maule, Universidad Católica del Maule, Talca, Chile. 7 Centro de Investigación en Recursos Naturales y Sustentabilidad, Universidad Bernardo O'Higgins, Santiago, Chile. 8 Instituto de Ecología y Biodiversidad, Ñuñoa, Chile.

Polyploidy is a widespread and relevant phenomenon in ferns, with over 95% of homosporous fern species being polyploids (Wood et al., 2009; Barker and Wolf, 2010). Despite this prevalence, ferns remain one of the most understudied cytogenetic groups. This discrepancy can often be attributed to the challenges of using the mitotic chromosome squash technique, originally designed for angiosperms (personal observation). While squash preparations are considered the most precise method for assessing ploidy level and chromosome number (Kirov et al., 2014; Nakato et al., 2016; Singh, 2016; Windham et al., 2020), they present several difficulties when applied to seedless plants like ferns (Ramirez-Castillo et al., in press). Knowing the exact chromosome number of a species is especially important in incompletely resolved tribes like the Cheilanthoideae (Pteridaceae), as it can provide key insights into phylogenetic relationships (Levin, 2002; Clark et al., 2016; Windham et al., 2020). In recent years, efforts have been made to resolve the phylogenetic relationships of South American Cheilanthoides uncovering new species and polyploid complexes (Sosa et al., 2021, Hernández et al., 2015; Ponce and Scataglini, 2018). Traditional cytogenetic tools and accurate morphological techniques are needed to characterize the hidden diversity within the group. Here, we uncover a diploid-tetraploid complex in Cheilanthes mollis, a poorly explored desert-inhabiting fern in northern Chile, newly developed and refined mitotic chromosome squash technique, as well as geometric morphometrics and gametophyte reproductive strategies characterization

P.0537 Character evolution of modern taxa as a tool for fossil assignments: the case of Cretacifilix fungiformis (Dryopteridaceae)

Ledis Regalado[1], Harald Schneider[2], Patrick Müller[3], Alexander R. Schmidt[1]

1 University of Göttingen, Göttingen, Germany. 2 Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun, Yunnan, China. 3 Amber Study Group, Geological-Palaeontological Museum of the University of Hamburg, Hamburg, Germany.

Cretacifilix fungiformis, a fossil fern from mid-Cretaceous Kachin amber from Myanmar, was previously assigned to the eupolypod ferns based on the presence of sporangia with a vertical annulus and sporangial stalks 2–3 cells thick, along with monolete spores with a distinct perine. However, the proposed affiliation of this fossil to derived families of eupolypods remained unclear due to the inaccessibility of the holotype and the insufficient documentation of relevant characters. We re-evaluated the relationships of this fossil taxon based on additional leaf fragments recently discovered from the same amber deposit. We assessed identifiable features of the fossil species through an ancestral character state reconstruction using a comprehensive, time-calibrated phylogeny of the eupolypod ferns. Our morphological evaluation supported the placement of *C. fungiformis* within the eupolypod ferns and our character state reconstruction of extant eupolypod families and genera recovered morphological similarity of *Cretacifilix* to the closely related genera *Arachniodes* and *Dryopteris*, supporting an assignment of this fossil genus to the species-rich family Dryopteridaceae within the Polypodiineae.

P.0538 Development and description of the gametophytic phase of a selection of species of the genus Parablechnum (Polypodiopsida)

Guillermo Santos[1], Carmen Prada[1], Luis G. Quintanilla[2], Sonia Molino [1,3], Rafael Medina[1]

1 Dept. Biodiversidad, Ecología y Evolución, Facultad de Ciencias Biológicas, Universidad Complutense de Madrid, Spain. 2 Dept. Biología y Geología, Física y Química inorgánica, Universidad Rey Juan Carlos, Madrid, Spain. 3 Dept. de Biociencias, Facultad de Ciencias, Biomedicina y Salud, Universidad Europea de Madrid, Spain.

Ferns and lycophytes are unique among land plants in having both generations of their life cycle (gametophyte and sporophyte) living as independent organisms. This independence is reflected in multiple differences among them, from ecological needs to physiological functions, and even distribution patterns. Thus, it is not possible to fully understand a fern species without knowing both phases. However, the gametophyte of many ferns is very little studied, and often completely unknown. Furthermore, previous studies have found that the development and traits of the gametophyte may provide characters of taxonomic value. Here, we present a case study within the genus *Parablechnum*. This genus belongs to the Blechnaceae, and contains about 68 species, mostly distributed in the Austropacific region and the Neotropics. Although the sporophytic phase of most species of the genus is completely described, the gametophyte remains an enigma, this phase is completely unknown and we do not know what importance it may have for the taxonomy and biology of *Parablechnum*. In this work, we studied the development of eight *Parablechnum* species from the Neotropical diversification centre. Spores were sown in mineral agar during field work to maintain their viability until culture under controlled conditions (22°C, 12-hour day/night photoperiod). The results indicate that all the studied species have a *Vittaria*-type germination and *Adiantum*-type cordate development. The eight species formed male, female, and hermaphrodite gametophytes. In most of them, there were no glandular hairs, a typical trait of many Blechnaceae gametophytes and in some cases with the presence of antheridiogen. The cultured gametophytes will be used for further genomic work developed under a Hyb-Seq approach to check whether the use of haploid tissue simplifies the bioinformatic processing of polyploid taxa sequences.

P.0539 Synopsis of native Lycophytes (Lycopodiopsida) and Ferns (Polypodiopsida) from Chile

Javian Gallardo-Valdivia[1], Marcelo D. Arana[2], Gloria I. Rojas[3], Paulette I. Naulin[1]

1 Universidad de Chile, Santiago, Chile. 2 Universidad Nacional de Río Cuarto, Córdoba, Argentina. 3 Museo Nacional de Historia Natural. Santiago, Chile.

The knowledge of the state of the art of national floras enables decision-making for conservation purposes. Lycopodiopsida (clubmosses) and Polypodiopsida (ferns), classically known as "pteridophytes," correspond to the first terrestrial plants with a developed system of conducting tissues in the sporophyte. They represent the second largest group of vascular plants in terms of diversity, estimated at 12,000 species globally, while in Chile, the diversity of this group is estimated at 160 specific and infraspecific taxa, mainly distributed in the temperate-humid zones of the country. The objective of this work is to present the pteridological richness of the flora of Chile. A comprehensive literature review was conducted in specialized literature, in addition to the examination of specimens from herbaria (CONC, SGO and EIF). The results show that the Chilean pteridoflora consists of 164 specific and infraspecific taxa distributed in 23 families and 57 genera, representing 2.9% of the vascular flora of Chile. 35.4% are endemic species, while 64.6% are native. Although the Chilean pteridoflora is relatively small considering the global diversity, its taxa exhibit high singularity, mainly due to long periods of isolation and vicariance during the evolutionary history and biogeography of the flora.

P.0540 Taxonomic revision of Equisetum (Equisetaceae) in Chile

Javian Gallardo-Valdivia[1], Marcelo D. Arana[2], Gloria I. Rojas[3], Paulette I. Naulin[1]

1 Universidad de Chile, Santiago, Chile. 2 Universidad Nacional de Río Cuarto, Córdoba, Argentina. 3 Museo Nacional de Historia Natural. Santiago, Chile.

The genus *Equisetum* is the only living representative of the family Equisetaceae, of the order Equisetales, subclass Equisetidae, Polypodiopsida. The distribution of the group is cosmopolitan, with 18 species reported globally, while in Chile classically three native species have been reported (*Equisetum giganteum* L, *Equisetum pyramidale* Goldm., and *Equisetum bogotense* Kunth). Type specimens housed at B, BM, BR, FR, G, P and S were reviewed online and through JSTOR. Also, the collection of CONC and SGO which include nomenclatural types were reviewed. Additionally, the protologue of all taxa cited for Chile were reviewed. The genus *Equisetum* in Chile is represented by three species: *Equisetum xylochaetum* Mett., *Equisetum pyramidale* Goldm., and *Equisetum bogotense* Kunth. According to the descriptions of *Equisetum giganteum* L., none of the specimens deposited in the SGO and CONC herbaria match the taxon in question, corresponding most of cited specimens to *E. pyramidale* in the central-southern zones of Chile, while specimens collected in the northernmost regions correspond to *E. xylochaetum*. After reviewing the type specimens and the literature associated with the protologues of the taxa, *E. giganteum* is excluded from the flora of Chile, while *E. pyramidale* (endemics of central Chile) and *E. xylochaetum* endemics to the Atacama Desert in southern Peru and northern Chile are both recognized as a valid species.

P.0541 Systematics of the Elaphoglossum dendricola Clade (Elaphoglossum sect. Lepidoglossa, Dryopteridaceae), a Neotropical group of ferns

Lucia Vargas-Longas [1,2]Alejandra Vasco[2]

1 Texas Christian University, Fort Worth, USA. 2 Botanical Research Institute of Texas, Fort Worth, USA.

Elaphoglossum is one of the most diverse fern genera, with more than 600 species pantropically distributed. Historically, the genus has represented a taxonomic challenge mainly because of the large number of species and the similarity among them. Less than 15% of the species in the genus have been the subject of detailed taxonomic revisions; therefore, species limits are not well understood, and many species remain undescribed. Molecular phylogenetic hypotheses have served as a framework to focus on smaller coherent clades for monography. Our recent phylogenetic reconstructions, based on chloroplast markers, found a clade within *Elaphoglossum* sect. *Lepidoglossa* distinguishable by morphological characters, with an interesting geographic distribution, and a convenient size for a taxonomic revision. We called this group the *Elaphoglossum dendricola* Clade. This research aims to overcome some of the challenges in the study of *Elaphoglossum* by focusing on resolving the systematics and taxonomy of the *E. dendricola* Clade and by assessing the conservation status of its species. The clade has around 13 already described species under at least 22 validly published names. Herbarium revision also indicates that there are at least six putatively undescribed species. Species of this clade are characterized by long-creeping ascending rhizomes with long, curly scales and scaly leaves with resinous dots and round or acute apex. Diagnostic characters to distinguish among species are mostly based in the morphology of mm-long scales of rhizomes, petioles, and leaves. The clade is mostly distributed over 2,400 m in Panama and in the Tropical Andes, both biodiversity hotspots of conservation priority. Taxonomic revisions are essential to understand and document the diversity and distribution of species on Earth, and to provide good and expert baseline information to support decisions that help their conservation.

P.0543 Beneath the surface: the sporoderm evolution of homosporous ferns using sculptural and wall-stratification characters

Agustina Yañez[1], Ignacio H. Escapa[2], Gonzalo J. Marquez[3], Michael Sundue[4]

1 Museo Argentino de Ciencias Naturales (MACN-CONICET), Ciudad de Buenos Aires, Ar-

gentina. 2 Museo Paleontológico Egidio Feruglio, Chubut, Argentina. 3 Universidad Nacional de La Plata Buenos Aires, Argentina. 4 Royal Botanic Garden Edinburgh, Scotland, UK

Spores have long been used as a source of characters in fern systematics, primarily to circumscribe genera and families using spore wall sculpturing. Spore sizes have also been relied upon to infer ploidy. In some groups, the evolution of spore features has been studied through the reconstruction of ancestral states using a molecular phylogenetic framework. Most of these studies have relied on surface characters observed with SEM and LM and have not taken into account wall-stratification information (observed with TEM), which informs the homology of sculptural elements. In this work we studied characters of spore wall sculpture and stratification including: surface sculpturing, as well as the number of layers and their structures in order to infer the origin of the sculpturing. Our aim was to detect broad evolutionary patterns related to the characteristics of the walls that constitute the sporoderm in homosporous ferns. We studied 724 species using data from Tryon & Lugardon (1991) which we optimized onto the comprehensive phylogeny of Testo & Sundue (2016). Our main findings are that: 1. Both the ornamented exospore and perispore (constituting the spore sculpture) appeared several times in evolution, 2. In most groups, two layers constitute both the exospore and the perispore, 3. The most common type of exospore is "Blechnoid", characterized by a compact inner exospore and a bistratified outer exospore, while the most common perispores are solid or cavate. Our results provide new insight to the evolution of different ornamental and wall-structural configurations in the ferns. Moreover, it provides a framework to evaluate paleopalynological assignments and interpretations of fossil spores.

References: Testo W, Sundue M. 2016. A 4000-species dataset provides new insight into the evolution of ferns. Mol Phylogenetics Evol 105.Tryon AF, Lugardon B. 1991. Spores of the Pteridophyta: Surface, Wall Structure, and Diversity Based on Electron Microscope Studies.

S.063. FLORAL NECTAR: POLLINATION SYNDROMES, PRODUCTION ATTRIBUTES, REGULATION EVOLUTION.

P.0544 Unraveling the effects of long-term exposure to fungicides on the growth performance of ecologically important nectar yeasts

Sergio Quevedo-Caraballo[1], Clara de Vega[2], Bart Lievens[3], Sergio Álvarez-Pérez[1]

1 Universidad Complutense de Madrid, Madrid, Spain. 2 Universidad de Sevilla, Seville, Spain. 3 Katholieke Universiteit Leuven, Leuven, Belgium.

Fungicides are nowadays indispensable to global food security, and among them, 14α-demethylase inhibitors (DMIs) are a mainstay of modern agriculture due to their widespread use against fungal pathogens of diverse crops. Unfortunately, DMI residues can disperse and persist in the environment and potentially affect pollinators and non-target fungi, including the yeast communities inhabiting the floral nectar of Angiosperms. Some nectar-yeast species have shown to be of outstanding ecological importance as mediators of animal-plant interactions, and investigations are therefore required to unravel the specific effect of fungicides on nectar-yeast performance. We analysed the effect of long-term exposure to sublethal concentrations of imazalil, a DMI fungicide widely used worldwide, on the growth performance of the cosmopolitan nectar-specialist *Metschnikowia reukaufii* (Ascomycota), a yeast species of high ecological importance. Three yeast populations each composed of 10 *M. reukaufii* strains isolated from floral nectar of Mediterranean plants were inoculated into culture broths mimicking natural nectars containing different imazalil concentrations (0, P.31, 0.125, and 0.5 μg/ml). After a 3.5-day incubation, an aliquot of the cultures corresponding to the DMI-exposed and DMI-free control treatments was transferred to new vials with the same media to simulate yeast dispersal by insects, and this operation was repeated twice a week for 16 weeks. The results demonstrated that the overall yeast cell count (by microscope counting) and the number of viable cells (colony forming units on agar plates) were significantly determined by imazalil concentration, the exposure time, and the interaction between these two factors. DMI fungicides can, therefore, significant and negatively impact the ability of nectar yeasts to thrive in their habitat. Future research should address other effects that long-term exposure to fungicides can have on nectar microbial populations and how agrochemicals indirectly disrupt plant-pollinator communication mediated by nectar yeasts.

Filling the gaps in Bracken fern: genetic variability, relationships, and climate requirements of South American populations

Agustina Yañez[1], Sylvia Kinosian[2], Vanina Salgado[1], Jessica Viera Barreto[3], Juan F. Rodriguez Cravero[1], Pedro B. Schwartsburd[4], M. Mónica Ponce[5], Diego G. Gutierrez[1], Carlos Mendes[6], Michael Sundue[7, 8, 9],Paul G. Wolf[10]

1 División Plantas Vasculares, Museo Argentino de Ciencias Naturales (MACN-CONICET), Ciudad de Buenos Aires, Argentina. 2 Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, USA. 3 División Plantas Vasculares, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, Buenos Aires, Argentina. 4 Laboratory of Systematics and Evolution of Plants, Department of Plant Biology, Federal University of Viçosa, Viçosa, Brazil. 5 Instituto de Botánica Darwinion, Buenos Aires, Argentina. 6 Centro de Estudios de la Crisis Ambiental Global, Instituto Venezolano de Investigaciones Científicas, Miranda, Venezuela. 7 Royal Botanic Garden Edinburgh, Scotland, U.K. 8 The Pringle Herbarium, Department of Plant Biology, University of Vermont, Burlington, USA. 9 Botanical Research Institute of Texas, Fort Worth, USA. 10 Department of Biological Sciences, University of Alabama in Huntsville, Huntsville, USA.

The bracken fern (*Pteridium*, Dennstaedtiaceae) is a cosmopolitan fern genus of aggressive disturbance colonizers. Bracken is also toxic to many livestock animals, and the control of this species is of agricultural interest. The taxonomy of *Pteridium* has been described in multiple schemes, ranging from one to four species with numerous subspecies and varieties. Recent work has focused on the worldwide distribution and systematics of the bracken fern, but South America has been poorly represented. Here, we present the first continent-wide sampling and analysis of *Pteridum esculentum* (= "*P. arachnoideum*"), a southern hemisphere diploid species. Within South America *P. esculentum* has several morphotypes, distinguished into subspecies by variation in indument and lamina architecture. In this study we use double digest restriction site-associated DNA sequencing (ddRADSeq) to assess the phylogenetic relationships of *P. esculentum* subspecies. Additionally, we evaluate their potential distribution and climatic niche to detect ecological requirements. We found a striking genetic homogeneity for the species, being able to support only two morphotypes from molecular data. We propose an east-west geographic pattern that explains the relationships between populations and, in contrast to previous studies, we detected differences with *P. esculentum* from Australia. Finally, although the morphological subspecies did not show differentiation in their climatic niche, the Amazonian and northern South American populations could constitute a different ecotype.

P.0545 Flower traits, flower visitors and breeding systems of Nicotiana glauca: a climate change comparison

Francisco Maldonado Vargas[1], Mónica Móraes Ramírez[1], Sissi Lozada-Gobilard[1,2]

1 Instituto de Ecología, Unidad de Botánica (Herbario Nacional de Bolivia - LPB), Universidad Mayor de San Andrés, La Paz, Bolivia. 2 Department of Biology, Lund University, Lund, Sweden.

Climate change in the last decades has caused a decline of pollinators affecting plant-pollinator interactions worldwide. When pollinators are scarce, plants might change strategies into selfing and invest less resources into flower traits related to advertising (e.g., flower size) and reward (e.g., nectar). In this study we compare whether patterns of flower advertising, nectar production, sugar concentration and daily flower visitors changed after 25 years in six populations of *Nicotiana glauca* in the dry valleys and Puna of La Paz city (Bolivia). We hypothesize that changes in climate reduced the availability of pollinators during the day, affecting the pollination and breeding system of *N. glauca*. After 25 years, we resampled six natural populations and measured flower morphology (corolla width, length, tube length), nectar volume, sugar concentration, and observed flower visitors three times per day. We expect to find less pollinator visitation rate and a decrease in flower size and nectar volume in the current populations compared to those collected 25 years ago. Additionally, we estimate the degree of dependence of pollinator of *N. glauca* measuring the capacity of produce fruits without pollination and measuring the anther-stigma distance. If pollinator visits are reduced, we expect to find indication of selfing (short anther-stigma distances to facilitate self-fertilization) as a strategy to cope with stressful conditions. Preliminary results show that patterns of pollinators and nectar production are very similar to those found 25 years. Nectar volume varies during the day decreasing in volume and sugar concentration at the end of the day. The main visitors are *Xilocopa sp., Apis mellifera* (both robbers), and hummingbirds *C. coruscansa and A. chiniogaster* as legitimate pollinators. However, a lot of variation was observed between populations and whether the degree of compatibility within populations relates with the pollinator visitation rate and flower traits remains to be tested.

P.0546 Towards sustainable agriculture: unravelling the complex interplay of landscape, pollinators, and crop quality in rapeseed crops

Pablo Neira[1,2], Meanie Morales[1,2], Sergi Munné-Bosch[1,2], José M Blanco-Moreno[1,2], F. Xavier Sans[1,2.]

1 Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Facultat de Biologia, Universitat de Barcelona, Barcelona, Spain. 2 Institut de Recerca de la Biodiversitat, Universitat de Barcelona, Barcelona, Spain.

Agricultural intensification, which alters landscape structure and composition, influences pollinator abundance, and in consequence impacts the service of pollination. This service maintains biodiversity and ensures food security. Our study examines the effects of pollinator visitation rate (wild bees and honeybees) and three landscape features—crop diversity (eRg), percentage of semi-natural habitats (SNH), and Mean Field Size (MFS)—on pollination efficiency across twenty-two rapeseed fields scattered in arable-dominated landscapes differing in eRg, MSF and SNH. In each field, we assessed insect pollination and set up a pollinator-exclusion experiment to disentangle their effects on rapeseeds quantity (number of seeds per pod and seed weight) and quality (oil content, vitamin E, and pigments) in different landscapes. Multi-model inference emphasizes the distinct impact of agricultural landscape and of pollinator visitation rate on seed quantity and quality. eRg and the pollinator visitation rate, play pivotal roles for both crop production parameters. Discrepancies between plants with and without pollinator-exclusion experiment are evident, particularly in quantity parameters, oil content, γ-tocopherol levels, and seed pigment contents, underscoring the positive influence of pollinators on seed production. Other quality parameter, total vitamin E, respond significantly to landscape variables. They increase with eRg and decrease with MFS and SNH and unaffected by exclusion treatments. In summary, landscapes with diverse crops with high pollinator visitation rates, enhance seed quantity and quality, reflected in quantity parameters, oil content and γ-tocopherol levels. Meanwhile, total vitamin E levels only correlate positively with crop diversity. These findings guide actions to enhance plant-pollinator interactions through the landscape, propose improved agro-landscape schemes and fostered interdisciplinary studies on landscape-insect-crop interactions.

Burjassot, Spain. Contact: mahonmar@alumni.uv.es 2 Instituto Cavanilles de Biodiversidad y Biología Evolutiva (ICBiBE) – Departamento de Botánica y Geología, Universitat de València, Burjassot, Spain. 3 Departamento de Micología, Real Jardín Botánico (CSIC), Madrid, Spain. 4 Departamento de Ciencias de la Vida, Universidad de Alcalá, Alcalá de Henares, Spain.

S.064. FLORAL POLYMORPHISMS AS A RESEARCH TARGET FOR NATURAL SELECTION

P.0547 Stylar polymorphism and the incompatibility system are maintained across ploidy levels of the Linum suffruticosum s.l. complex

Ana Afonso[1], Juan Arroyo[2], João Loureiro[1], Mariana Castro[1], Catarina Siopa[1], Sílvia Castro[1]

1 Centre for Functional Ecology, Associate Laboratory TERRA, Department of Life Sciences, University of Coimbra, Coimbra, Portugal. 2 Departamento de Biología Vegetal y Ecología, Universidad de Sevilla, Sevilla, Spain.

Whole genome duplications (WGDs) may significantly affect the arrangement of sexual organs in flowers and associated traits and are known to break reproductive self-incompatibility mechanisms, allowing selfing in polyploids and counteracting the minority cytotype exclusion. Additionally, changes in reproductive traits will be particularly relevant in polyploid species with complex breeding systems, such as heterostyly, a polymorphism which promotes outcrossing and reduces sexual self-interference in hermaphroditic flowers. Recently, we found a remarkable cytogenetic diversity in *Linum suffruticosum s.l.*, a distylous polyploid complex (diploids, tetraploids, hexaploids, octoploids and decaploids) from a genus with about 40% of heterostylous species. Here, we used *L. suffruticosum* as study system for exploring the variation in heterostylous reproductive traits after WGDs. Morph frequencies were recorded, and the sexual organs were measured in flowers obtained from populations representing each of the five cytotypes. Experimental crosses within cytotypes (selfing and intra- and inter-morph crosses) and crosses between diploids and tetraploids from a parapatric contact zone were performed. Results showed strong self- and within-morph-incompatibility, and most populations showed isoplethy with no correlation between population size and deviations in style-morph proportions. Thus, no breakdown of the distyly and incompatibility system was detected across the five cytotypes. In addition, pollen flow among cytotypes appears to be possible since there is an overlap between reciprocal sexual organs and pollen tubes reaching the bottom of the style in inter-cytotype crosses. This study highlights the importance of ecological and genetic mechanisms in shaping the diversity of reproductive traits in *L. suffruticosum s.l.* and the importance of further studies integrating genome size, breeding system and phylogenetic analyses to unravel the evolutionary scenarios that have occurred in *L. suffruticosum s.l.*

P.0548 Comparative floral anatomy and evolution of species of Clusia sect. Cordylandra and sect. Phloianthera with similar unusual androe

Ana Cláudia Alencar[1], José Elvino Nascimento-Jr.[1], Volker Bittrich[2], Diego Demarco[3], Maria do Carmo E. Amaral[2]

1 Department of Natural Science, Federal University of São João del Rei, São João del Rei, Brazil. 2 Department of Plant Biology, University of Campinas, Campinas, Brazil. 3 Department of Botany, University of São Paulo, São Paulo, Brazil.

The sections *Cordylandra* and *Phloianthera* (*Clusia* L., Clusiaceae) are both known for some time to be monophyletic, but their relationship and internal phylogeny is poorly known. The species of both sections are dioecious. The flowers offer resin from stamens or staminodes for pollinators, exclusively so in sect. *Cordylandra*, additionally pollen in male flowers of some species of sect. *Phloianthera*. Species with a similar unusual androecium morphology, disciform or conical-crateriform, occur in both sections, leading some authors to treat *Cordylandra* and *Phloianthera* as a single section. The resemblance raises questions regarding the adaptive value of such androecia and the floral evolution within the genus *Clusia*. We investigated morphological and anatomical flower characters of both sections to look for similarities and possible differences. Anatomical sections of the androecium and the stigma from both sections were studied. We observed that the very unusual androecia in *Cordylandra* and *Phloianthera*, although morphologically similar, are anatomically distinct. Based on a new molecular phylogeny, five morphological characters of the androecium of two species of each section were used for the reconstruction of ancestral character states. Species from *Cordylandra* and *Phloianthera* with a disciform androecium were the first to diverge within each clade. As the phylogeny suggests a sister-group relationship of both sections, this kind of androecium is possibly of shared evolutionary origin. On the other hand, species from these sections with conical-crateriform androecium are more derived, surprisingly suggesting an independent evolution of this very unusual morphology. A possible advantage could be the enlargement of the surface, important for attracting pollinating bees. However, there exists an important difference in these androecia, as in sect. *Cordylandra* the whole surface offers a resin-pollen ixture, but in sect. *Phloianthera* the upper part offers only pollen, as resin secretion is restricted to the base.

P.0549 Effect of ovary locule number on seed production and predation in populations of Cistus ladanifer L. (cistaceae) in the Madrid region, Spain

Yoel Aroca-Martínez[1], Diana Zugasti-Hervás[1], Marcos Moreno-Rabadán[1], María D. Jiménez[1], Juan A. Delgado[1]

1 Universidad Complutense de Madrid, Madrid, Spain.

There is a great variation in the number of ovary locules per flower in *Cistus ladanifer* L. Cistaceae. In fact, this variation takes place not only among populations, but also between individuals and even within individuals. In this study we assess the variation in the number of locules of the ovary in this Mediterranean woody plant which is an obligate seeder with a strong dependence upon seeds available in the soil bank for post-fire seedling establishment. Our aim is to assess the variation in the number of ovary locules, seed production and seed pre-dispersal predation at population, individual and intraindividual levels in five localities in the Madrid Region (Central Spain). Sampling followed a hierarchical pattern, with random selection of ten individuals per population, two branches per individual and five fruits per branch (500 fruits in total). We observed that the number of ovary locules did not influence the potential quantity of seeds yielded by each fruit or the rates of insect predation. Instead, the potential seed production by the fruit was mainly correlated with the number of seeds per ovary locule. The variability in the number of seeds dispersed per fruit among populations was solely determined by the pre-dispersal predation rate, remaining unaffected by both the number of seeds produced or the number of locules in the fruit. These findings suggest that variation in locule count is not subject to either positive or negative selection, as there appears to be no advantage or disadvantage in terms of seed yield saved from insect predation.

P.0550 Variation in reproductive traits among three Thymus species exhibiting gynodioecy

José Carlos del Valle[1], David Doblas-Pruvost[1], Francisco Javier Jiménez-López[2], Javier López-Tirado[3], Diego Nieto-Lugilde[3], María Ángeles Ortiz-Herrera[1], Regina Berjano[1]

1 Departamento de Biología Vegetal y Ecología, Universidad de Sevilla, Seville, Spain. 2 Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos, Madrid, Spain. 3 Departamento de Botánica, Ecología y Fisiología Vegetal, Universidad de Córdoba, Córdoba, Spain.

Species of thymes have evolved a mating system in which selfing hermaphrodites and females coexist. Whereas hermaphroditism promotes mate diversity, females are obligate outcrossers that only contribute to the next generation through ovules. In addition, numerous studies have demonstrated that female flowers are generally less attractive to pollinators compared to hermaphroditic ones. Hence, the percentage of female plants relative to hermaphrodites plays a key role in genetic diversity, population structure, and species distribution. In addition, both the ability to *self*-crossing and *pollen or pollinator limitation* interact to shape outcrossing rates and, therefore, genetic variability. We focused on the *Thymus* Sect. Mastichina composed by three taxa: *T. albicans* is native to the southern Iberian Peninsula and share a significant portion of its restricted distribution range with the rare *T. mas-*

tichina subsp. donyanae, while *T. mastichina* subsp. *mastichina* has a broader distribution range that spans the entire Iberian Peninsula. We analyzed the floral morphology in 41 populations of these three taxa to evaluate differences in floral morphology both within and among species, and specially between sex morphs. We also examined each species' sex ratios, selfing rates and seed set to discern putative correlation patterns between the frequency of sex ratio and reproductive success. In sympatric populations, we also studied putative episodes of hybridization among these three closely related taxa. For this purpose, we examined those individuals with an intermediate morphology between the two sympatric species. Additionally, morphological differences were concurrently investigated alongside with genomic sequencing approaches (Hyb-Seq), as well as we analyzed the biotic interactions with pollinators and florivores. Our study attempts to shed light on how interdependent traits, such as the abundance of female plants, may influence the fitness and long-term persistence of a species.

P.0551 Divergence in floral phenotype and mating preferences within a self-compatible species population

Celia Vaca-Benito[1], Camilo Ferrón[2], A. Jesús Muñoz Pajares[1], Mohamed Abdelaziz[1], Ana García-Muñoz[1]

1 University of Granada, Granada, Spain. 2 University Rey Juan Carlos, Madrid, Spain.

Phenotypic variation is the substrate for the action of natural selection, so it is not surprising to find differences in morphology and even in mating patterns among the individuals of a single population. Since pollinators are closely associated with floral phenotypes and reproductive strategies in flowering plants, they are important selective agents responsible for the gene flow within populations and the maintenance of such diversity. We observed a strong inter-individual variation in a wild population of Erysimum repandum after two years of phenotypic measurements and fitness estimation in tagged individuals. Although this species is described as a Brasicaceae species showing the common traits of selfing syndrome, we found a wide range of flower size from small to large flowers with intermediate sizes. Larger flowers were associated with a significant increase in nectar production and a higher frequency of pollinator visits. We found an increase in fitness in individuals with large flowers when pollination was mediated by insects while they produced fewer seeds when grown in pollinator exclusion. In contrast, individuals with small flowers showed no differences in fitness between self and cross-pollination. Our results suggest the existence of variation in mating preferences within this population, associated with differences in flower size and differences in nectar production. These contrasting patterns of pollination may influence the genetic structure of this population whose individuals could be following divergent evolutionary trajectories as a consequence of the accumulation of genetic differences.

P.0552 A range-wide flower color polymorphism driven by soil and climatic factors

Kathleen M. Kay[1], Dena L. Grossenbacher[2]

1 Department of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA. 2 Department of Biology, California Polytechnic State University, San Luis Obispo, USA.

The maintenance of polymorphism in fitness-associated traits is an enduring puzzle in evolutionary biology. Variation in flower color, a visible and often genetically simple phenotype, has played an outsized role in evolutionary biology yet remains perplexing. Floral pigments like anthocyanins are well-known to influence pollinator attraction. However, they may also confer tolerance to abiotic stressors such as harsh soils, extreme temperatures, low precipitation, or ultraviolet radiation. In such cases, environmental variation in abiotic stressors over space or time could lead to the maintenance of flower color variation within species. We predict flower color frequencies in natural populations respond to interactive effects of multiple environmental stressors; however, the effects of individual abiotic factors are often investigated in isolation. Using a comparative approach, we test whether multiple abiotic variables predict flower color in *Leptosiphon parviflorus* (Polemoniaceae), a species with pink and white flower color morphs determined by a single genetic locus. We use > 1,000 community scientist-powered iNaturalist observations and in-depth field studies to assess morph frequency, soil chemistry, and climate. For iNaturalist observations across the geographic range of *L. parviflorus*, we find the probability of flowers being pink is greater in locations with serpentine-derived soil, especially when local annual temperatures are higher, precipitation is lower, and UV radiation is higher. Moreover, across 21 field sites we find a higher frequency of pink morphs in sites with low Ca:Mg ratios and high concentrations of nickel and cobalt (i.e., serpentine soil), higher annual temperatures, and lower precipitation. In combination with prior work on *L. parviflorus* showing pink-flowered plants have an advantage in dry years, we conclude that spatial variation in climate and soils and temporal variation in precipitation contributes to the maintenance of flower color polymorphism across the range of *L. parviflorus*, likely through pleiotropic effects on earlier life stages.

P.0553 Molecular basis and population genetics of petal loss in Capsella bursa-pastoris (Brassicaceae)

Sofya D. Koblova[1], Maria D. Logacheva[1], Anna V. Klepikova[1], Aleksey A. Penin[1]

1 Laboratory of Plant Genomics, IITP RAS, Moscow, Russia.

We studied petal loss in a young tetraploid species of hybrid origin, Capsella bursa-pastoris (Brassicaceae). This family is renowned for its floral structure stability, yet some genera show alterations from the common bauplan that mostly include petal and stamen number deviations, arguably displaying an evolutionary trend for corolla reduction. Within C. bursa-pastoris, multiple geographically isolated accessions share the same Lepidium-like (lel) phenotype, characterized by petal loss (1). We inferred the population structure from over 60 accessions, tree topology largely matched previous reports and clade structure correlated with accession geography. All of the investigated apetalous isolates belonged to the European group of accessions. Lepidium-like lines did not form a single clade; this assumes that their occurrence is not due to recent dispersal of a single successful accession but rather emerged independently or is due to retained ancestral polymorphism. We focused on one of the petal-loss accessions, lel4-msk, for further genetic analysis. Identified associated genomic regions did not contain any known petal development factors and were independent from genes involved in the decandric phenotype (2). A total of four candidate loci were identified, three in non-syntenic regions of C. orientalis- and C. rubella/grandiflora-descending subgenomes' Chr1 and one in Chr4 of C. orientalis origin; it suggests that distortion of a single homeolog is enough for the phenotype emergence. This might be due to ortholog subfunctionalization or to pseudogenization of responsible genes' homeologs. Hence, petal loss in C. bursa-pastoris is a unique system for studying both genome evolution in polyploids and morphological evolution in Brassicaceae.

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P.0554 The unique SI type in heterostylous Linum pubescens as a starting point in understanding evolutionary aspect in the genus Linum

Hanna Levchuk[1], Michael Lenhard[1]

1 Institute of Biochemistry and Biology, University of Potsdam, Potsdam, Germany.

Heterostyly is the phenomenon where a population consists of two (distyly) or three (tristyly) types of flowers differing in the height of pistils and stamens. In such populations it is often virtually impossible to obtain seeds from self-pollination, suggesting that there is a mechanism preventing the formation of viable seeds from such pollination to prevent inbreed depression. This phenomenon is called self-incompatibility (SI). Later it was established that distyly is controlled by a specific region (S locus), which includes several genes that are inherited in a linked manner and control the manifestation of heterostyly and self-incompatibility. A particularly interesting taxon for understanding the evolutionary process of heterostyly and self-incompatibility is the genus *Linum*, among whose representatives there are both self-compatible homostylous species and self-incompatible species with different types of heterostyly: distyly and style-height dimorphism. We found that one of the Linum species, *L. pubescens* is in fact a tristylous species. In addition, according to divergence time analysis this species is one of the oldest and may be the source species of the genus *Linum*. To confirm the tristyly nature of this species, all variants of intraspecific crosses were performed and it was found that this species is SI, as in all variants of self-pollination no seeds were obtained and even pollen tube growth was not observed. In intramorph crosses involving L and S morphs, complete SI was also observed, but if at least one of the parents was an M-morph, seeds were formed but were not viable. A similar picture was observed in intermorph crosses, but in legitimate pollination, fully viable seeds were formed. Thus, continued research on this species will allow us to understand the evolutionary processes occurring in the population of heterostylous species.

P.0555 Flower colour dimorphism in Anemone palmata

N.L. Rodríguez-Castañeda[1], M.L. Buide[2], M. Arista[1], E. Narbona[2], P.L. Ortiz[1]

1 Departamento de Biología Vegetal y Ecología, Facultad de Biología, Universidad de Sevilla, Seville, Spain. 2 Departamento de Biología Molecular e Ingeniería Bioquímica, Universidad Pablo de Olavide, Seville, Spain.

Flower colour polymorphisms are infrequent yet prevalent across angiosperms, and their persistence might be attributed to various forms of balancing selection mechanisms. *Anemone palmata* predominantly exhibits plants with yellow flowers, while populations with coexisting white-flowered plants have also been observed. The distribution of *A. palmata* morphs was studied throughout its geographical range. We also carried out a characterisation of their colours as perceived by their main pollinators and determined which pigments are responsible for them. Furthermore, we compared the morphs in terms of their vegetative and sexual reproductive traits, pollinator attention and fitness. We found that *A. palmata* is widespread throughout the western Mediterranean region, but white-flowered plants were only recorded in populations in Portugal and SW Spain, where they occurred at low frequencies. Yellow flowers had a characteristic UV pattern, with the centre absorbing UV and the periphery reflecting it, whereas the white morph had no such pattern. Carotenoids were only present in the yellow flowers and were responsible for this colouration, whereas UV absorbing flavonoids were present in both morphs and were responsible for the UV bullseye pattern. We show that flower colour traits allow both morphs to be discriminated by their pollinators, even though both morphs are similar in other attraction-related traits. Pollinators, mainly Hymenoptera and Diptera, generally preferred the yellow morph, but there was a partitioning of insect groups between the two colour morphs and a marked constancy in flower colour during their visits. Clonal propagation and sexual reproduction coexisted in both morphs, although the white morph had lower female fitness. The maintenance of this polymorphism, despite the lower pollinator visitation rate and female fitness of white-flowered plants, could be attributed to the mechanisms of pollinator partitioning and colour constancy of pollinators. In addition, the clonal propagation of white-flowered plants may further facilitate this phenomenon.

P.0556 Transitions from monomorphism to dimorphism in mirror-image flowers: A theoretical approach

Marco Saltini[1], Spencer C.H. Barrett[2], Eva E. Deinum[1]

1 Mathematical and Statistical Methods - Plant Science Group, Wageningen University, Wageningen, The Netherlands. 2 Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, Canada.

Enantiostyly is a type of floral asymmetry in which the styles of flower are either deflected to the left or right side of the floral axis (mirror-image flowers). Phylogenetic evidence indicates that in several monocotyledonous lineages, dimorphic enantiostyly (all flowers of a plant have the same style orientation) has evolved from monomorphic enantiostyly (flowers within a plant have both stylar orientations). Here, we use a modelling approach based on adaptive dynamics to study the emergence of dimorphism in a population of plants with monomorphic enantiostyly under gradual evolution. Our results indicate that, depending on the balance between inbreeding depression following geitonogamy, pollination efficiency, size of the daily floral display, and plant density, dimorphism can evolve from an initial, monomorphic population. In general, the newly-emergent dimorphic population is stable against invasion of a monomorphic mutant. However, our model predicts that under certain environmental conditions, e.g., a decline of pollinators or scarcity of resources, dimorphic enantiostyly may revert to a monomorphic state.

P.0557 The length and frequency of quantitative floral spur governs assortative mating in a Aquilegia species

Mingliu Yang[1], Spencer C. H. Barrett[2], Zhi-Qiang Zhang[1]

1 Institute of Biodiversity, School of Ecology and Environmental Science, Yunnan University, Kunming, Yunnan, China. 2 Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, Canada.

The influence of floral traits on nonrandom mating within a population has been extensively explored in previous studies. Despite most of floral traits vary continuously and are usually distributed unimodally within a natural population, whether and how these quantitative floral traits affect mating remains unclear. Here, we investigate mating patterns in a natural population of *Aquilegia rockii*, a self-compatible insect-pollinated herb with quantitative variation in spur length. We employed a combination of pollinator observation, manipulated pollination, and mark-based paternity analyses to assess the effects of spur length and flower quantity per plant on the mating system and reproductive success. Our findings indicate that both spur length and its frequency within the population positively influence outcrossing opportunities, siring diversity, and pollen dispersal distance. Moreover, a significant positive assortative mating was observed, regardless of selfing events. Our results suggested that even limited natural variation in quantitative floral traits can lead to nonrandom mating in natural populations. This study holds significant implications for understanding the maintenance of floral phenotype through stabilizing selection.

S.065. FLORAL SPECIALIZATION AND THE GENERALISED NATURE OF POLLINATION INTERACTIONS

P.0558 Evaluation of plant-pollinator interactions in the Brazilian Atlantic Forest

Sara S. Domingos[1], Nícolas A. P. Ricci [2], Larissa de O. Leite[3], Marina Wolowski[4], Leandro Freitas[5], Kayna Agostini[1]

1 Universidade Federal de São Carlos, Araras, Brazil. 2 Colégio Objetivo, Santa Bárbara d'Oeste, Brazil. 3 Universidade Estadual de Campinas, Campinas, Brazil. 4 Universidade Federal de Alfenas, Alfenas, Brazil. 5 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil.

The Brazilian Atlantic Forest is one of the most diverse forests in regions with a humid tropical climate, however it is one of the most threatened ecosystems in the world, due to the deforestation process. Given the current global biodiversity crisis, plant-pollinator interactions are fundamental to ecosystem regulation and maintenance. Here, we conducted a data survey of plant-pollinator interactions in the Atlantic Forest, adopting biodiversity data standards. A systematic review of the literature was carried out on the Web of Science, Dimensions and SciElo platforms, up to September 2023, resulting in 317 references, of which 265 have been compiled to date. The interaction database standard of the Brazilian Plant-Pollinator Interactions Network (REBIPP) was used to compile each interaction (http://db.rebipp.org.br/). We recorded 1,595 plant species interacting with 1,507 animal species, totaling 9,010 interactions. Among the 135 botanical families sampled, Bromeliaceae (14.4%), Fabaceae (8.7%) and Asteraceae (7.8%) had the highest number of species. The animals were divided into 39 functional groups, with bees (46.6%), butterflies (12.8%) and wasps (7%) being the most diverse and with the highest number of established interactions. This reinforces patterns found for local works in the Atlantic Forest but also demonstrates the diversity of less frequent groups (e.g., bat) and a high diversity of pollinator species. This data will be included in the REBIPP database and can be used by policymakers to support actions and strategies for the conservation of the Brazilian Atlantic Forest.

P.0559 Pollination of steady-state blooming Centropogon granulosus (Campanulaceae: Lobelioidae) by the traplining Buff-tailed Sicklebill

Mannfred M. A. Boehm[1], David Guevara-Apaza[2], Jill E. Jankowski[3], Quentin C. B. Cronk[1]

1 Department of Botany and Biodiversity Research Centre, University of British Columbia, Vancouver, British Columbia, Canada. 2 Facultad de Ciencias Biológicas, Universidad San Antonio Abad del Cusco, Cusco, Peru. 3 Department of Zoology and Biodiversity Research Centre, University of British Columbia, Vancouver, British Columbia, Canada.

The Andean bellflowers ('centropogonids', Lobelioidae) comprise a highly diverse recent radiation, mediated in part by the evolution of different pollination niches. Most remarkably of all, one diverse clade has evolved with extremely curved flowers ('eucentropogonids') and these species are predicted to be pollinated exclusively by one of two parapatric species of Sicklebill hummingbirds (*Eutoxeres*). Whereas pollination by the northernmost species (White-tipped Sicklebill, *E. aquila*) is relatively well-documented, very little is known about its southern congener, Buff-tailed Sicklebill (*E. condamini*). In this study we focused on the floral biology of *Centropogon granulosus* C.Presl, a eucentropogonid thought to be pollinated by Buff-tailed Sicklebill in the southern portion of its range. Using camera traps and a pollination exclusion experiment, we determined the visitors to *C. granulosus*, and the effect of hummingbird-exclusion on fruit development. Because phenological types may also mediate floral specialization, we quantified anthesis rates in the context of pollinator behaviour. We confirm that Buff-tailed Sicklebill is a visitor to *C. granulosus*, and that visitation is necessary for fruit development. Buff-tailed Sicklebill was the only legitimate pollinator during this study, supporting the notion that *C. granulosus* has a highly specialized pollination biology mediated by floral curvature. We quantified anthesis rates and found variation spanning one flower per 1.88 to 7.22 days. Flowering rates were unequivocally linear and conformed to the 'steady state' phenological type. We recorded 12 Buff-tailed Sicklebill visits to *C. granulosus* over the course of >1800 hours of monitoring effort, indicating traplining behaviour. As predicted by its floral morphology, *C. granulosus* is exclusively pollinated by Buff-tailed Sicklebill. We also present preliminary evidence for the congruence between phenological type and hummingbird foraging behaviour as a driver of specialization in this mega-diverse clade of Andean bellflowers.

P.0560 Evolution of the pollination system and floral signalling in nocturnal flowers of the Cereeae tribe (Cactaceae)

Sinzinando Albuquerque-Lima[1,2], Daniela C. Zappi[3], Nigel P. Taylor[4], Isabel C. Machado[1]

1 Federal University of Pernambuco, Recife, Brazil. 2 Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China. 3 University of Brasília, Brasilia, Brazil. 4 Federal University of São Carlos, Sorocaba, São Paulo, Brazil.

Cactaceae species with nocturnal anthesis belong to a group that has a close relationship with pollination by bats and hawkmoths. This family includes species that exhibit a wide range of morphological and floral cues, allowing interaction with different pollinators. In addition to differences in flower morphology, cacti have unique characteristics such as spine-covered branches and, in some cases, they have a structure called cephalium from which the flowers emerge. With this distinct pattern, these structures can influence interactions with pollinators. Another factor that can influence pollination relationships within species is genetic factors such as hybridisation. Based on these assumptions, Cereeae proved to be an excellent model to understand questions related to the evolution of nocturnal pollination in the family and the role of environmental and genetic factors in the relationship between cacti and pollinators. Using multiple approaches and field collections in eastern Brazil, we present unprecedented data that provide a leap forward in understanding the biology and ecology of pollination in Cactaceae. We investigate the pollination system of the species of the tribe, with emphasis on chiropterophily, from a floral morphological perspective. We found a strong similarity in the morphology of the species and confirmed with field observations for the first time pollination by bats in 14 taxa. We also investigated a case of natural hybridisation, where we found that the flowers of the hybrids are intermediate and the signalling compounds may remain the same as those of the parents, but may also show new traits. From an olfactory cue's perspective, we investigated how olfactory signalling can vary between different taxa within the tribe, from complete absence to a floral bouquet dominated solely by sulphur compounds. Considering the role of the cephalium in cacti, we found an interesting pattern of cephalium orientation in different species of nocturnal and diurnal cacti.

P.0561 A novel case of ant pollination in Synedrellopsis grisebachii (Asteraceae), a ruderal plant with very inconspicuous flowers

Pedro Q. Dantas[1], Volker Bittrich[1], Maria do Carmo E. Amaral[1]

1 Department of Plant Biology, University of Campinas, Campinas, Brazil.

Synedrellopsis grisebachii Hieron. & Kuntze is a common ruderal species in urban ecosystems in the city of Campinas, southeast Brazil. The species has small capitula protected by two foliaceous involucral bracts. Each very inconspicuous capitulum comprises four minuscules florets: a pair of pistillate florets and a pair of bisexual florets. Their corolla tube measures approximately 2 mm long. Due to the minuteness of its flowers and its creeping habit, flowering individuals are easily overlooked. Despite being common and flowering year-round, the reproductive biology of *S. grisebachii* is poorly known. The present study aims to understand the reproductive system and pollination of *S. grisebachii*. In our investigation, we inferred the breeding system through the pollen-ovule ratio analysis. Additionally, we conducted experiments to evaluate the influence of floral visitors on the reproductive success. Furthermore, we photographed *S. grisebachii* possible pollinators and studied the floral anatomy of the distinct florets. We observed that floral nectaries are present only in pistillate flowers. Our results show that *S. grisebachii* pollen-ovule ratio is not one of a typical obligate autogamous species. Plants to which floral visitors had unrestricted access present greater reproductive success as indicated by fruit set. Minute ants are the only regular floral visitors and appear more interested in pistillate than bisexual florets, matching with the presence of nectaries only in pistillate florets. These results integratively corroborate that *S. grisebachii* is primarily or exclusively pollinated by ants, representing a novel and rare case of myrmecophily. Further studies of this common but mostly overlooked weedy species are under way. The present study serves as an example and a reminder of the biological discoveries that can be made in typical urban ecosystems.

P.0562 Bridging boundaries: the enduring harmony between plants and pollinators defies isolation and geographical distance on tropical mountains

Yasmine Antonini[1], Cristiane Martins[1], Fernanda Vieira da Costa[2], Marina do Vale Beirão[3], Rosana Maria Pereira Rocha[1]

1 Laboratório de Biodiversidade, Departamento de Biologia do Instituto de Ciências Biológicas da Universidade Federal de Ouro Preto, Minas Gerais, Brazil. 2 Departamento de Ecologia da Universidade Federal de Brasília, Distrito Federal, Brazil. 3 Laboratório de Ecologia de Insetos, Departamento de Genética, Ecologia e Evolução da Universidade Federal de Minas Gerais, Minas Gerais, Brazil.

Ecological communities consist of species that are joined in complex networks of interspecific interaction. These interactions often form and dissolve rapidly, but this temporal variation needs to be better integrated into our understanding. One of these causes could be habitat isolation and across isolated mountaintops, several biotic and abiotic factors influence community assemblages of interacting species, leading to a shift in species distribution, functioning, and, ultimately, topologies of species interaction networks. However, empirical studies of distance-driven plant-pollinator networks in mountain tops are rare, particularly in tropical ecosystems. Here, we use an empirical plant-pollinator system to examine the spatial distribution of plant communities and the interaction with the potential pollinators in three tropical mountaintops, in Brazil. To this end, we tested whether geographical distance and natural isolation between mountaintop areas affect the structure of interaction networks, the beta diversity of plant communities, pollinators, and the beta diversity of plant-pollinator interactions. We expect plant communities to show more significant dissimilarity in species composition between areas than communities of flower-visiting insects. The turnover component will be mainly responsible for the beta diversity of communities and interactions. In addition, we expect to find modular and specialized networks and no variation in the structure of the interaction networks between the different mountain tops. We found that the dissimilarity of plant communities is more significant than the dissimilarity of insect communities, that turnover is the component responsible for such dissimilarity, and that there are no significant differences in the beta diversity of interactions. We also found that the interaction networks are constant in space, with highly modular topologies and little nesting, with considerable specialization, and with insects more robust to extinction. In addition, we showed a high diversity of insects associated with the flowers, with bees being the primary pollinators, followed by ants and flies.

P.0563. Optimising the pollination of Vicia faba

Charlotte Apsey[1], Beverley J. Glover[1]

1 Department of Plant Sciences, University of Cambridge, UK.

Vicia faba is a legume crop grown across the world for both animal feed and human consumption and is hugely important within food security due to its high protein content. Optimising its yield is therefore of particular interest. Focussing on floral traits to attract more pollinators demonstrates great potential to improve yield while also increasing biodiversity. Insect pollinators are invaluable in agriculture, however populations worldwide are declining at an alarming rate. This decline is predicted to have detrimental effects, not only on agriculture but also on food security and human health. Farmers are being encouraged to use techniques to promote pollinators and provide greater resources to them, such as growing wildflower margins around their crops. Mass flowering crops like *V. faba* hold huge potential to aid in slowing this decline as they are significant nectar sources for foraging insects in agricultural landscapes. This project aims to identify breeding targets to enhance pollination of*Vicia faba*while also increasing the support this crop can provide to vital pollinators. In particular, the scent and UV patterning of four commercially important *V. faba*-lines is explored using a combination of analytical, molecular genetic and behavioural ecology techniques. The effect of these traits on the behaviour and visitation rates of bumblebees (the main pollinator of*V. faba*) was observed both in lab conditions as well as out in the field. Additionally, this project investigated the impact of flower-rich margins on yield; whether margins attract more pollinators and generally increase the pollinator populations in the area or whether they actually distract pollinators away from the crop.

P.0564 Traditional pollination syndrome: the most important plants morphological traits for predicting pollinators.

Xiao Zhang[1], Ana Claudia Araújo[2,*], Neil A. Brummitt[2,**]

1 Imperial College London, Silwood Park, Buckhurst Road, Ascot, UK. (xiao.zhang22@imperial.ac.uk)
*2 Natural History Museum, Cromwell Road, South Kensington, London, UK, *a.araujo@nhm.ac.uk, **n.brummitt@nhm.ac.uk.*

Traditional pollination syndromes are widely referred when predicting pollinators, but its validity have been often questioned. Identifying the pollinators of the plant species can help to infer their potential extinction, as threatened plant species may affect the survival of their pollinators, and vice versa. Therefore, it is valuable to systematically test the traditional pollination syndromes and find the most important plant traits in predicting pollinators. In this study traditional pollination syndromes information, extracted from published empirical studies, was comprised into a validation dataset, ordination to visualise and compare the syndromes and indicator species analysis (ISA) to detect the deterministic traits for prediction was applied. Based on the most relevant traits validated, the second step was to construct a dataset with such traits for randomly selected plant species listed from Chinese and North America online floras. The morphological traits were collected by machine learning (ML) process from taxonomic descriptions, complemented by manual searching. The species evaluated presenting comparable traits were grouped using hierarchical clustering. Ordination of the validation dataset showed somewhat different but overlapped groups of syndromes, not supporting a clean-cut of traditional pollination syndromes. Yet, ISA showed that flower colour and shape are informative traits for predicting pollinators. Morphological traits have the potential to be the main indicators of pollination syndromes.

P.0565 Flowering synchrony modulates pollinator sharing and places plant individuals along a competition–facilitation continuum

Blanca Arroyo-Correa[1], Ignasi Bartomeus[1], Pedro Jordano[1,2]

1 Dept. Integrative Ecology, Estación Biológica de Doñana, Sevilla, Spain. 2 Dept. Biología Vegetal y Ecología, Facultad de Biología, Universidad de Sevilla, Sevilla, Spain.

Indirect interactions among species within ecological communities govern ecological and evolutionary processes as much as, or even more, than direct effects. In insect-pollinated plant communities, indirect interactions between plants can be mediated by shared pollinators, and may influence plant fitness, population growth and community structure. As individuals are the entities actually interacting in nature, rather than species, downscaling from species to individuals is essential to understand the underlying processes promoting these indirect interactions. We combined empirical data on plant–pollinator interactions collected in Mediterranean shrublands with a novel modelling framework to assess how the patterns of heterospecific and conspecific pollinator sharing between plant individuals are generated and their fitness implications. We found that the effects of flowering synchrony on pollinator sharing among conspecific and heterospecific plant individuals outperformed those of spatial distance. Our results revealed that plant individuals that shared more pollinators with conspecifics were also involved in a higher pollinator sharing with heterospecifics. For most plant species, the sharing of pollinator species between heterospecific plant individuals produced positive mean fitness outcomes, as long as plants did not share many pollinator interactions, which had negative effects on their fitness. At the level of plant individuals, we found that specific combinations of conspecific and heterospecific pollinator sharing lead to distinct reproductive outcomes that placed each individual along a competition–facilitation continuum. Interestingly, most plant species included a higher proportion of individuals likely experiencing competition compared to those potentially involved in facilitation processes. Our contribution provides novel insights into the factors responsible for local-scale indirect interactions within communities and their individual-level functional consequences. Such intricate patterns of indirect interactions have far-reaching implications, as the transitions of plant individuals along competitive or facilitative processes mediated by shared mutualists may contribute significantly to the functioning and coexistence of ecological communities.

P.0566 A case of study on the pollination ecology and reproductive biology of Masdevallia striatella (Orchidaceae: Pleurothallidinae)

Noelia Belfort-Oconitrillo[1,2], Melania Fernández[1], Diego Bogarín[1], Alfredo Cascante[3], Adam P. Karremans1

1 Jardín Botánico Lankester, Universidad de Costa Rica, Cartago, Costa Rica. 2 Orchid Conservation Project, Bosque de Paz Biological Reserve, Bajos del Toro, Alajuela, Costa Rica. 3 Escuela de Biología, Universidad de Costa Rica, San Jose, Costa Rica.

Studying pollination and reproductive strategies in Orchidaceae has been considered key to elucidating evolutionary processes and pollinators' role in the family's diversification. Diptera interacts with the family's most diverse subtribes, potentially pollinating >8000 orchid species. However, there are significant information gaps, especially in the Neotropical region. Pleurothallidinae is a fly-pollinated megadiverse subtribe, with *Masdevallia* as the third most diverse genus (>600 species). Little is known about *Masdevallia* pollination, with scarce evidence of effective pollinaria removal, little documentation on the diversity of secretory glands related to the pollination mechanism, and just a few studies addressing the type of reproductive system. Understanding the pollination and reproductive ecology of *Masdevallia* species can contribute to a better understanding of evolutionary relationships in Pleurothallidinae and Diptera's role in the group's radiation. This work focuses on *Masdevallia striatella*, an endemic species from Costa Rica and western Panama. We recorded various floral visitors distributed in three classes (Insecta, Arachnida, and Gastropoda) and seven orders of invertebrates, with Diptera being the most abundant. However, effective pollinators belong only to Lauxaniidae (Diptera), with at least three species in the genera *Poecilominettia* and *Xenochaetina*. There is a wide variety of papillary and glandular trichomes and stomata on the perianth of *M. striatella*, with contents that vary between proteins, lipids, insoluble polysaccharides, and simple sugars, with several possible sites for producing and releasing functional volatile substances to attract visitors and guide pollinators into the flower interior. In addition, this study evidences the presence of nectar composed of glucose and fructose accumulating at the base of the lip, suggesting a myophily pollination syndrome. Finally, *M. striatella* is highly self-compatible, although unable to self-fertilize autonomously, with some mechanisms that can prevent self-pollination.

P.0567 Temporal variation of floral traits in shaping plant-pollinator interactions in the southern Western Ghats, India.

Sachin Bhaskar[1], Manish R[1], Ricarda Scheiner[2], Ingolf Steffan-Dewenter[3], Hema Somanathan[1]

1 School of Biology, Indian Institute of Science Education and Research, Thiruvananthapuram, Kerala, India. 2 Department of Behavioral Physiology and Sociobiology, Biocenter, Universität Würzburg, Am Hubland, Würzburg, Germany. 3 Department of Animal Ecology and Tropical Biology, Biocenter, Universität Würzburg, Am Hubland, Würzburg, Germany.

In recent decades, pollination research has shifted from studies of single-species pollination to a community-level approach. Floral traits can shape the structure of plant-pollinator interactions. Specific traits like color, shape, size, symmetry, and resource traits may be better suited to some pollinators than others, potentially structuring pollinator communities. The southern Western Ghats, India, is known for high endemism and diversity of plants, though community-level plant-pollinator interactions are little studied. In an ongoing study in this region, we are examining how floral traits structure plant-pollinator interactions and whether this trait-pollinator association changes over seasons.144 line transects (100*2m) covering a region of approximately 30 km², were laid in landscapes dominated by settlement, agriculture, or forest to observe plant-pollinator interactions across seasons (pre and post-monsoon, 2023-24). 18 floral traits involved in visual attraction and rewards, were recorded for flowers observed in the transect walks. Pollinator functional groups observed, were ants, stingless bees, solitary bees, carpenter bees, honeybees, beetles, butterflies, and birds. 357 species of flowers were observed in the pre-monsoon season, here the observations were dominated by stingless bees and honeybees, accounting for 47% of total pollinator visits. Preliminary analyses of a few floral traits (floral shape) revealed that beetles visited trap-shaped flowers (4% of the total flower species in the study community) in a high proportion, directing specialized interactions. Stingless bees and honeybees visited most floral shapes, except tubular and trap-shaped flowers, showing some degree of generalization. Further analysis and seasonal comparison are currently underway.

P.0568 Pollination syndromes in Passiflora L.

Laetitia Carrive[1], Anaëlle Hulbert[1], Paul Simion[1], Maxime Rome[2]

1 Université de Rennes, Rennes, France. 2 Université Grenoble Alpes, Grenoble, France.

Flower specialization to pollinators is thought to be a key process in flower evolution, as it increases pollination efficiency. And when flowers evolve to the same type of pollinators, it seems that some floral traits frequently change or appear together. The concept of pollination syndromes was created to describe sets of traits associated to pollinator types (e.g., Bees and wasps, beetles, mammals, hummingbirds, etc.). Pollination syndromes have been debated for a long time, but they might be useful to understand plant natural history. Here we study *Passiflora* (e.g., passion fruit species), where switches of pollination syndromes might have occurred several times, and that has a great variety of pollinators. The complex ecology of those tropical lianas and their peculiar flower morphology raises many questions about their floral evolution. Phylogeny and classification in the genus *Passiflora* L. is still somehow unstable, so anew phylogenetic framework was build using published sequences and pollination syndrome evolution was reconstructed with ancestral states reconstruction first and character correlations tests. We discuss the existing molecular data and their phylogenetic power. Floral evolution is discussed in the light of pollination knowledge and the relevance of pollination syndromes is evaluated for this group. We state that passifloras are a good tropical model for flower evolution in regard to pollinator interactions.

P.0569 A preliminary study on reproductive ecology and life history of Veratrum in Taiwan

Ssu-Han Chiu[1], Jer-Ming Hu[1, 2]

1 Institute of Ecology and Evolutionary Biology, National Taiwan University, Taipei, Taiwan. 2 NTU Herbarium, National Taiwan University, Taipei, Taiwan.

Veratrum (Melanthiaceae) species are perennial plants, many with medicinal properties, and there are 25 accepted species predominantly distributed in the Northern Temperate regions. There are two species found in Taiwan, *Veratrum formosanum* O.Loes. and *V. shuehshanarum* S.S.Ying, both are endemic to the island and are primarily habitat in open grasslands in the Central Mountain Range at 2,200-3,600 m and at the Datun Mountain at 800 to 1,100 m in northern Taiwan, displaying a northern descent phenomenon. The most distinctive feature between the two lies in the colour of their flowers. *V. formosanum* displays purple flowers, while *V. suehshanarum* has light green ones, with a few intermediate forms observed. No reproductive or phylogenetic studies for the two taxa in Taiwan have been studied. Field observations were conducted from June 2022 to December 2023 at various localities in Taiwan. The results showed that the population of *V. shuehshanarum* is significantly fewer than that of *V. formosanum*. Four individuals of *V. shuehshanarum* in known localities were recorded in the fieldwork and from historical records. The flowering period for both species occurs from mid to late June to mid-August, with fruiting occurring from late July to October. Flowering and fruiting in higher altitudes are delayed by 2 weeks compared to Datun Mountain, likely influenced by temperature differences. Pollinators of *Veratrum* are primarily members of (1) Diptera, such as Syrphidae, Tipuloidea, and other fly species; (2) Lepidoptera, including moths; and (3) Coleoptera, represented by ladybugs. After the fruiting period in October, the plants gradually wither, disappearing above ground. The individuals survived through winter with underground bulbs, while regrowth and budding typically happened around February of the following year.

P.0570 The floral scent chemistry of Philodendron cipoense (Araceae) ensures diversity of pollinating cyclocephaline beetles (Melolonthidae)

Pinheiro-Costa, B[1,2], Maia, A.C.D[3]., Oliveira, R[4]., Schlindwein, C[5].

1 Departamento de Botânica, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil. 2 Centro de Investigación de Estudios Avanzados del Maule, Universidad Católica del Maule, Talca, Chile (Current address). 3 University of Corsica, Laboratory of Sciences for the Environment, Ajaccio, France. 4 146 Tenente Vitorino street, Belo Horizonte, MG, Brazil. 5 Departamento de Botânica, Grupo Plebeia-Ecologia de Abelhas e da Polinização, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

Highly specialized pollination interactions have been documented in cantharophilous Araceae, where only one or a few cyclocephaline beetle species are effective pollinators, ensuring fruit set. Volatile organic compounds (VOCs) play a crucial role in mediating these specialized mutualisms, as demonstrated by both field and laboratory-controlled experiments. Given that selective attractiveness is achieved through single or simple combinations of VOCs, a prominent hypothesis suggests that the employment of ‘private communication channels’ may be widespread in aroid-cyclocephaline beetle interactions. These channels could be pivotal for reproductive isolation, speciation, and the rapid diversification of both plants and their pollinators. We investigated the role of floral scent in attracting pollinators of Philodendron cipoense Sakur. & May, an endangered rupicolous species endemic to the Espinhaço mountain range, in mid-eastern Brazil. Qualitative and quantitative analyses of floral scent chemistry were conducted, followed by field experiments to assess the attractiveness of key scent compounds to potential pollinators. Chemical analysis of floral scent samples revealed a perfume predominantly composed of (Z)-jasmone, p-vinylanisole, and isojasmol, collectively comprising 97% of the mixture. The presence of a limited set of major VOCs, despite overlapping with those of other cyclocephaline beetle-pollinated taxa, enables P. cipoense to attract a diverse array of specialized pollinators, including Cyclocephala atricapilla, C. variolosa, Chalepides dilatatus, and Erioscelis sp., thereby ensuring pollination success for the species. In field experiments, we successfully attracted both female and male specimens of Cyclocephala atricapilla and C. celata to (Z)-jasmone. Our findings demonstrate that the floral scent of P. cipoense plays a critical role as an olfactory cue for pollinator attraction. The presence of a diverse range of pollinators is facilitated by the chemically convergent scent and olfactory preferences of selected species of cyclocephaline beetles.

P.0571 Hawkmoth pollination in the Afrotropics: frequency, evolutionary patterns and timeline of Darwin's famously predicted guild

João Farminhão[1,2,3], Géromine Collobert[4], Marie Savignac[3], Simon Verlynde[5], Brigitte Ramandimbisoa[6], Laura Azandi[3,6], Nirina Rajaonarivelo[7], Benoît Perez-Lamarque[4], Arsela Todivelo[7], Vincent Droissart[3,6,8,9], Porter P. Lowry II[4], Olivier Lachenaud[3,10], Florent Martos[4], Tariq Stévart[3,6,10]

1 Jardim Botânico da Universidade de Coimbra, Coimbra, Portugal. 2 Centre for Functional Ecology, Laboratório Associado TERRA, Departamento de Ciências da Vida, Universidade de Coimbra, Coimbra, Portugal. 3 Herbarium et Bibliothèque de Botanique africaine, Université libre de Bruxelles, Brussels, Belgium. 4 Institut de Systématique, Evolution, Biodiversité, Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France. 5 New York Botanical Garden, Bronx, New York, United States of America. 6 Missouri Botanical Garden, Africa & Madagascar Department, St. Louis, United States of America. 7 Ambatovy, Environment Department, Moramanga, Madagascar. 8 AMAP Lab, Univ. Montpellier, IRD, CNRS, CIRAD, INRAE, Montpellier, France. 9 Plant Systematics and Ecology Laboratory, Higher Teachers' Training College, University of Yaoundé I, Yaoundé, Cameroon. 10 Botanic Garden Meise, Meise, Belgium.

The world-renowned pollination system of the long-spurred orchid *Angraecum sesquipedale* from Madagascar and the long-tongued hawkmoth *Xanthopan praedicta* is the best-known example of the predictive power of evolutionary ecology, yet the relative importance of coevolution and pollinator shifts for the origin of the deepest nectar tubes is still debatable. Recently, an orchid in the genus *Solenangis* bearing the longest spur of any flowering plant, relative to flower diametre, was discovered in Madagascar. In the aftermath of this exceptional discovery, which expands Darwin's famously predicted pollination guild, the frequency and phylogenetic diversity of sphingophily in the Afrotropics is comprehensively reviewed for the first time. Based on flower colour, structure and depth, we identify 697 species in Tropical Africa and 320 species in Madagascar as presumably sphingophilous. The proportion of hawkmoth-pollinated species in the flora of Madagascar (2.9%) is almost double the one found in mainland Tropical Africa (1.6%). By establishing a parallel between floral depth and proboscis length, we propose a new terminology for the different pollination niches within sphingophily. Based on this overview, we pinpoint some spatial patterns in hawkmoth pollination and we present hypotheses to account for the apparent higher diversity of sphingophilous plants in some habitats and bioregions in the Afrotropics. Additionally, a timeline of hawkmoth pollination evolution in the Afrotropics is presented.

P.0572 Classical and 3-D pollination syndromes of Aquilegia

Anna-Sophie Hawranek[1], Maria von Balthazar[1], Gregor Traun[1], Anne Le Maître[1], Marion Chartier[1], Jürg Schönenberger[1]

1 University of Vienna, Vienna, Austria.

Flowers in the genus *Aquilegia* are pentamerous with two whorls of petaloid perianth organs. The organs differ greatly in shape (flat vs. spurred) and, in most species, also in colour. In Asia and Europe *Aquilegia* flowers are mostly pollinated by bumblebees and bees, while in North America shifts to hummingbirds and hawkmoths have occurred repeatedly. In earlier studies, typical bee, hummingbird or hawkmoth syndromes have been described for different *Aquilegia* species. However, as field observations have shown, *Aquilegia* flowers are almost always visited by a number of different pollen and nectar collectors, and some

Aquilegia species seem to exhibit mixed pollination systems. In a first step, we established for each species its "classical" pollination syndrome (bee-hummingbird-hawkmoth) based on general floral traits such as perianth colour, spur length etc. In a second step, we also considered additional floral traits that are involved in the physical interaction between plant and pollinators such as position of the reproductive organs in relation to the whole flower, flower orientation etc. Furthermore, we distinguished between nectar- and pollen-collecting pollinators in our analyses. Finally, to better understand the floral evolution through pollinator-driven selection, we used X-ray computed tomography and identified additional, 3-dimensional shape traits possibly resulting from the adaptation to one or more types of pollinators.

P.0573 The role of breeding systems in diversification of Melastomataceae.... enough information?

Francisco Javier Jiménez-López[1], L. Patricia C. Morellato[2]

1 Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos, Madrid, Spain. 2 Phenology lab, Biodiversity Department, Center of Research on Biodiversity Dynamics and Climate Change, Universidade Estadual Paulista, Rio Claro, São Paulo, Brazil.

Diversity of flowering plant species can be promoted by multiple factors. Among them, breeding systems can play a fundamental role, since self-fertilization dynamics can enhance reproductive isolation and fix genotypes in a few generations. Therefore, in those angiosperm families with high variability of reproductive systems could play a fundamental role in their diversification and distribution. In this sense, the Melastomataceae, a large tropical family, may be a good model to evaluate this phenomenon. Among other aspects, this family includes species with all options of sexual and breeding systems, from apomixis to dioecy (obligate outbreeders, e.g. in the genus *Miconia*). However, the study of breeding systems seems to be outdated in plant biology. The rate of species for which precise breeding or mating system studies have been carried out is surprisingly low. This aspect is also unbalanced among the different tropical regions where Melastomataceae are distributed and among the different tribes. Therefore, we must be prudent in the evaluation of breeding systems in the diversification of this family.

P.0574 Repeated switching between pollination by sciarid and mycetophilid fungus gnats associated with the radiation of Arisaema in Japan

Satoshi Kakishima[1,2], Tetsuya Matsumoto[3], Kenji Suetsugu[4], Yudai Okuyama[2]

1 Showa University, Fujiyoshida, Japan. 2 National Museum of Nature and Science, Tsukuba, Japan. 3 Ibaraki University, Mito, Japan. 4 Kobe University, Kobe, Japan.

The adaptation to pollinators is a key factor in the evolution of floral traits and plays a crucial role in adaptive radiation. In Japan, the genus *Arisaema* (Araceae) exhibits significant diversification, possibly through adaptation to pollinators. Recent studies have indicated that many *Arisaema* species attract species-specific fungus gnat pollinators (Mycetophilidae and Sciaridae), and differences in pollinator assemblages serve as an important mechanism for reproductive isolation between species. In this study, we conducted a molecular phylogenetic analysis using genome-wide SNP data of *Arisaema* species to understand the relationships between inflorescence morphological traits and pollination mode. We identified several instances where previously recognized species were polyphyletic, with major pollinators varying among different lineages within those species, despite having similar inflorescences. Additionally, we identified six distinct clades, and interestingly, within some of these clades, we discovered species that are pollinated by mycetophilids and others by sciarids. This pattern suggests the occurrence of parallel pollinator shifts within the genus *Arisaema* in Japan. These findings support the hypothesis that that adaptation to fungus gnats is a major driver of *Arisaema* diversification in the Japanese archipelago. Moreover, the distinct fungus gnat pollinator fauna among species with similar inflorescence morphology underscores the potential importance of inflorescence odor in pollination. Consequently, we plan to further analyze the chemical components of the inflorescence odor in future studies.

P.0575 Disentangling the drivers of plant-pollinator interactions

Jose B. Lanuza[1], Henriette F. Morgenroth[1], Raymond Umazekabiri[1], Marc Hoffmann[1], Panagiotis Theodorou[1,2], Robert Paxton[1,2], Isabell Hensen[1,2], Robert Rauschkolb[1,3], Christine Römermann[1,3], Oliver Schweiger [1,5], Martin Freiberg[1,4], Tiffany Knight[1]

1 German Centre for Integrative Biodiversity Research, Halle-JenaLeipzig, Leipzig, Germany. 2 Institute for Biology, Martin-Luther-UniversityHalle-Wittenberg, Halle, Germany. 3 Institute of Ecology and Evolution with Herbarium Haussknecht and Botanical Garden, Friedrich Schiller University Jena, Jena, Germany 4 Systematic Botany and Functional Biodiversity/Botanical Garden, Institute of Biology, Leipzig University, Leipzig, Germany. 5 UFZ-Helmholtz Centre for Environmental Research, Department of Community Ecology, Halle, Germany.

Flowering plants exhibit an astonishing diversity of reproductive structures, which shapes how they interact with their pollinators. However, to what extent reproductive traits or other drivers like phenology and species abundances shape plant-pollinator interactions is still an open question. To disentangle the relative effects of species phenology, abundances and traits in plant-pollinator interactions, we compared pollinator visitation rates, diet breath, specialization from plant species that vary in reproductive traits, phenology and abundances. To do this, we observed plant-pollinator interactions for a whole flowering season in three different botanical gardens located in an urban setting. We anticipate that the ecological role of the different plant and pollinator species are largely driven by their phenological overlap and abundance, and only certain taxonomic groups are strongly influenced by trait matching processes. Our results highlight the relevance of considering multiple mechanisms to understand plant-pollinator interactions.

P.0576 Relationships between floral traits' originality and plant fitness along gradients of landscape disturbance

Amparo Lázaro[1], Indradatta de Castro-Arrazola[1], Carmelo Gómez-Martínez[1], Ørjan Totland[2]

1 Mediterranean Institute for Advanced Studies (UIB-CSIC), Global Change Research Group, Esporles, Spain. 2 Department of Biology University of Bergen, Bergen, Norway.

Floral traits favour pollination by attracting pollinators and maximizing pollinator efficiency. Therefore, floral traits may be at least partially responsible for among-species differences in pollinator visitation and fitness. However, the attractiveness of floral traits for pollinators might depend as well on the community context in which the pollinators make foraging decisions. In this work, we explore for the first time the extent to which the originality and uniqueness of species' floral traits within their communities, influence their pollinator visits and fitness. For this, we sampled plant-pollinator interactions and plants' seed production in 20 Mediterranean and 24 Temperate communities along gradients of habitat loss. We then used multivariate techniques to estimate the originality (i.e., distance to the centroid of community's functional trait hypervolume weighted by plant abundance) and the uniqueness (i.e., distance to closest neighbour) of species' floral traits in each community and sampling date, and related these variables to pollinator visits and fitness. Our results showed that weighted originality consistently decreased total pollinator visits in both study systems. Although the uniqueness of floral traits always had stronger effects on visitation in disturbed landscapes (i.e., lower percentage of natural habitats) compared to more conserved landscapes, the effect differed between study systems. In disturbed Mediterranean communities, uniqueness reduced visitation, while uniqueness increased pollinator visits in Temperate disturbed communities. The effects of originality on fitness also differed between study systems, with a negative effect in the Mediterranean communities and a positive effect in the Temperate ones, which might be explained by differences in species richness between study systems. On the contrary, the positive effect of uniqueness on fitness in disturbed landscapes was similar for both systems, suggesting the benefits of niche partitioning particularly in these landscapes. Our study highlights the context-dependent effects of floral traits on pollinator visits and plant fitness.

P.0577 Flavonoid composition of red flowers affects pollinator attractiveness.

Melissa León-Osper[1], Mª Luisa Buide[1], Montserrat Arista[2], Pedro L. Ortiz-Ballesteros[2], Victor Rossi[3], Katie Conrad[3], Justen B. Whittall[3], Amelia Fuller[3], José C. del Valle[2], Eduardo Narbona[1].

1 Pablo de Olavide University, Seville, Spain. 2 Seville University, Seville, Spain. 3 Santa Clara University, Santa Clara, USA.

Red flowers have traditionally been associated with bird pollination because birds perceive long-wavelength colors, whereas hymenopterans exhibit lower sensitivity in the yellow-red band. This association gave rise to the "bee-avoidance" hypothesis, which proposes that flowers evolved red colors to deter visits from hymenopterans. However, we recently demonstrated that not all red-flowered species follow this strategy, as some showed reflectance spectra with a secondary reflection peak in the UV band, increasing visibility for bees. Because the flower reflectance spectrum is mainly affected by floral pigments, we propose that pigment composition plays a relevant role in triggering changes in pollination strategies in red flowers. To further investigate this hypothesis, we collected samples from red-flowered species in the Mediterranean California (hummingbird-pollinated) and Spain (bee-pollinated). We measured the reflectance spectra and performed spectral analysis to assess the conspicuousness of red flowers for both pollinators. Additionally, we examined their absorbance spectra and identified main floral pigments through HPLC-LC-MS. Our findings revealed that bird-pollinated red flowers had lower UV reflectance compared to bee-pollinated ones, making them more perceptible to birds and less discernible to bees. Furthermore, bird-pollinated red flowers showed higher concentrations of UV-absorbing flavonoids, probably leading to the absence of UV-reflectance in these flowers. We also identified differences in anthocyanin visible pigmentation between bird- and bee-pollinated red flowers. Whereas the predominant anthocyanin in bird-pollinated flowers was pelargonidin, bee-pollinated flowers exhibited equal amounts of cyanidin and delphinidin. Finally, we found that reflectance properties of pelargonidins are better adapted to the visual systems of both pollinators. Differences in pigment composition between red flowers from California and Spain suggest apparent strategies to attract their respective target pollinators. Our results suggest that the concentration of UV-absorbing flavonoids and the type of anthocyanins play a crucial role in the evolution of red flowers in California and Spain.

P.0578 Exploring chemical diversity of floral scent in wild tobacco in light of genus evolution

Maria Alice M.S. Couto[1*], Geraldo L.G. Soares[1], Caroline Turchetto[1,2]

1 Department of Botany, Bioscience Institute, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil. 2 Pos graduate Program of Genetics and Molecular Biology (PPGBM). Department of Genetics, Bioscience Institute, Universidade Federal do Rio Grande do Sul, Brazil.

Plant-pollinator relationship drives floral diversity. Among many floral signals, flower scent is used to attract and ensure an efficient pollination system. *Nicotiana* is a diverse genus in terms of floral phenotypes. The evolution of the genus was closely impacted by the relationship with pollinators, through floral specialization and hybridization, arising new species. *Nicotiana* is a genus with a wide variation in floral shape and color, with hybridization resulting in transgressive phenotypes impacting pollination-related visual traits. In this review, we investigated how phylogeny and pollination systems impact the floral blend of *Nicotiana* species. A bibliographic review was carried out for 30 years of floral volatiles emissions studies and organized on circadian rhythms. The results of 18 studies investigating floral volatiles in 19 species of *Nicotiana* were revised. For each study, we retrieved information concerning methodology, volatile compounds present, circadian rhythm, and pollination systems. In total, 179 compounds were found, including mono- and sesquiterpenoids, nitrogenous compounds, and benzenoids. Most allopolyploid species lack floral emissions data, and total circadian emissions in *Nicotiana* are still underrepresented. The results suggest that pollination systems have a major similarity in emissions in night-pollinated flowers. However, phylogeny still has a role in scent emission for species with conflicting pollination systems.

P.0580 How do flower visitors, and a subset of true pollinators, respond to environmental variables in Chilean highbush blueberry crops?

Pinheiro-Costa, B[1]., Cortes-Rivas, B.[2], Mesquita-Neto, J.[2]

1 Programa de Doctorado en Salud Ecosistémica, Centro de Investigación de Estudios Avanzados del Maule, Universidad Católica del Maule, Talca, Chile. 2 Laboratorio Ecología de Abejas, Departamento de Biología y Química, Facultad de Ciencias Básicas, Universidad Católica del Maule, Talca, Chile.

Highbush blueberry (Vaccinium corymbosum L.: Ericaceae) is a globally important buzz-pollinated crop in which animal pollinators, particularly those capable of sonicating flowers, play an important role in ensuring high quality fruit production. However, without a clear distinction between visitors and pollinators, the functional roles of the antagonists (pollen and nectar thieves) and neutrals are mixed with the mutualistic partners (pollinators) of the plant. Pollinators adapt foraging behavior through time and space, focusing their efforts to maximize pollen collection, and therefore are susceptible to variations in local environmental conditions. We hypothesize that the daily activities of flower visitors compared to true pollinators of highbush blueberry crops are differentially influenced by local environmental and temporal variables. The frequency of flower visitors was measured in four highbush blueberry orchards in southern Chile. The daily activity was estimated by 10-minute observations at five-time intervals (10:00-11:59, 12:00-13:59, 14:00-15:59, 16:00-17:59 and 18:00-19:59) while temperature, light intensity, and wind speed were measured. True pollinators were distinguished from non-pollinators based on number of intraspecific pollen depositions on the stigma per visit relative to the control of unvisited flowers (bagged flowers). Among the measured variables, only luminosity and time of day significantly accounted for the frequency of flower visitors to blueberry flowers. Considering only the subset of true pollinators, temperature played a role in influencing their frequency of visiting blueberry flowers, in addition to the variables affecting the frequency of flower visitors. In contrast, only specific time intervals (10:00-11:59 and 12:00-13:59) differed in the presence of true pollinators. Therefore, the frequency of true pollinators in blueberry flowers was significantly more affected by temperature and luminosity fluctuations than all flower visitors. Although other external factors may affect pollinator frequency, these results are particularly important to predict the occurrence of true pollinators in blueberry crops with important implications for crop management.

P.0581 The invasive bumblebee Bombus terrestris (Linnaeus, 1758) disrupts the adaptive function of heteranthery by indiscriminately visiting the pollinating and feeding anthers of Senna arnottiana flowers

Juliana O. Rego[1,2], Victor Hugo Monzón[2], José N. Mesquita-Neto[2*]

1 Jardim Botânico da Fundação de Parques Municipais e Zoobotânica de Belo Horizonte, Belo Horizonte, Minas Gerais, Brasil. 2 Laboratorio de Ecología de Abejas, Departamento de Biologia y Quimica, Facultad de Ciencias Básicas, Universidad Católica del Maule, Talca, Maule, Chile.

Heteranthery, the presence of different types of anthers on the same flower, is a floral adaptation that aims to balance the need for pollinators to gather pollen as a food resource while also ensuring sufficient pollen for pollination. We investigate the role of heteranthery in the pollination of *Senna arnottiana* flowers and how it affects the behavior and effectiveness of visiting bees, with a specific focus on the impact of the invasive bumblebee *Bombus terrestris*. *Senna arnottiana* is a shrub with hermaphrodite flowers that has two long pollinating anthers, one medium anther, four short feeding anthers, and three staminodes. We observed variations in anther size and found that long anthers contained the most pollen and were the most fertile, producing more fruits and seeds.

Different bee species visit *S. arnottiana* flowers, and their foraging behavior varies. Native bees, including *Centris cineraria*, *Caupolicana* sp., and *Cadeguala occidentalis*, preferentially visit short anthers, while *B. terrestris*, an exotic bumblebee, forages from both short and long anthers without distinction. This behavior by *B. terrestris* disrupts the adaptive significance of heteranthery by mixing the roles of pollination and feeding anthers, potentially affecting the plant's reproductive success. Despite the higher stigma contact by *B. terrestris*, its indiscriminate foraging behavior hinders the efficient transfer of pollen to the stigma, reducing its role as an effective pollinator. The study highlights the negative impact of invasive species like *B. terrestris* on native plant-pollinator relationships and the need to consider the complex dynamics of these interactions in conservation efforts. The results provide empirical evidence in support of the "division of labor" hypothesis in *S. arnottiana* and emphasize the potential disruption of this relationship by exotic pollinators.

P.0582 Orientation of four and eight pollinia in Epidendreae and Maxillarieae (Epidendroideae, Orchidaceae)

Hilda R. Mosquera-Mosquera[1], Rosa M. Valencia Barrera[2], Carmen Acedo[3]

1 Faculty of Sciences, University of Tolima, Ibagué, Colombia. 2 Faculty of Biological and Environmental Sciences, University of León, León, Spain.

The orientation of superposed or juxtaposed pollinia in Orchidaceae is an important but little-studied topic. It is related to the position and dehiscence of the anther, the rotation of the thecae, and the number of pollinia. In the subfamily Epidendroideae, two states of pollinia orientation occur. Still, probably they are not the result of the same process and/or transformation of the characters indicated for the complete family in the literature. This research analyzes and describes the orientation of the pollinia based on the position and dehiscence of the anther of 34 species belonging to the tribes Maxillarieae (*Anguloa, Sudamerlycaste, Lycaste, Maxillaria, Caluera, Ornithocephalus, Sphyrastylis, Pescatoria, Chondroscaphe, Cochleanthes, Dichaea, Galeottia, Huntleya, Kefersteinia*) and Epidendreae (*Brassavola, Cattleya, Caularthron, Dimerandra, Encyclia, Epidendrum, Laelia, Prosthechea, Scaphyglottis*), and five subtribes (Laliinae, Lycastinae, Maxillariinae, Oncidiinae, and Zygopetalinae). Pollinaria from fresh samples and herbarium specimens were investigated. The pollinaria were extracted and photographed with a Nikon 11.25X stereomicroscope with a Nikon Dxm1200 camera. The images were processed with NIS-Elements F 2.20 software. All the analyzed samples have incumbent anthers and introrse dehiscence, but *Dimerandra buenaventurae* has erect anthers. In most of the species of Zygopetalinae studied their four pollinia are superposed, except in *Maxillaria egertoniana,* having juxtaposed pollinia. In the members of the subtribe Laeliinae, in both cases, four or eight pollinia have a juxtaposed orientation. Other studies have indicated the following relationship: latrorse anther/superposed pollinia and introrse anther/juxtaposed pollinia. Our results allow inferring that the orientation of the pollinia may obey the occurrence of longitudinal and transverse septa that produce the locules within the anther and where the pollinia are organized, the presence of operculate anthers to facilitate the release or deposition of the pollinia on pollinators, and not exclusively the position or the dehiscence of the anther.

P.0583 Orchid pollination and fecundity: a comparison between deceptive and rewarding species

Ludovica Oddi[1], Valeria Fochi[1], Asja Cucchietti[1], Alex Salvadego[1], Karl Duffy[2], Consolata Siniscalco[1]

1 Department of Life Sciences and Systems Biology, University of Turin, Torino, Italy. 2 Department of Biology, Complesso Universitario di Monte Sant'Angelo, University of Naples Federico II, Naples, Italy.

The fecundity of pollinator-dependent orchids is affected by different factors in food-deceptive and -rewarding species. Indeed, rewarding orchids can rely on nectar production to attract pollinators, whereas deceptive species take advantage of other factors, such as floral mimicry and community density. In this study, we tested whether the inflorescence morphological characteristics and the local conspecific and non-conspecific density influence pollination and fecundity in the rewarding orchids, *Gymnadenia conopsea* (two different sites) and

Spiranthes spiralis, and in the deceptive orchids, *Neotinea tridentata* and *Dactylorhiza sambucina*. We measured the plant height and the number of flowers of 50 individuals per species, together with the distance to each of the nearest five conspecific and non-conspecific plants in five populations in Piedmont, along an altitudinal gradient, from the bottom valley to the alpine horizon. Furthermore, we examined whether pollen removal, pollen deposition and fruit set varied according to the measured variables. We observed that plant height and the number of flowers had a positive significant effect on the number of visited flowers and fruits only in rewarding species. We also found that the number of visited flowers was significantly linked to the fruit set of rewarding orchids, whereas we did not observe the same pattern in deceptive species. The distance from conspecific and non-conspecific species did not show any significant effect on both pollinator visiting and fruit set. Results suggest that plant height and the number of flowers increase orchid success in capsule production in rewarding species, which also showed a strong link between pollinator visiting and fruit set. On the contrary, in deceptive species the number of visited flowers was not correlated to the fruit set, since pollinators spend less time on flowers decreasing the probability of pollination success. The role of species density and vegetation structure needs further investigations.

P.0584 Breakthroughs on the reproductive biology and the taxonomy of Lavatera acerifolia (Malvaceae), an endemic shrub to Canary Islands

María Olangua-Corral[1], Lluís García Mir[2], Olga Férnandez-Palacios[1], Rosa Febles[1], Javier Fuertes Aguilar[2]

1 Jardín Botánico Canario "Viera y Clavijo"-CSIC, Las Palmas de Gran Canaria, Spain. 2 Real Jardín Botánico-CSIC, Madrid, Spain.

As part of NEXTPOL and MACFLOR projects, we were studied the reproductive biology and several micro-morphological characters in *Lavatera acerifolia* Cav. (=*Malva canariensis*), a Canarian endemic species with two varieties. Likewise, *L. acerifolia* is an endangered, redlisted species. Inicially, we have undertaken a 2-year comparative studies on floral phenology and changes of micro-morphological attributes of hermaphrodite flower in this caducous woody shrub. As a novelty, seventeen morphological characters of the flower were daily analyzed along the floral development, providing a more objective criterion to establish the developmental stages. Floral phenology was divided into sven stages (plus fruiting period), being four of them pre-anthesis (S0-S3) and three post-anthesis (S4-S6; this starts when petals are fully open and androecium is accessible). The total life-span of a single flower was 32 days, on average. *L. acerifolia* takes 28d for the petal to achieve the maximum size before floral anthesis, while pollination period lasted only 4d. In all cases, hermaphrodite flowers present short protandry and partial herkogamy. Flowers of *L. acerifolia* exhibit an entomophilous pollination syndrome (punctual concentration of nectar between calyx-petals base, colour guides in the nail of the whitish petal, pollen with spines +pollen-kit and stigma with papillae). In addition, Pollen-Ovule ratio and pollen size were analyzed to compare with the pollination syndrome for both varieties. In all cases, P-O ratios are moderately low, showing a facultative Xenogamy *sensu* Cruden (1977). Controlled hand pollination treatments were carried out evaluate the breeding system and self-incompatibility (SI) of *L. acerifolia*. On the other hand, morphological and biometric differences of flowers and seeds were detected for *L. acerifolia* and its variety *hariensis*, with possible taxonomic implications.

P.0585 Pollen analysis of stingless bee honey from the Peruvian Amazon

Rossana Paredes[1], Daniel Meza Huamán[2]

1 Laboratorio de Palinología y Paleobotánica, Laboratorios de Investigación y Desarrollo-LID, Universidad Peruana Cayetano Heredia, Lima, Perú. 2 Laboratorio de Palinología y Paleobotánica, Laboratorios de Investigación y Desarrollo-LID, Universidad Peruana Cayetano Heredia, Lima, Perú.

Honey is consumed for medicinal, culinary, religious and diverse purposes, being a natural product with global demand. Meliponiculture involves the management and breeding of stingless bees which produce honey with greater medicinal properties compared to the honey of other bee species. In Peru, there is a knowledge gap in the composition of honey produced by stingless bees, which is considered a higher quality product by local producers reflected in the high price of the product in the national market. For this reason, this work seeks to determine the botanical content of the honey produced by stingless bees of the Peruvian Amazon by conducting a melissopalynological analysis. Pollen from Melastomataceae, Myrtaceae and Elaeocarpaceae botanical families were very frequent in the samples, while pollen from Asteraceae and Convolvulaceae botanical families were rare. Pollen concentration class values per 10 g of honey varied from rich to poor. In general, the interactions between bee keepers, bees and honeys were different between the two studied Amazonian regions: in the lowland region, beekeepers produce stingless bee honey mainly as an additional economic activity, and in the highland region mainly for personal consumption. More melissopalynological studies on stingless bees and their honey in Peru are needed to promote the complementation of scientific and traditional knowledge in the use and commerce of bioproducts.

P.0586 Anatomical modifications of figs along the reproductive cycle of a Brazilian fig tree (Ficus citrifolia Mill., Moraceae)

Felipe P. Ramos[1,2*], Jackeline V. Silva[1,2], Ana Julia Peracini[1,2], Simone P. Teixeira[2]

*1 Faculty of Philosophy, Science and Letters of Ribeirão Preto, University of São Paulo, Ribeirão Preto, Brazil. 2 Faculty of Pharmaceutical Sciences of Ribeirão Preto, University of São Paulo, Ribeirão Preto, Brazil. *felipepramos@usp.br*

The fig trees (*Ficus*) and the minuscule Agaonidae wasp participate in a mutualistic interaction that has selected a series of convergent adaptations on both organisms, like the concurrent development of the figs and their pollinators, which has been divided into five biological phases (A to E). This work aims the study of anatomical modifications that occur in the fig, with emphasis on the laticifer, throughout the reproductive cycle of *F. citrifolia* Mill., a species widely distributed in Brazil. To this end, figs in all phases of the cycle were collected and processed for anatomical (light microscopy) analysis. The fig mesophyll initially shows parenchyma and vascular bundles that still have not reached their final dimensions. In phases B-C, the tissues expand; in D-E, some cells of the parenchyma die, turning the intercellular spaces wider, and the fiber walls become thicker. A branched laticifer travels through the mesophyll. Its walls are pecto-cellulosic and its latex is dense and has polysaccharides on stages A-C. In B-C, the laticifer becomes vacuolated and multinucleated. In phases D-E, the secretory structure persists, showing winding cell walls, vacuolated cytoplasm, and less dense latex. Phenolic idioblasts can be widely found in all phases of the inflorescence, especially below the epidermis and in the perianth of pistillate and staminate flowers. Increased compounds in the latex and thickening of the fibers by C-phase probably reduce oviposition by fig parasitic wasps. The programmed death of the parenchyma cells allows the fig to expand and decreases its stiffness in the later stages of the cycle. Despite the persistence of the laticifer, the decrease of latex products probably makes the fruit more palatable for consumption by dispersing animals. Such anatomical changes occurring in the fig are typical of an endozoochoric fruit (infructescence).

P.0587 Phenology, floral morphology and reproductive biology of the endangered Azorean endemic Azorina vidalii (Campanulaceae)

Rúben M. C. Rego[1], Mónica Moura[1], Luís Silva[1], Guilherme Roxo[1], Alejandra G. Herrezuelo[1], Roberto Resendes[1], Magui Olangua-Corral[2]

1 Universidade dos Açores, Ponta Delgada, Portugal. 2 Jardim Botânico Canario "Viera y Clavijo", Las Palmas de Gran Canaria, Spain.

In the Azorean endemic *Azorina vidalii* (Campanulaceae), selfing within a flower might be compromised by morphologic and sexual self-Incompatibility (SI) mechanisms, however, the same is known to occur within an inflorescence, in other Campanulaceae. Additional information about the breeding systems of this endangered species is lacking, therefore, we aimed to study the reproductive biology of *A. vidalii*, assessing its seasonal and floral phenology, morphology, and breeding strategies. Using samples from fourteen populations, throughout the nine Azorean islands, 21 morphological characters were measured and subjected to detailed multivariate and univariate analyses, supported by light and scanning electron microscopy, and the reproductive systems were studied using Pollen/ovule (P/O) ratios and pollination tests. Flowering in *A. vidalii* generally occurs in August, starting earlier in July, in Santa Maria Island, following a fruiting period that lasts until November/December. The flower exhibits protandry, with basal nectaries and a secondary pollen presentation site in the style. The highest variation among the measured morphologic characters in both open flowers and buds was detected in the androecium (anther filaments: 23.0% and anther width: 50.2%, respectively). Some characters in the corolla and reproductive whorls appear to be strongly related, in terms of their dimensions, the same applying to the calyx and ovary. Additional variation was found in the number of pollen grains, ovules, and seeds, among individuals. The P/O ratios showed a tendency for crossing in *A. vidalii* (facultative xenogamy), but the pollination tests showed individuals with different breeding systems within the population studied, with some exhibiting alogamic reproduction, and others favouring xenogamy. Some of the variation observed can be attributed to external environmental factors, such as those related with the flowers' age, after opening (stigma's receptivity and the action of SI mechanisms, during the pollination efforts), temperature, presence of developing fruits or possible scarcity of pollinating agents.

P.0588 Plant polyploidy effects on floral traits and the pollination niche

Nathália Susin Streher[1], Keren Halabi[2], Itay Mayrose[2], Tia-Lynn Ashman[1]

1 University of Pittsburgh, Pittsburgh, USA. 2 Tel Aviv University, Tel Aviv, Israel.

Polyploidy (whole genome duplication) is a major evolutionary process in flowering plants yet the consequences for a significant mutualistic interaction with pollinators is unclear. The increased DNA quantity resulting from whole genome duplication causes larger cells and slower cell division which can impact floral phenotype and flowering phenology-- traits that mediate plant-pollinator interactions. For instance, larger flowers and longer flowering time may affect pollination generalization and also have cascading effects on the structure of the entire plant community. By leveraging herbarium specimens and published plant-pollinator networks, we aim to elucidate the effects of plant polyploidy pollination niche from two different perspectives. Specifically, we asked: 1) do polyploids have larger flowers and broader pollination niches than diploids or does this depend on mating system or its interaction with ploidy? 2) does the percentage of polyploids within communities affect plant-pollinator network structure? We tested the first question on 40 Brassicaceae species. Our results indicated that mating system moderated the influence of ploidy on morphological features associated with pollination generalism but that response in terms of pollination generalism (inferred from diversity of pollen/stigmas) was more variable. For the second question, we analyzed 316 weighted bipartite plant-pollinator networks and revealed that polyploid-rich communities exhibit significantly higher nestedness and lower modularity. These effects, however, do not appear to propagate to increased connectance and enhanced robustness to extinction and are mostly indirect-- being mediated by the frequency of self-compatible plants in the community. Taken together our work is revealing the myriad and nuanced ways that polyploidy affects species and their roles within pollination networks.

P.0589 Reproductive biology of two related species of southern Iberian Peninsula: Cathissa reverchonii and C. villasina

Amanda Tercero Araque[1], Luis Ruiz Valenzuela[1], Carlos Salazar Mendías[1]

1 Universidad de Jaén, Jaén, Spain.

Cathissa *reverchonii* (Lange) Speta (=*Ornithogalum reverchonii* Lange) and *C. villasina* C. Salazar, Tercero & Mart.-Azorin are related geophytes that have been confused for 35 years, until the recent description of *C. villasina* as a local endemic species in the Sierra de Las Villas (Jaén province, Andalusia, Spain) in southeastern Iberian Península (Tercero et al. 2023). On the other hand, *C. reverchonii* is an endemic species in southwestern Iberian Peninsula and northern Africa, it has been evaluated as NT according to IUCN threat categories, while *C. villasina* is an endangered species (EN). Futhermore, *C. reverchonii* is included in Annex IV-B of the European Habitats Directive as "vulnerable", but *C. villasina* currently lacks any legal protection. In this work, the mating system of these two species is studied. The pollen/ovules ratio (P/O) is calculated and compared with the results of fruiting and seed production after induced self-pollination and cross-pollination done in experimental garden. Additionally, pollen viability is analyzed over time using the tetrazolium chloride test (TTC), and stigma self-compatibility, fruiting of individuals at field and floral visitors are observed. According to the criteria given by Cruden (2000), the P/O ratio (1000-1170) indicates that both species are facultative xenogamous. However, the low fruiting of hand cross-pollination (between 2-6%) shows that these species are obligate xenogamous with self-incompatible stigmas (Self-Compatibility Index = 0.10). Pollen remains viable up to 16 days after anthesis in both species. The pollinators visitation rate was low, being *Hymenoptera* the main group in both cases. Understanding the reproductive biology of threatened species can provide information to develop appropriate conservation strategies. References: Tercero-Araque A, Martínez Azorín M, & C Salazar-Mendías (2023). *Cathissa villasina* (*Hyacinthaceae*), a new endemic species from the southeastern Iberian Peninsula. Plant Biosyst. 157(3): 516-529; Cruden, RW (2000). Pollen grains: why so many? Plant Syst. Evol. 222:143-165

P.0590 How does pollinator size affect the pollen fate of a buzz-pollinated plant?

Amanda V. da Silva[1], Anselmo Nogueira[1], Vinicius G. Brito[2], Laura C. Leal[3]

1 Center of Natural and Human Sciences, Federal University of ABC, São Bernardo do Campo, Brazil. 2 Department of Ecology, Conservation and Biodiversity, Federal University of Uberlândia, Uberlândia, Brazil. 3 Department of Ecology and Evolutionary Biology, Federal University of São Paulo, Diadema, Brazil.

Animal-pollinated plants exchange floral rewards by pollen transportation. However, flower visitors' traits influence the quality of pollen transfer and, consequently, the male and female reproductive performance. For instance, larger bees provide better pollen transportation than smaller ones. While the effect of pollinator size has been studied from the female component of plant fitness, the male component remains undervalued. This study aims to fill such a gap, evaluating the influence of bees' body size on the male performance of the buzz-pollinated *Chamaecrista latistipula* (Fabaceae). We hypothesized that smaller bee species (1) are less efficient pollinators and (2) have a less steep pollen carryover curve than larger bee species. To evaluate the pollination efficiency and pollen carryover, we performed 32 rounds of simulations of flower visitation using one mimetic individual of a small or large bee. We attached these bees to a mini shaker, which simulated the vibrations of each bee species when visiting *C. latistipula* in nature. We found that large bees removed 1.7 times more pollen grains from the anthers and deposited almost 1.5 times more pollen grains in the stigma of *C. latistipula* than small bees. We also found that the pollen carryover curve was steeper for large than small bees, and the number of pollen grains deposited over multiple visits was higher for large bees. Thus, although larger bees remove more flower resources than the smaller ones, they provide a more effective service of pollen transportation than smaller bees. It indicates that as higher the frequency of pollen-flower visitation by larger bees, the higher the performance of male plant function. Our results highlight that pollinator traits, such as body size, can be an important tool for predicting the impact of bee diversity decline on the outcome of plant-pollinator interactions in natural and modified habitats.

P.0591 Uncovering a novel obligate pollination mutualism endemic to Japan

Marika Yamaguchi*[1], Namiki Kikuchi[1,2], Takahiro Yoshida[1], Yudai Okuyama[3], Noriaki Murakami[1]

1 Tokyo Metropolitan Univ., Hachioji City, Japan. 2 Toyohashi Museum of Natural History, Toyohashi City, Japan. 3 Tsukuba Botanical Garden, NMNS, Tsukuba City, Japan.

Coevolution is a dynamic process in which multiple organisms interact and exert mutual evolutionary influence on one another, and this phenomenon has captured the interest of evolutionary biologists. One of the most prominent examples of coevolution is the intricate relationship between flowering plants and their pollinating insects, the most diverse group of terrestrial organisms on Earth. Among the various mutualistic plant-insect relationships, one of the most highly interdependent and fascinating interactions is known as "obligate pollination mutualism." In this symbiotic relationship, certain insects feed on the seeds of host plants during their larval stage and later act as pollinators for the host's flowers. This unique association has been identified in only eight cases. Obligate pollination mutualism not only provides valuable insights into the mechanisms driving floral diversity, but also serves as an important model for studying the intricacies of biological interactions and coevolution. Our study focuses on the Japanese endemic obligate pollination mutualism between *Macrostemon* plants (classified in *Chrysosplenium* series *Macrostemon*) and *Nipponorhynchus* sawflies (family *Tenthredinidae*). The larvae of the two *Nipponorhynchus* species, *N. bimaculatus* and *N. mirabilis*, have been documented as specialized seed feeders on two plant species, *Chrysosplenium macrostemon* var. *shiobarense* and *C. echinus*, both of which belong to the *Macrostemon* series. In addition, adult *Nipponorhynchus* sawflies possess an elongated proboscis of a unique structure classified as "Type 8" within the order Hymenoptera, distinct from the other seven functional proboscis types. This specialized proboscis might be an adaptation for accessing nectar hidden deep within flowers, and has evolved through interactions with *Macrostemon* flowers. Our study showed that these sawflies are the primary and effective pollinators of *Macrostemon* flowers, confirming that these plants and insects are in an obligate pollination mutualism. We will present the progress of our research on this novel interaction.

P.0592 Pollinator-mediated connectivity in fragmented urban green spaces - tracking pollen grain movements in the city centre

Barbara Płaskonka[1], Marcin Mazurkiewicz[1,2], Mateusz Skłodowski[1,3], Marcin Zych[1], Katarzyna Roguz[1]

1 Botanic Garden, Faculty of Biology, University of Warsaw, Warsaw, Poland. 2 Białowieża Geobotanical Station, Faculty of Biology, University of Warsaw, Warsaw, Poland. 3 The National Botanic Gardens of Ireland, Dublin, Ireland.

Cities are expanding rapidly and emerging as complex ecosystems. This expansion of urbanized areas has resulted in the alteration and fragmentation of several natural habitats. Recent studies have shown that cities support a significant level of biodiversity. This unexpected role of cities holds promise for advancing knowledge of urban ecosystems and promoting their conservation. In particular, the connectivity of plant populations through pollen transfer is crucial for the long-term persistence of insect-pollinated plant species. In this study, we tracked pollen movement areas in four isolated patches of urban greenery in urbanized area using quantum dots. We studied *Fritillaria imperialis* (spring) and *Hemerocallis* sp. (mid-summer). Our research revealed frequent pollen transfer between small, isolated flowering patches, even when these locations were not connected by green corridors. Common elements found in urban ecosystems, such as streets, trails, and pavements, did not stop the dispersion of pollen grains. Moreover, the migration pathways of pollen grains varied for each species according to different factors. For *F. imperialis*, the key factor was the proportion of green areas in proximity to the study location, whereas for *Hemerocallis* it was the proportion of green areas, the distance between study sites, and the frequency of pollinator visits. Our study demonstrates that small isolated plant populations exchange pollen due to pollinator movement, indicating that these small populations may serve as stepping stones for pollinators among larger populations.

S.066. FLORAS AND DIVERSITY OF EASTERN ASIA

P.0593 Assessment of wood specific gravity, carbon content of southern Guinea savanna vegetation zone of Kogi State

Fatimoh O. Ademoh[1], Anthony I. Odiwe[2], Ikechukwu J. Muohalu[2], Moses A. Afolabi[2]

1 Department of Plant Science and Biotechnology, Delta State University of Science and Technology, Ozoro, Nigeria. 2 Department of Botany, Obafemi Awolowo University, Ile- Ife, Nigeria.

A crucial component of the ecology of tropical vegetation is wood specific gravity. It incorporates numerous facets of a tree's mechanical characteristics, and its key factor in biomass estimation when assessing carbon stock globally. This study determined the wood specific gravity (WSG), Carbon content, and above-ground biomass (AGB) of woody species encountered in twenty-seven (0.16 ha) sample plots in the Nigerian southern Guinea savanna of Kogi State. WSG of the stem cores of species was determined from the oven-dry wood mass and green volume. Carbon concentration in the AGB was determined by oven-drying each woody stem core at 105°C to constant weight before analysis. The WSG of 135 (32 shrubs and 103 trees) species was determined with a range of 0.52 g/cm3 to 0.83 g/cm3 and 0.42 g/cm3 to 0.90 g/cm3 for shrubs and trees respectively. Thirty-five rare species were encountered in the vegetation. Among the shrubs, *Anthonotha macrophylla*had the highest (0.83 g/cm3) WSG, and the lowest was *Rauvolfia vomitoria* (0.52 g/cm3). Among the trees *Pterocarpus soyauxii* (0.90 g/cm3) had the highest WSG and *Adansonia digitate* (0.42 g/cm3) had the lowest. Carbon content ranged from 21.65% (*Cola millenii)* to 94.88% (*Sterculia setiga)* among the trees, 25.39% *(Euphorbia kamerunica*) to 71.90% (*Pyrenacantha staudtii)* among the shrubs. For shrubs, *Euphorbia kamerunica* has the highest AGB (49P.6±P.0) and *Dombeya buettner i*had the lowest (16.17±4.80 Kg). For the trees, *Croton penduliflorus* had the highest biomass (7859.61±P.0) and *Trichilia emetica* had the least biomass (13.84±7.93 kg) respectively. Within and among species in the vegetation, the study showed that variation occurred in the specific gravity, AGB, and carbon content.

P.0594 Genus Thismia section Sarcosiphon (Thismiaceae) in Thailand

Isareyakorn Chantapram[1], Alisa Nakkaew[2], Sahut Chantanaorrapint[1]

1 PSU-Herbarium, Prince of Songkla University, Hat Yai, Songkhla, Thailand. 2 Molecular Biotechnology and Bioinformatics, Prince of Songkla University, Hat Yai, Songkhla, Thailand.

Thismia section *Sarcosiphon* sensu lato include species whose inner tepals connate to form a mitre above the flower opening, and lacking any filiform appendages on the top of the mitre. Members of the section are mainly found in Southeast Asia, particularly the Malesian floristic region. This study aims to revise *Thismia* section *Sarcosiphon* in Thailand, based on herbarium specimens and recent collections from field surveys. Plant materials are searched systematically in several localities that were mostly selected in advance based on our previous experiences. Morphological characters are observed and the phylogenetic relationships of section *Sarcosiphon* is also investigated. Eight species are recognized including *Thismia angustimitra*, *T. brunneomitroides*, *T. lacerata*, *T. mirabilis*, *T. nigricans*, *T. obtusa*, *T. sridithiana*, and *T. submucronata*. In addition, *Thismia clandestina* is excluded from the Thai flora. The phylogenetic analyses reveals that the section *Sarcosiphon* sensu lato is not fully monophyletic and separated into two clades: vermiform root clade and coralliform root clade. Species with vermiform roots and outer tepals well developed nest in sect. *Thismia*. While the coralliform roots species with reducing outer tepals sister to a clade of sect. *Geomitra*.

P.0595 Floristic Diversity of Rubiaceae in the Flora of Pan-Himalaya

Tao Chen[1], Mudavath Chennakesavulu Naik[2], Yiying Liao[1], Jianyou Li[1], Mary Ann Bautista[1], Saroji Barik[3], Qiang Wang4

1 Shenzhen Fairy Lake Botanical Garden, Shenzhen, China. 2 Andhra Pradesh State Biodiversity Board, Andhra Pradesh, India. 3 North-Eastern Hill University, Shillong-793022, India. 4 Institute of Botany, Beijing, China.

The Pan-Himalaya region covers a broad area from West China in the east, along the range in Bhutan, India, Nepal and Southern Tibet in the middle, to parts of Pakistan and Afganistan in the west. It enjoys the mostly diverse habitats sustaining a number of hot spots of biodiversity. There are 72 genera and 355 species (including infraspecific taxa) in the family Rubiaceae according to preliminarily floristic diversity analysis. Genera with higher species diversity are *Galium* (49 species), *Hedyotis* (14), *Ixora* (9), *Lasianthus* (13), *Leptodermis* (36), *Mussaenda* (10), *Mycetia* (8), *Ophiorrhiza* (30), *Psychotria* (13), *Rubia* (26) and *Wendlandia* (14). The upcoming Rubiaceae volume for the Flora of Pan-Himalaya would be the ultimately detailed diversity accounts of the family.

P.0596 A pattern of anagenetic speciation is observed in Ulleungdo liverleaf (Hepatica maxima, Ranunculaceae) genomic analysis

Myoung-Suk Cho[1], Seung-Chul Kim[1]

1 Department of Biological Science, Sungkyunkwan University, Suwon, Korea.

Anagenesis has been considered as the prominent speciation mode of endemic plant lineages on Ulleung Island, Korea. Despite unclear progenitor species, *Hepatica maxima* Nakai endemic to Ulleung Island is presumed as one of anagenetically speciated species on the island. Its taxonomic identity has been recognized by its morphological differences from other *Hepatica* species (i.e., larger sized achenes and leaves, biennial or annual leaves and glabrous surface of achenes) through previous numerical and palynological studies. However, the genetic diversity and population structure of *H. maxima* as well as its phylogenetic relationship to other continental *Hepatica* species, *H. asiatica* and *H. insularis* have not been investigated thoroughly to infer its origin and evolution. In this study, we conducted population genetic and phylogenetic analyses employing genotyping-by-sequencing (GBS) method based on broad sampling, including 13 populations of *H. maxima* (194 individuals) from Ulleung Island and 3 populations of *H. asiatica* (21) from Korean Peninsula, and 4 populations of *H. insularis* (49) from other Korean archipelagos (Jeju-do, Hong-do and Gageo-do). The results of phylogenetic reconstruction and population genetic structure analyses based on GBS-derived SNP data revealed the monophyly of *H. maxima* with robust support (100% BS), although its continental progenitor lineage was not determined concretely. Within *H. maxima* on Ulleung Island, population genetic structuring and geographical patterns were found among western, eastern and central populations. Comparing with *H. asiatica* and *H. insularis*, significant reduction in genetic diversity was found in the populations of *H. maxima* on Ulleung Island. This study provides additional insight into broadening our knowledge in the genetic consequence of anagenetic speciation of Ulleung Island plant endemics.

P.0597 Watching the South China Sea - Siamkiama (Iridaceae), a new genus for Iris speculatrix based on molecular and morphological data

Manuel B. Crespo[1], Mario Martínez Azorín[1], Evgeny V. Mavrodiev[2]

1 Department of Environmental Sciences and natural Resources, University of Alicante, Alicante, Spain. 2 Florida Museum of Natural History, University of Florida, Gainesville, USA.

Iris speculatrix is a remarkable species endemic to the southern part of China that was described from the coastal mountains near Hong Kong. The preliminary molecular data did not resolve confidently its phylogenetic position and placed it as strongly sister to the beardless irises (the "*Xiphion* clade" sensu Wilson). That position was first assumed to be highly sequence-divergent regarding the remaining members in there, though consistent with morphology. Nonetheless, classical placement of that species was confusing, and some authors placed it among the "Evansia irises" (either in *I.* sect. *Crossiris* = genus *Evansia*, or *I.* sect. *Lophiris* = genus *Lophiris*), or among the "Chinenses irises" (genus *Zhaoanthus*). However, relationships to the "Evansia irises" were questioned by some authorities based on the reduced entire crest of *I. speculatrix* seeming only a raised ridge. Further, important morphological characters connected it to members of the "Chinenses irises" and separated it from the above cited "*Xiphion* clade" (i.e. slender wiry rhizomes, shiny leaves, spreading falls, discrete central ridge on standards, oblong entire stigma, or seeds with fleshy wing-like appendage). Also, the chromosome number (2*n*=44) is peculiar in the context of that group. In this context, our research on an expanded sampling of the "*Iris*-flower clade" including entire sequences of *I. speculatrix*, recovered it as strongly sister to members of the "*Xiphion* clade", which is congruent with previous phylogenies. This fact together with the morphological and chromosomal divergence regarding members of that broad clade supports a treatment according with the multigeneric arrangement of the "*Iris*-flower clade", as published by the authors. Hence, we propose to accommodate the concerned southern Chinese plant in a new genus, *Siamkiama* M.B.Crespo, Mart.-Azorín & Mavrodiev. Molecular, morphological and biogeographical evidence is presented to support such treatment.

P.0598 Impatiens in Shaanxi, China: from herbarium to field

Zhangjie Huang[1], Peiliang Liu[1]

1 Key Laboratory of Resource Biology and Biotechnology in Western China, Ministry of Education, Northwest University, Xi'an, China.

Shaanxi is the last province in China whose updated regional flora is yet to be published due to historical underestimation in surveys of biodiversity. Being a precursory contribution to the Flora of Shaanxi, the authors conducted a comprehensive study on *Impatiens* in Shaanxi and adjacent areas, notably the Qinling-Bashan Mountains. The investigation integrates literature review, specimen inspection, field research as well as analyses at both morphological and molecular phylogenetic level (utilizing nuclear ITS and plastid *trnL-trnF*, *atpB-rbcL*, *psbA-trnH* sequence). Through these methodologies, the study leads the description of several species in the genus new to science and resolves taxonomic ambiguities surrounding *I. notolopha*. Meanwhile, the distribution of *I. nasuta* and *I. compta* in Shaanxi is clarified. Our data also elucidate morphological and biogeological distinctions between *I. linocentra* and *I. pterosepala*. Moreover, three species are herein reported as new records of Shaanxi.

P.0599 Floristic diversity of Overa-Aru Wildlife Sanctuary in Kashmir Himalaya

Tajamul Islam[1], Anzar A. Khuroo[1], Irshad A. Nawchoo[1]

1 Department of Botany, University of Kashmir, Srinagar, India.

Protected areas are one of the prime repositories to conserve biodiversity and furnish life-supporting ecosystem services. The Overa-Aru wildlife sanctuary is one of the largest protected areas in terms of area in Kashmir Himalaya, however little is known about its biodiversity. Here we present an integrative study on floristic diversity of this sanctuary. In terms of taxonomic composition, a total of 397 taxa (392 species, 1 subspecies, 3 varieties and 1 forma) belonging to 254 genera in 76 families are recorded from the sanctuary. A new species, *Swertia pahalgamensis* has been described from the sanctuary. In addition, the utilization of plants in the sanctuary for precious ecosystem provisioning services such as fuel, fodder, medicine, and the community perception of these services have been studied. Hopefully, this comprehensive study will be immensely useful in guiding suitable conservation strategies and management decisions of this protected area in the region, with lessons for elsewhere.

P.0600 Vascular plants in the Tyumen Region, Western Siberia

Igor V. Kuzmin[1]

1 University of Tyumen, Tyumen, Russia.

Tyumen Region is located in southwestern of the Western Siberia, beyond the mountains of the Middle Urals. This is a large (160.122 sq. km) and inaccessible territory, where natural zones change when moving from north to south. Southern taiga and subtaiga are located in the north. Forest-steppe is located in the south. Wild and cultivated plants of this territory have never been fully studied. We studied all publications, old herbaria (LE, LEGB, MW, MHA, NSK, TK, etc.) and collected our own herbarium (50000 specimens). Based on the results of the work, a checklist was compiled that provided a critical review of 2041 taxa. The checklist includes 1222 wild species, subspecies and aggregate species (native and alien, including 21 native species also in cultivation); 46 wild hybrids; 15 species whose diaspores are intentionally introduced, but they are not cultivated and germinate on their own; 462 cultivated species and 59 hybrids. 55 microspecies are noted inside aggregates. 122 wild and 1 cultivated species, 11 hybrids were excluded from the flora because they were incorrectly indicated in the literature. 10 species are excluded from the wild flora, but are grown. 36 species and 2 hybrids discovered in adjacent territories are potentially possible for our flora. Our research has shown that even in flat areas, plant habitats are dependent on the terrain and local climate. Comparison with data from 100-300 years ago showed a change in the species composition of plants due to climate change. Nowadays, southern steppe species are actively spreading to the north, but sudden weather changes prevent them. Boreal thermophobic species are becoming rarer. The history of settlement of a region also has implications for plant composition. The richest local floras are found in Tobolsk, the old capital of Siberia, and in Tyumen, the most ancient city in Siberia.

P.0601 First record of natural hybrids of Dryopteris from Korea

Chang Shook Lee[1], Kanghyup Lee[2], Chae Eun Lim[3], Chunghee Lee[4], Kyong-Sook Chung[5]

1 Department of Science Education, Ewha Womans University, Seoul, Korea. 2 Korea National Arboretum, Pocheon, Korea. 3 National Institute of Biological Resources, Incheon, Korea. 4 Korea National Arboretum, Pocheon, Korea 5. Department of Medicinal Plant Science, Jungwon University, Goesan, Korea.

The genus *Dryopteris* Adans. (Dryopteridaceae), known as wood fern, contains 225 to 300 species that are widely distributed in the temperate Northern Hemisphere. The genus has the highest species diversity in eastern Asia and is one of the largest genera in Dryopteridaceae. The base chromosome number of *Dryopteris* is n=41, but polyploidy is common; and *Dryopteris* is considered extremely prone to hybridization. The potential roles of reticulate evolution and polyploidy in the genus have long been recognized. In Korea, hybrids of *Dryopteris* have been unknown so far. However, we have recently found two new hybrids and seven unrecorded hybrids (*D.* x *fujipedis*, *D.* x *kominatoensis*, *D.* x *mayebarae*, *D.* x *mitui*, *D.* x *watanabei*, *D. crassirhizoma* x *D. monticola*, and *D. monticola* x *D. uniformis*) in Korea. For one new hybrid, *D. goeringiana* x *D. lacera* is newly given based on their morphology. Their morphology is newly found from Yeongwol, Korea, which is distinguished by several vegetative characters such as shrunken upper parts of lamina with sporangia, widest pinnule bases, and decreased teeth of segment margins. We have extensively analyzed one new hybrids and relative taxa of *Dryopteris* populations from China, Japan, and Korea. Descriptions and illustrations of these hybrids and photographs in the habits are provided. Furthermore, phylogenetic analyses of the hybrids should be clarified to evaluate the relationships of evolution among parental taxa.

P.0602 First record of three fern taxa from Korea: Crepidomanes bipunctatum, Coniogramme affinis, and Asplenium capillipes

Chang Shook Lee[1], Kanghyup Lee[2], Youngsim Hwang[3], Kyong-Sook Chung[4]

1 Department of Science Education, Ewha Womans University, Seoul, Korea. 2 Korea National Arboretum, Pocheon, Korea. 3 Geobook, Seoul, Korea. 4 Department of Medicinal Plant Science, Jungwon University, Goesan, Korea.

For the first time, three fern species were found in Korea. *Crepidomanes bipunctatum* (Hymenophyllaceae), *Coniogramme affinis* (Pteridaceae), and *Asplenium capillipes* (Aspleniaceae) were collected from the forests in Jeju-do island, Taebeck, and Samcheok, Gangwondo. *Crepidomanes bipunctatum* (vernacular name: 'Teol-goe-bul-i-kki') was distinguished from other Korean congeners of the genus by stipes winged almost to the base, short hairs, submarginal false veinlets continuous, ovate to oblong, pinnae with entire or slightly crisped margins and obtuse or acute apexes, narrowly elliptic involucres. *Coniogramme affinis* (vernacular name: 'San-go-bi-go-sa-li') was distinguished by having summer-green, pinnule margin dense, sharp and fine teeth, hydathodes slightly thicker than veins, extending to tips of teeth and fused with teeth pinnae arrangement. The last, *Asplenium capillipes* (vernacular name: 'Gag-si-kko-li-go-sa-li') was similar to *A. tenuicale* Hayata, but it was distinguished from the other taxa of *Asplenium* by smaller sizes, triangular laminae, missing extended gemmiferous rachises, basal acroscopic pinnules largest, cordiform or elliptic, and entire margins. Descriptions and illustrations of the three taxa and their photographs in the habitat are provided along with a key to the species of *Crepidomanes, Coniogramme,* and the similar taxa with *A. capillipes* of *Asplenium* from Korea.

P.0603 First comprehensive floristic survey using a belt transect method on Iriomote Island, Okinawa, southern Japan

Akiyo Naiki[1], Takenori Yamamoto[2], Koji Yonekura[3], Takuto Shitara[4], Hironori Toyama[5], Shuichiro Tagane[2], Atsushi Abe[3], Yui Kajita[1], Naoko Sashimura[1], Masaharu Amano[3], Ryo Furumoto[6]

1 Tropical Biosphere Research Center, University of the Ryukyus, Okinawa, Japan. 2 The Kagoshima University Museum, Kagoshima University, Kagoshima, Japan. 3 Department of Plant Science, Okinawa Churashima Foundation Research Institute, Okinawa, Japan. 4 Tama Forest Science Garden, Forestry and Forest Products Research Institute, Tokyo, Japan. 5 College of Arts and Sciences, J. F. Oberlin University, Tokyo, Japan. 6 Forest Tree Breeding Center, Forestry and Forest Products Research Institute, Ibaraki, Japan.

There has been limited information available about the flora of Iriomote Island (Okinawa, Japan), despite its rich forest ecosystems and designation as one of the World Natural Heritage Sites in 2021. To gain a better understanding of the vascular flora of Iriomote Island, quantitative and comprehensive surveys were conducted using a belt transect method (5m x 100m, 208 sites placed approximately per square kilometer, covering the whole island) and general samplings. A new list of vascular plant species, distribution maps for each species, a species richness map, and a vegetation map were made for the island based on the survey data. 1,375 species of vascular plants (1,109 native and 266 alien species) were identified on the island, including three newly recorded native species to the island and two to Japan. The observed number of vascular plant species per belt transect was 40 to 166. The species richness within a belt transect was higher in the northeastern and south-central higher-elevation parts of the island and lower in the peripheral regions and the downstream areas of large rivers. Through our survey, 183 species of endangered plants listed in the Red List by the Ministry of the Environment, Japan, were confirmed. They occurred mainly in limestone areas on the island's periphery or in valleys, especially on rock walls and earthen cliffs near waterfalls in the inland areas. The number of endangered species per belt transect ranged from 0 to 11, with an occurrence rate of 0 to 7.4%, and 84% (175/208) of the belt-transect surveyed sites showed at least one endangered plant. The species richness was weakly correlated with the number of endangered species. On the island's periphery, some locations in lowland forests possessed several endangered species, while they had a low number of the total species within a belt transect.

P.0604 Floral Composition and Diversity of Ultramafic Forests in Homonhon Island, Eastern Samar, Philippines

Roanne B. Romeroso[1,2], Jorge Anton D. Ordas[3], Danilo N. Tandang[4,5], Ian A. Navarrete[6], Cecilia B. Moran[1, 3]

1 The Graduate School and Research Center for the Natural and Applied Sciences, University of Santo Tomas, Manila, Philippines. 2 Department of Biology, College of Science, University of Eastern Philippines, Northern Samar, Philippines. 3 Department of Biological Sciences, College of Science, University of Santo Tomas, Manila, Philippines. 4 Botany Division, Philippine National Museum of Natural History, Manila, Philippines. 5 Biodiversity Program, Taiwan International Graduate Program, Academia Sinica and National Taiwan Normal University, Taipei, Taiwan. 6 Department of Environmental Science, Southern Leyte State University, Hinunangan Campus, Ambacon, Southern Leyte, Philippines.

The Philippines has suffered tremendous deforestation due to rampant anthropogenic impacts such as mining. In particular, the forests of Homonhon Island are threatened by mining activities. In this study, we assessed its ultramafic vegetation's floristic composition and diversity to initiate its conservation efforts on Homonhon Island. In five sampling areas on the island, we have documented 181 species in 148 genera and 83 families, with 176 native species. Twenty-two species are classified as threatened based on the IUCN. On the other hand, in DENR-DAO 2017-11, 38 are classified as threatened. Homonhon Island exhibits a very high species diversity overall, and the forests in Barangay Bitaugan revealed the highest species diversity among the sampled areas. *Alstonia macrophylla* and *Terminalia surigaensis* chiefly dominates the island's forests. Despite being threatened by mining, Homonhon Island's ultramafic forests exhibit a diverse floristic composition worthy of protection. It serves as a sanctuary for many of the Philippines' highly threatened species. Its local government agencies should implement strict protection and management policies to prevent further disturbance to its flora. We can anticipate this study to be used in the restoration, rehabilitation, and conservation of the remaining forest on the island.

P.0605 Unveiling the enigmatic world of Impatiens of Western Himalayas: exploring diversity, endemism and habitat preferences

Ashutosh Sharma[1], Wojciech Adamowski[2], Noorunissa S. Begum[1], K. Ravikumar[1]

1 FRLH Herbarium, The University of Trans-Disciplinary Health Sciences and Technology, Bengaluru, India. 2 Białowieża Geobotanical Station, University of Warsaw, Białowieża, Poland.

Impatiens Riv. ex L. (Balsaminaceae) commonly known as 'balsams' is among the largest, diverse and complex genera of angiosperms with more than 1000 species, most of which are distributed in Africa, Southeast Asia and India. In India, the genus is represented by about 280 species with the Western Ghats and the Himalayas being hotspots with very high endemism. *Impatiens* in the Western Himalayas comprises 38 species, half of which are endemic and one third of these endemics are only known from century old herbarium records with incomplete descriptions. In fact, a few species are solely known by their types e.g. *Impatiens violoides* Edgew. ex Hook.f., *I. reidii* Hook.f., and *I. vexillaria* Hook.f. Taxonomic study of balsams solely based on herbarium specimens has been greatly hampered as the main distinguishing floral characters like shape of spur, lower sepal and colour of corolla are often untraceable in herbarium specimens which sometimes also leads to errors in delimiting the species. Thus, owing to difficulties in identification of *Impatiens* species it was also referred as '*a terror to botanists*' by Sir J.D. Hooker. Based on our extensive field surveys in the Indian Western Himalayan region from 2018–23 covering different habitats and altitudinal range (700–4,500 m elevation) we present here species diversity of *Impatiens* in Western Himalayas along with species morphology, endemism, habitat preferences and change in composition of the species along altitudinal gradients.

P.0606 Yield performance and regeneration of alfalfa experienced the monsoon season in the Jianghuai region of China

Jiaqing Li [1,2], Zhenwu Wei [1,2], Xueyang Min [1,2], Chuanjie Wang [1,2], Haowen Cheng [1,2]

1 College of Animal Science and Technology, Yangzhou University, Yangzhou, China. 2 Institute of Grassland Science, Yangzhou University, Yangzhou, China.

Cultivated alfalfa, as a legume crop originating from the temperate continental climate region, is often cultivated in China in the northwestern part of the country, where the diurnal range is large. In the southeastern China, where summers are rainy, there is a lack of reports on alfalfa yield and growth before and after the entry of the monsoon season. This study describes research on the growth of cultivated alfalfa in Jianghuai region of China in June-July. The dynamics of grass yield, protein accumulation, and SPAD values were investigated in 4 rainfed farmed alfalfa materials that were experimentally proven to be suitable to the climate of the Jianghuai region, represented by Yangzhou. Additionally, the number of stems per plant, leaf area, and FW/DW ratio before cutting were ascertained, as were variations in plant height over the monsoon season. The results demonstrated significant differences in grass yield of cultivated alfalfa before and after the monsoon season ($p <$ P.01); additionally, it was established through fitting a linear function of plant height that the Huaiyang No. 4 alfalfa, a new cultivar cultivated at the Yangzhou, and BC regenerated more quickly than the other two (*p* < P.5); The protein accumulation results indicated that, with the exception of BC, the materials under test differed in growth changes to varying degrees; there were no statistically significant differences in the FW/DW harvested from the various materials, nor in the 2 results comparing the number of stems per plant during the growth of regenerated plants over the rainy season and between SPAD. The findings demonstrated that grown alfalfa in the Jianghuai region can adapt to its unique growing conditions; yet it may be affected to variable degrees by heavy precipitation during the monsoon season, which could have an impact on output and protein accumulation.

P.0607 Taxonomy of the largest lycophyte genus Selaginella in China

Xianchun Zhang[1]

1 The National Herbarium, Institute of Botany, Chinese Academy of Sciences, Beijing, China.

Selaginella is the sole genus of the lycophyte family Selaginellaceae, with about 800 species all over the world, but mainly centered in tropical humid forests. Molecular phylogenetic studies resolved the monophyly of *Selaginella* and divided it into seven subgenera. Although the infrageneric classification has been settled, the species level taxonomy is very unclear, especially in the species rich subgenus *Stachygynandrium* and some species complexes or groups. Recently we adopted an integrative taxonomy approach and successfully revised the taxonomy of some difficult groups, such as the *Selaginella helvetica* group, *S. labordei* group, *S. delicatula* group, *S. monospora* group, *S. tamariscina* group and *S. sanguinolenta* group. First, we studied herbarium collections, literatures, type specimens, and collected materials from the type locality if possible. Second, we performed morphological observations by microscope and morphometric analysis such as linear discriminant analysis (LDA) and principal component analysis (PCA). Third, chloroplast and nr DNA markers were sequenced using different analysis methods including concatenation and coalescent-based methods, the concatenation phylogenetic trees were constructed using Neighbor-joining (NJ), maximum likelihood (ML) and Bayesian inference (BI) methods, and coalescent-based phylogenetic trees generated by software ASTRAL. Additionally, Flow CytoMetry (FCM) was used to detect genome size variation and polyploidization, MaxEnt model was used to predict the probability distribution of the target species based on existing occurrence records. Combining morphology, molecular, cytological, and ecological evidence, we proposed species delimitations and recognized formal taxa according to nomenclature rules.

S.067. FROM DEVELOPMENTAL SWITCHES TO BROAD EVOLUTIONARY TRAJECTORIES: UNDERSTANDING MECHANISMS OF SEX DETERMINATION

P.0608 Decoding sexual plasticity in dioecious plant-Cannabis sativa as a case study

Adrian S. Monthony[1,2,3,4], Marilou Ledeuil[5], Maxime de Ronne[1,2,3,4], Olivia Carlson[6], Susan Murch[6], Davoud Torkamaneh[1,2,3,4]

1 Département de phytologie, Université Laval, Québec, Canada. 2 Institut de Biologie Intégrative et des Systèmes, Université Laval, Québec, Canada. 3 Centre de recherche et d'innovation sur les végétaux, Université Laval, Québec, Canada. 4 Institut intelligence et données, Université Laval, Québec, Canada. 5 Faculté des Sciences, Université Catholique de Lyon, Lyon, France. 6 Chemistry, University of British Columbia, Kelowna, Canada.

This research explores the phenomenon of sexual plasticity in *Cannabis sativa* L. (cannabis), wherein plants develop sex organs opposite to their sex chromosome karyotype. As a dioecious plant with a XX/XY sex chromosome complement, cannabis typically exhibits sex organ development concordant with its genetic sex. However, sexual plasticity has been observed in response to ethylene, leading us to hypothesize a key role of ethylene-related genes (ERGs) in controlling this plasticity. Despite the apparent critical role of ethylene, the interplay between phenotypic and chromosomal sex, and the ERGs involved in the biosynthesis and perception of ethylene remain largely unexplored. This study delineates the phenotypic effects of ethylene and its inhibition on cannabis, from seedling to flowering, while also detailing *in silico* and transcriptomic approaches that, for the first time, model the ethylene biosynthesis and signaling pathways in cannabis. We present the results of transcriptomic changes during flowering, where transcriptomes from plants treated with ethylene and its signaling inhibitors were analyzed over the course of floral induction. Together with metabolomic data from key ethylene precursors in our plants, we provide a detailed look at the role of ethylene biosynthesis and signaling during sexual development in cannabis. Our model elucidates the mechanisms by which ethylene and ERGs govern sex determination and plasticity in both XX and XY cannabis plants. Our research not only sheds light on the complex sexual development of cannabis but also offers a model for investigating sexual plasticity in other important dioecious plant species.

P.0609 The transition from dioecy to monoicy in liverworts is a case of convergent evolution

Giacomo Potente[1], Yasui Yukiko[2], Rachel N. Walstead[3], Jane Grimwood[3], Jeremy Schmutz[3], Jim Leebens-Mack[4], Eita Shimokawa[2], Tomoha Tanaka[2], Yuka Umeya[2], Shogo Kawamura[2], Katsuyuki T. Yamato[5], Katsushi Yamaguchi[6], Shuji Shigenobu[6], Masaki Shimamura[7], Takayuki Kohchi[2]and Peter Szovenyi[1]

1 Dept. of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland. 2 Kyoto University, Kyoto, Japan. 3 Hudson Alpha Institute for Biotechnology, Huntsville, University of Georgia, Athens, USA. 5 Kindai University, Kinokawa, Japan. 6 Trans-Scale Biology Center, National Institute for Basic Biology, Okazaki, Japan. 7 Hiroshima University, Hiroshima, Japan.

Sex chromosomes have evolved independently in many groups of plants and animals. Genetic sex determination ensures obligate outcrossing that may confer advantages against selfing. In liverworts, sex is expressed in the haploid phase and genetically determined by the presence of a single U (female) or V (male) sex chromosome. The UV sex determination is ancestral in liverworts and represents the oldest sex chromosome system ever described (430 million years old). Although the transition to monoicy occurred repeatedly in liverworts, its genomic basis has been investigated only in one species (*Ricciocarpos natans*). Here we report on the chromosome-scale genome assembly of the monoicous liverwort *Marchantia quadrata*, which diverged from the dioicous *M. polymorpha* 125 million years ago. We show that the *M. quadrata* genome consists of eight large and one (9th) small chromosome (1/10th of the size of the large eight chromosomes). The eight large chromosomes are collinear with the eight autosomes of *M. polymorpha* showing many intra- but few inter-chromosomal rearrangements. By contrast, the small 9th chromosome contains genes homologous to the *M. polymorpha* V chromosome. Many genes homologous to U-chromosome genes of *M. polymorpha* are absent from the *M. quadrata* genome or are relocated to the autosomes, including the major sex determining gene (*Feminizer, BPCU*). These results imply that the transition from dioecy to monoicy was achieved by the translocation of few crucial U-genes to the autosomes and the loss of the U chromosome, while a larger proportion of V-linked genes was retained on a segment of the V chromosome as chromosome 9. Our findings are remarkably similar to the recent observation made on *R. natans*, raising the possibility that genomic changes underlying the transition from dioecy to monoecy in liverworts may be highly predictable.

S.068. FROM MULBERRIES TO FIGS: STUDIES IN THE EVOLUTION OF MORACEAE

P.0610 Vegetative and flower structures: Moraceae inflorescences and its link to plant shape

Thibaud Gaudry[1,2], Yves Caraglio[1], Artémis Anest[1]

1 AMAP, Univ Montpellier, CIRAD, CNRS, INRAE, IRD, Montpellier, France. 2 University of Montpellier, Montpellier, France.

Moraceae is one of the largest and most diversified Angiosperm families. Some genera within the family, such as the genus Morus, are recognised as having a highly conserved inflorescence: the fig. The acquisition of this inflorescence type likely involved radiation within this genus. However, vegetative structural features in the family Moraceae are often disregarded: while the fig is an extremely conserved innovation, the Morus genus has been shown to express a huge variety of architectures, defined by Hallé et al. (1978) as the spatial and temporal arrangement of plant organs across space and through time, which is stable at the species scale. Plant architecture is acknowledged as holding traits resulting from environmental selection and has also been attributed as a factor increasing speciation rates under specific biotic conditions (e.g., herbivory). The vegetative structural diversity of the genus Morus and the entire family Moraceae may thus have played a decisive role in explaining its current species diversity. In this study, we used descriptions of inflorescences in relation to plant structure, along with comparative phylogenetic analyses, to establish the first relations between plant vegetative diversity and inflorescence conservatism in the genus Morus and inflorescence diversity in the whole Moraceae family. Here, we propose that sexual reproduction efficiency might have been supported by an effective space occupation strategy and functional partitioning within the whole plant architecture.

P.0611 Secretion dynamics in the laticifer system of Dorstenia cayapia Vell. (Moraceae)

Felipe P. Ramos[1,2*], Simone P. Teixeira[2]

*1 Faculty of Philosophy, Science and Letters of Ribeirão Preto, University of São Paulo, Ribeirão Preto, Brazil. 2 Faculty of Pharmaceutical Sciences of Ribeirão Preto, University of São Paulo, Ribeirão Preto, Brazil. *felipepramos@usp.br*

Secretory structures produce, storage and/or release specialized metabolites that mediate the interaction between plants and their environment. Studying the detailed cellular events in the secretion process are crucial for a better understanding of their functions. In this study, we aimed to characterize the microscopic diversity of forms involved in laticifer differentiation and latex production in *Dorstenia cayapia* Vell. This monoecious widely distributed herb is relevant due to its pollination by small insects and the presence of white milky latex, a significant characteristic of Moraceae. Developing staminate and pistillate inflorescences were processed for anatomical (light microscopy) and ultrastructural (transmission electron microscopy) analyses. The laticifer is articulated, branched, and occur close to the vascular bundles. The precursor laticifer cells are numerous, with ameboid nuclei, pecto-cellulosic walls and dense cytoplasm that contains dictyosomes, rough endoplasmic reticulum, plastids, amyloplasts and mitochondria. Microtubules are observed rearranging plasma membranes, possibly allowing the branching of the laticifer. Developing laticifer cells show a high number of small vacuoles, which later fuse to form a massive vacuole. The cytoplasm of fully developed laticifers is less dense, maintains the ameboid nuclei, and the latex is found exclusively inside vacuoles. Most organelles persist but are less frequent. As the vacuoles expand and fill with latex, the nuclei and organelles get closer to the cell wall. In the pistillate inflorescences, the latex appears to become denser as the floral organs develop. Laticifer growth and latex production are events that happen simultaneously. The cytoplasm reduction may be associated to a degree of autophagy, commonly described in articulated laticifers. Despite that, the persistence of dictyosomes, endoplasmic reticulum and mitochondria reveals a constant production of latex. Our data show that several metabolites found in the latex of *D. cayapia* are continuously produced, indicating that they are not strictly tied to a specific laticifer developmental stage.

S.069. FUNCTIONAL ASPECTS OF NECTARMEDIATED PLANTPOLLINATOR INTERACTIONS

P.0612 Cross-taxon congruence between plants and bumblebees in mountain grasslands along an elevation gradient

Edoardo Asquini[1,2], Simone Ghassempour[2], Desiderato Annoscia[2], Davide Frizzera[2], Silvia Parenzan[2], Elisa Seffin[2], Tatiana Trifonova[2], Giacomo Trotta[2,3], Marco Vuerich[2,4], Pietro Zandigiacomo[2], Virginia Zanni[2,4], Francesco Nazzi[2,4], Francesco Boscutti[2,4]

1 University of Palermo, Palermo, Italy. 2 University of Udine, Udine, Italy. 3 University of Trieste, Trieste, Italy. 4 National Biodiversity Future Center, Palermo, Italy.

Climate change is one of the main causes of biodiversity loss worldwide. The alteration of plant and animal fitness and their range shift are prominent evidence of climate change ecosystem alterations. Climate-driven impacts on biodiversity are exacerbated by the interplay of climate change and land use and management. This research aims at parsing the congruence between plant and bumblebees' biodiversity in mountains grassland along an elevation gradient, here used as a proxy of the variation induced by climate change. The study was set in the South-Eastern Alps (Italy) where plant and bumblebee communities were sampled in 25 secondary grasslands distributed along an elevation gradient of 1,500 vertical meters (i.e. from 100 m to 1,600 m.a.s.l., 5 elevations x 5 mountain areas). Plant species were recorded in 10 x 10 m plots at the growing peak; bumblebees were sampled in the same areas on flowering plants, along a 100 m transect at four points during the season (May, June-July, August, and October). The preliminary results showed that plant diversity was mainly driven by elevation, evidencing a positive relationship between α and β diversity indices and elevation, while bumblebee diversity showed a weak response to elevation. Cross-taxon analysis suggests that plant and bumblebees diversities are linked together, but the strength of the correlation varies along the elevation. These preliminary results suggest that climate change might exert a direct effect on plant communities, potentially decreasing their diversity at different scales; the aftermaths on bumblebees' communities will thus be both indirect (i.e., mediated by plants) and direct (i.e., mediated by temperature and other environmental variables). This study provides some useful interpretative tools to inform concrete conservation actions in order to maintain the ecosystem's functionality.

P.0613 Composition of the floral nectar in Lithospermeae tribe (Boraginaceae) and their pollinators

Daniele Calabrese[1,2], Massimo Guarnieri[1], Massimo Nepi[1,2]

1 MAEC Lab - Department of Life Science, University of Siena, Siena, Italy. 2 National Biodiversity Future Center, Palermo, Italy

In recent years, a central role was recognized to the study of nectar chemistry in shaping the interactions between plants and pollinators. This work describes the chemical profile of the floral nectar of Mediterranean Lithospermeae used to identify possible associations with pollinators' guild. The pollinators that interact most with the studied Lithospermeae species are long-tongued bees (Apidae and Megachilidae families) but also specialized or non-specialized dipterans and moths and some short-tongued bees. A particular adaptation has been identified in some instances linking plant and pollinators in a very specialist relationship (e.g., *Andrena solenopalpa* and *Lithodora fruticosa*). The hexose-dominant profile of nectar is restricted to *A. purpurocaeruleum,* and it is associated with a purely generalist guild of pollinators. The sucrose-rich profile is typical of *Echium* species, and it is the most interactive, as well as the most widespread. The sucrose-dominant profile, typical of *Onosma* spp. it is the one that is the most dependent on specialist pollinators. The *Onosma* species, with corolla tubes up to 23mm, are visited only by species morphologically suited to reaching nectar, such as *Osmia apicata* (Megachilidae: Osminii). The amino acid profile is more diversified and not very constant among the Lithospermeae species of the collection. Among the most ubiquitous amino acids are histidine, valine and tyrosine. The concentrations also vary greatly, with proline being the most concentrated amino acid. In general, in the Lithospermeae species it seems that the floral morphology rather than the sugar and amino acid profile of floral nectar, describes the pollinator guild, nonetheless species with highly sucrose-dominant profile (>90%, i.e., *Onosma* species) are those most dependent on specific pollinators.

P.0614 Aging nectar candy – 17-year-old viscous nectar discovered on an herbarium sheet at University of Alaska Museum herbarium (ALA)

Stefanie M. Ickert-Bond [1], Massimo Guarnieri [2], Emanuelle Giordano [2], Massimo Nepi [2,3]

1 University of Alaska Museum of the North and Department of Biology and Wildlife, University of Alaska Fairbanks, Fairbanks, USA. 2 Department of Life Sciences, University of Siena, Siena, Italy. 3 NBCF, National Biodiversity Future Center, Palermo, Italy.

Nectar constituents have long been considered as a major factor influencing plant-animal mutualism. For many pollinators nectar represents the main source of carbohydrates, as well as a nutrient source of amino acids. The chemical composition of nectar also makes nectar attractive to nectar-infecting microorganisms and fends of some nectar robbers. Balancing these unique roles is paramount to maintaining the fragile plant-animal mutualism as a fitness benefit. Can these roles be extended to avoid spoilage of nectar in herbarium specimens? The primary goal of this study was to analyze the nectar constituents in 17-year-old viscous nectar candy in an herbarium sheet of *Arctous rubra* (Ericaceae). The chemical profiles of sugars and amino acids in the nectar samples included glucose, sucrose and fructose and a predominance of serine, alanine, proline and tyrosine over the other amino acids. The total concentrations of sugars and amino acids are by one order of magnitude lower as compared to the average content of these substances in floral nectar. The nectar contained extremely high concentrations of secondary metabolites, three orders of magnitude higher than previously reported for any nectar sample. We hypothesize that the extremely high concentrations of biogenic amines and the low concentrations of sugars and amino acids obtained from the 17-year-old nectar samples was accelerated in the 17-year time span since the flowers were collected, possibly by nectar-dwelling microorganisms. Although not often collected for the purpose of preserving nectar in flowers, this study shows another new use of (old) herbarium specimens.

P.0615 Chemical composition of floral nectar in Datura (Solanacea) species.

Evelin Buitrago [1], Vania Jiménez Lobato [1], Juan Núñez-Farfán [2], Violeta Patiño-Conde [3], José J. Virgen-Ortiz [4], Citlali Colín-Chávez [4].

1 Autonomous University of Guerrero-CONAHCYT-LANASE, Guerrero, Mexico. 2 National Autonomous University of Mexico, Mexico City, Mexico. 3 National School of Higher Studies Morelia Unit ENES, Morelia, Mexico. 4 CONAHCYT - Food and Development Research Center, A.C - CIDAM, Morelia, Michoacán, Mexico.

El género *Datura* (Solanaceae) es un grupo de hierbas anuales y arbustos perennes con sistema de apareamiento mixto. Filogenéticamente, se divide en dos grandes clados, que se diferencian en el tamaño de las flores. Las especies *de Datura* producen alcaloides tropano, siendo la escopolamina y la hiosciamina las más abundantes. Los alcaloides se sintetizan en las raíces, se almacenan en vacuolas y luego se trasladan a las hojas y las estructuras reproductivas, incluido el néctar floral. El néctar floral puede influir en interacciones tanto mutualistas como antagónicas. De esta manera, el néctar floral puede atraer a polinizadores especializados, disuadiendo a los herbívoros generalistas y a los ladrones de néctar. Asimismo, las características del néctar floral pueden controlar el crecimiento de microorganismos que modifican la composición química del néctar, afectando potencialmente la atracción y/o comportamiento de los polinizadores y el éxito reproductivo de las plantas. Se estudiaron cuatro especies *de Datura, dos de tamaño de flor grande* (*Datura discolor* y *Datura inoxia*) y dos de tamaño de flor pequeño (*Datura kymatocarpa* y *Datura pruinose*). La composición química del néctar de las flores y del tejido vascular (azúcares, aminoácidos y alcaloides) se determinó mediante HPLC. Los resultados indican una variación en la concentración de alcaloides entre el néctar floral y el floema, durante la ontogenia de las plantas y entre y dentro de las especies según su sistema de polinización. Los resultados también apuntan a algún tipo de regulación de la composición química que controla la diversidad y abundancia de la microbiota asociada. Asimismo, la concentración de azúcares y aminoácidos presentes en el néctar varía en el tiempo entre especies, dependiendo de las preferencias nutricionales del polinizador principal.

P.0616 Pollen micromorphology of Onosma stellulata Waldst. & Kit. (Boraginaceae), an endemic species of the Balkan Peninsula

Marina Mačukanović-Jocić[1], Snežana Jarić[2], Dragana Rančić[1], Maja Terzić[1]

1 University of Belgrade, Faculty of Agriculture, Department of Agrobotany, Belgrade, Serbia. 2 Institute for Biological Research "Siniša Stanković"- National Institute of Republic of Serbia, University of Belgrade, Serbia.

Palynomorphological characteristics of the Balkan endemic plant species, *Onosma stellulata* Waldst. & Kit., was described for the first time in order to contribute the taxonomy of Boraginaceae and melissopalynological investigation. The flowers were collected from plants growing on the cliffs of the Komarnica River Canyon in Montenegro, and pollen was analyzed using both, light microscopy and scanning electron microscopy. Pollen grains were found to be radially symmetrical and heteropolar with the distal and proximal poles being different in shape and aperture presence. They are small in size, with an average polar axis length of17.9±0.8 μm, and an equatorial diameter of 12.8±0.4 μm. The P/E ratio is 1.42, indicating prolate shape with circular to triangular convex outline in polar view. The aperture type is 3-syncolporate, with the colpal apices converging at the wider distal pole, and weakly defined pores positioned closer to it. Colpi range from 13.5 to 16.5 μm in length by 0.3 to 2.2 μm in width. Exine ornamentation was found as generally scabrate, predominantly in the equatorial area, with sparse perforations all over the surface. Sculptural elements, recognized as scabrae, range from 70 to 260 nm in length. Starting from the the narrowest equatorial region, where they are most densely distributed, towards the poles, scabrae appear smaller and rarer, being found sporadically at the proximal pole. Based on SEM micrographs, the average number of scabrae per 1 μm^2 in the central mesocolpial area is 14,4. The exine layer covering the aperture has noticeably distinct ornamentation of the same pattern as on the rest of the grain surface, but with more densely distributed scabrae. Based on LM observation, exine thickness is 1.2±0.3 μm in average.

P.0617 Standardizing the method for the description of microorganisms diversity in Onosma spp. nectar and their pollinators guild

Samuele Pignedoli[1], Daniele Calabrese[1,2], Massimo Nepi[1,2]

1 Department of Life Science, University of Siena, Siena, Italy. 2 National Biodiversity Future Center, Palermo, Italy.

The study of microorganisms inhabiting floral nectar and their influence on floral visitors has been extensively developed in the last decade. Nectar microorganisms modify nectar chemistry consuming sugars and amino acids, shaping a new nectar composition. Nectar acts as a selective filter against microorganisms due to its high sugar concentration and the presence of proteins and secondary compounds (NSC's), the latter not only act as antimicrobials but may also have a controlling function on visitors behavior. Studying the potential correlation between the diversity of microorganisms in nectar, on floral surfaces, and on visiting insects could provide valuable insights into the mutualistic relationship between visitors, nectar, and microorganisms. Standardizing a method for collecting and describing microorganisms from nectar, floral surfaces and visiting insects is thus necessary. The objective of this study is to outline effective sampling and sample manipulation methods that can simplify subsequent research. Plants of the genus *Onosma spp.* (Boraginaceae: Lithospermeae) can be particularly suited for this study, as they produce a significant amount of nectar and are pollinated by highly specific visitors. This feature offers an advantage by reducing random variables such as visits from generalist pollinators and the potential for significant errors caused by small nectar quantities.

P.0618 Deceptive vs. rewarding Orchids: a comparative analysis of reproductive strategies

Elvira Sahuquillo Balbuena[1], Eva Pardo[1,2], Manuel Pimentel Pereira[1]

1 Evolutionary Biology Research Group, University of A Coruña, A Coruña, Spain. 2 Evolutionary Biology Research Group, Interdisciplinary Centre of Chemistry and Biology, University of A Coruña, A Coruña, Spain.

Orchids represent one of the most diverse and widely distributed plant families, and they show remarkably different reproductive strategies and pollination mechanisms. Some orchids deceive their pollinators (sexual deception or mimicry), whereas others are nectariferous and offer rewards. This study explores the impact of plant and inflorescence architecture in the reproductive success of four food rewarding and deceptive orchids. We conducted a multivariate statistical analysis considering different morphological variables, such as plant size, inflorescence length and number of flowers, and using the number of ripe fruits as an indicator of reproductive success. We focused on four populations of two food-rewarding (*Coeloglossum viride* and *Gymnadenia conopsea*) and two deceptive (*Dactylorhiza cantabrica* and *Orchis mascula*) species from Serra do Courel (Lugo, NW Spain). Our results show significant differences in inflorescence length and number of flowers among the four species and between the two pollination strategies, as well as variations across populations. Deceptive species present larger inflorescence sizes, but fewer and larger flowers. This might suggest that pollinators are attracted through more prominent visual signals than in food-rewarding species. Conversely, taxa that offer floral rewards display shorter inflorescence lengths but a higher number of small flowers, a strategy possibly linked to increased reproductive success through the visitation of multiple flowers. In conclusion, this study shows the relevance of the analysed variables in the reproductive success of orchids, revealing specific adaptations to different pollination strategies depending on the species and the environment.

P.0619 A comparative reproductive study of sympatric Mussaenda taihokuensis and M. parviflora var. formosana (Rubiaceae)

David W. Taylor[1], Chia Hsin Tsai, Gregory J. Anderson[2], Jer-Ming Hu[3].

1 Department of Biology, University of Portland, Portland, USA. 2 Department of Ecology and Evolutionary Biology, University of Connecticut, USA. 3 Institute of Ecology and Evolutionary Biology, National Taiwan University, Taipei, Taiwan.

The approximately 200 species of *Mussaenda* (trees, shrubs, or lianas distributed in parts of Old World subtropics and tropics) are characterized in part by having some or all flowers of an inflorescence with one or more enlarged, white to colored, petaloid calycophyll(s), and there is evidence that these calycophylls are important in floral visitor recruitment in at least some *Mussaenda* species. However, *Mussaenda taihokuensis* Masamune, a Taiwan endemic, lacks these calycophyll(s), and we here compare aspects of its reproductive biology, including floral visitor recruitment, to that of the calycophyll-bearing and partially sympatric *M. parviflora* var. *formosana* Matsumura. Through crossing and selfing experiments, pollen viability studies, and SEM examination of stigmatic structures, both of these taxa were confirmed to be functionally dioecious, despite having morphologically hermaphroditic flowers. The size, coloration, UV reflectance, and other morphological features of flowers and inflorescences of functionally female and male individuals of both taxa were compared. Observations on floral phenology and measurements of nectar volume and sucrose concentration over the lifetime of flowers indicate that both of these taxa are adapted to diurnal pollination, which is supported by our multiple 24-hour floral visitor studies. Over 200 hours of floral visitor observation in three field seasons demonstrated that *M. parviflora* var. *formosana* is visited by both bees and butterflies whereas *M. taihokuensis* is almost exclusively visited by bees. No particular butterfly species was found to be a consistent visitor to *M. parviflora* var. *formosana*. A single species of carpenter bee was found to be the most consistent visitor to flowers of both taxa. The flowering season of *M. taihokuensis* was found to start earlier and to be shorter than that of *M. parviflora* var. *formosana*, including where these taxa grow sympatrically. Hybridization experiments between these taxa yielded fruit and seeds with embryos normal in appearance.

S.070. GENOMIC APPROACHES TO UNDERSTANDING THE ECOLOGY AND EVOLUTION OF SYMBIOTIC AND NONSYMBIOTIC MICROALGAE

P.0620 New species of symbiotic Symbiochloris (Chlorophyta) associated with four genera of lichens in the Iberian Peninsula

María Honrubia-Martínez[1], Patricia Moya[2], Sergio Pérez-Ortega[3], Francisco Gasulla[4], Eva Barreno[2], Isaac Garrido-Benavent[1]

1 Departamento de Botánica y Geología, Universitat de València, Burjassot, Spain. Contact: mahonmar@alumni.uv.es 2 Instituto Cavanilles de Biodiversidad y Biología Evolutiva (ICBiBE) – Departamento de Botánica y Geología, Universitat de València, Burjassot, Spain. 3 Departamento de Micología, Real Jardín Botánico (CSIC), Madrid, Spain. 4 Departamento de Ciencias de la Vida, Universidad de Alcalá, Alcalá de Henares, Spain.

The chlorophyte genus *Symbiochloris* was formally erected in the last decade to encompass a clade of free-living and/or lichenized coccoid green microalgae characterized by their lobed chloroplasts and particular reproduction type. The genus currently includes 10 species, of which some are involved in symbioses with a wide range of lichenized fungi, especially those forming relatively large foliose thalli in the genera *Crocodia*, *Lobaria*, *Lobariella*, *Dendriscosticta* and *Sticta*. A few *Symbiochloris* species have also been found in crustose and granular-verrucose lichens. Here, we performed phylogenetic and transmission electronic microscopy analyses to investigate the taxonomic identity of the phycobionts associated to four lichens occurring in Mediterranean forest ecosystems of the Iberian Peninsula: *Waynea stoechadiana* (Abbassi Maaf & Cl. Roux) Cl. Roux & P. Clerc, which forms minute, squamulose thalli, which are epiphytic on the bark crevices of oaks, olive and carob trees; *Phlyctis argena* (Ach.) Flot., which often occurs on oak bark and forms whitish, smooth and sorediate thalli; *Lecania naegelii* (Hepp) Diederich & van den Boom that forms epiphytic crustose and apotheciate thalli on the bark of several trees and shrubs; and *Leprocaulon quisquiliare* (Leers) M. Choisy, whose thalli are dimorphic, with the primary thallus forming soft, leprose-granular crusts on acidic to neutral soils. Despite these four lichens being unrelated phylogenetically and showing substantial differences in their morphology and reproduction mode, we found that they associated with at least three new, undescribed *Symbiochloris* species. These new species have been isolated into pure cultures that are kept at the Symbiotic Algae Collection of the University of Valencia (ASUV). Our findings serve as a precedent for the importance of the study of rare, minute lichens for unravelling the diversity of lichenized microalgae of the Mediterranean.

P.0621 Fungal, algal and bryophyte transport via bird vectors revealed using environmental DNA metabarcoding and microscopy

Niko R. Johansson[1,2], Ulla Kaasalainen[1], Jouko Rikkinen[1,2]

1 Finnish Museum of Natural History, Helsinki, Finland. 2 University of Helsinki, Helsinki, Finland.

Birds appear as intuitive dispersal vectors for various plants, fungi, algae and other organisms, but concrete evidence of bird-mediated transfer of biological material is scarce for most taxa. This is especially true for biota producing microscopic propagules, such as fungi, lichens, bryophytes and terrestrial algae. To produce concrete evidence on what taxa can be associated with bird vectors, we used a dual approach of light microscopy and environmental DNA metabarcoding to identify biological material present in bird feathers and feet. Firstly, fresh preserved bird specimens from the Finnish Museum of Natural History were screened with light microscopy. Secondly, swabs of live birds sampled during bird ringing were analyzed using environmental DNA metabarcoding targeting fungal taxa. Based on both surveys, a diverse set of transported organisms were identified. Using microscopy, most common recovered propagules were fungal spores, bryophyte fragments and lichen symbiotic dispersal units. eDNA survey identified diverse taxa with multiple ecologies and lifestyles, including wood-decaying fungi, saprotrophic and mycorrhizal fungi, plant and animal pathogenic fungi and lichenized fungi. Numerous terrestrial green algal species, symbiotic and non-symbiotic, were also discovered. Our results identify a large and diverse pool of species for which birds may function as a dispersal vector. For many taxa, this is the first evidence of their potential interaction with birds. Birds could be especially important in the dispersal of specialist taxa, providing directed transport to suitable microsites for establishment, or as strong fliers contribute to long-distance dispersal events.

P.0622 Relative abundance and the partner quality variation of Lotus japonicus-associated rhizobia in soil

Chiharu Ota[1], Masaru Bamba[2], Shusei Sato[2], Takashi Tsuchimatsu[1]

1 Department of Biological Sciences, Graduate School of Science, The University of Tokyo, Tokyo, Japan. 2 Graduate School of Life Sciences, Tohoku University, Sendai, Japan.

Interactions between legumes and rhizobia are the remarkable example of mutualism, in which rhizobia fix nitrogen in legume root nodules and legume plants allow them to grow in the nodules. The legume-rhizobia mutualism has often reported to be highly specific, such that a rhizobial species interacts with specific groups of legumes. It has also been suggested that there is extensive rhizobial variation in partner quality in terms of returning benefits to a partner. Since rhizobia in nodules are released back into soil, such host specificities and partner quality variation may influence the composition of microbiota in soil through the feedback of legume-rhizobia interactions. In this study, we used *Lotus japonicus* of natural habitats in Japan to quantify the relative abundance of its symbiotic rhizobia in soil and the differences in their performance on host growth. 16S rRNA amplicon sequencing analysis revealed that the abundance of *Mesorhizobium* bacteria, symbionts of *L. japonicus*, greatly varied among samples collected from the nearby local habitats. Inoculation experiments of the soil-extracted microbiome showed that the relative abundance of *Mesorhizobium* bacteria in microbiomes and the presence of *L. japonicus* in local habitats had significant positive effects on plant growth, supporting the influence of plant-soil feedback on the relative abundance and partner quality of rhizobia.

S.072. GENOMICS OF LOCAL ADAPTATION.

P.0623 Migration and interbreeding shaped the phylogeography and niche adaptation of the ancestral grass Brachypodium stacei

Campos Cáceres[1,2], Ernesto Pérez-Collazos[1,2], Antonio Díaz-Pérez[1,3,4], Diana López-Alvarez[1,5], Ali Oumouloud[6], Luis Mur[7], John Vogel*[8], Pilar Catalán[1,2]

1 Departamento de Ciencias Agrarias y del Medio Natural. Escuela Politécnica Superior de Huesca. Universidad de Zaragoza, Huesca. Spain. 2 Grupo de Bioquímica, Biofísica y Biología Computacional (BIFI-UNIZAR y EEAD-CSIC). 3 GESPLAN S.A., Las Palmas de Gran Canaria, Spain. 4 Universidad Central de Venezuela, Instituto de Genética, Facultad de Agronomía, Maracay, Venezuela. 5 Universidad Nacional de Colombia, Facultad de Ciencias Agropecuarias, Departamento de Ciencias Biológicas, Palmira, Colombia. 6 Institute Agronomique et Vétérinaire Hassan II, Agadir, Morocco. 7 Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Edward Llwyd Building, Aberystwyth, UK. 8 DOE Joint Genome Institute, Berkeley, USA.

The annual diploid species *Brachypodium stacei* is the most ancestral lineage of the *Brachypodium* grass model genus but also the less investigated taxon of the *B. distachyon* complex. *B. stacei* shows a wide circum-Mediterranean distribution, ranging from Macaronesia to Israel. Our study aimed to uncover the phylogeographic history of 17 *B. stacei* populations (46 individuals) using a genome-wide SNP data set and full plastome sequences. Phylogenetic and genetic structure analysis of nuclear SNP data revealed the existence of six main genetic groups, indicating a successive diverging pattern of *B. stacei* lineages from Sicily and Balearic Islands to Greece, Canary Islands, Israel, and the western Mediterranean. Coalescence-based dating analysis revealed a very recent split of *B. stacei* lineages from the crown ancestor in the Late Quaternary (0.27 Ma), suggesting the occurrence of repeated extinctions followed by radiation of young populations. Genetic diversity estimators indicated low levels of population genetic diversity and high selfing rates for this strongly inbred species. However, phylogenomic analysis using whole plastome sequence data showed incongruent evolutionary relationships of population samples with those retrieved by the nuclear data, pointing to the plausible existence of interbreeding and chloroplast capture events between populations. Dispersal and demographic models of *B. stacei* populations selected the best scenario for an early split of sister lineages in the western Mediterranean continental islands and the Canary Islands, followed by two independent colonization events to the eastern Mediterranean region by LDD, and bottlenecking events. Climatic data suggest that *B. stacei* is adapted to warm climatic conditions in the southern Mediterranean region although ecological niche models differentiated between an aridic Eastern niche, a less aridic Western niche, and a Macaronesian-type niche. Our findings indicate that the phylogeography of *B. stacei* populations was shaped by recent radiations, extinctions, long-distance dispersal events, occasional interbreeding, and adaptation to local climates.

P.0624 Chromosome level genome assembly of Megacodon stylophorus identified two rounds of whole genome duplications in tribe Gentianeae.

Chunlin Chen[1,2], Minghui Kang[2], Pengchuan Sun[2], Landi Feng[2], Jianquan Liu[2]

1 Escuela Politecnica Superior de Huesca, Universidad de Zaragoza, Huesca, Spain. 2 Key Laboratory for Bio-Resources and Eco-Environment, College of Life Science, Sichuan University, Chengdu, China.

Whole genome duplications are increasingly being unraveled in the diversification of many plant clades and were associated with plants adapting to extreme environments. However, the extent to which whole genome duplications influenced the species radiation of plants in the harsh Qinghai-Tibet Plateau is largely unknown. Here, we generated a chromosome-level genome assembly of *Megacodon stylophorus* from tribe Gentianeae, an iconic plant lineage that is widespread among the Qinghai-Tibet Plateau. The assembled genome size of *Megaco-*

don sylophorus is 2,240.42 Mb, with a scaffold N50 length of 164.5Mb. We revealed two rounds of whole genome duplications specific to tribe Gentianeae based on synteny analysis and *Ks* analysis. In addition, we further identified eight aspects of high-altitude adaptation based on gene family expansion analysis and positive selection analysis. Specifically, seven out of the eight aspects were contributed from gene family expansion, which is likely resulted from the two rounds of whole genome duplication events. Our results highlight the role of whole genome duplication in the radiation of plant lineages occurring in the Qinghai-Tibet Plateau.

P.0625 Thermal effects on the origin and establishment of Arabidopsis arenosa

Yu Cheng[1], Filip Kolář[1,2], Roswitha Schmickl[1,2]

1 Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic. 2 Institute of Botany, Czech Academy of Sciences, Průhonice, Czech Republic.

The effect of temperature on the establishment of polyploidy has been a long-term mystery, and it has been hypothesized that polyploids are better adapted to temperature extremes than their diploid progenitors. Given the increasing challenges that plants and animals face due to global warming, this study explores polyploids' molecular basis of their adaptation to thermal fluctuations, using *Arabidopsis arenosa* from the family Brassicaceae as the model system. This species crosses multiple temperature zones along its distribution, and its various intraspecific lineages adapted to diverse environmental conditions, including northern latitudes. In this study, I utilized genotype-environment association analysis and 222 genome-sequenced diploid and 410 tetraploid populations (total 632 individuals) to investigate the impact of harsh environments on the adaptation of *A. arenosa*, namely selected genes. Based on the initial findings from this analysis, significant differences in single nucleotide polymorphisms strongly associated with the coldest temperature in the coldest month were observed between diploids and tetraploids. Our preliminary findings indicate that genes strongly associated with cold temperatures in tetraploid *A. arenosa* encompass both stress response and DNA regulation. This dual focus may explain why tetraploids exhibit a robust adaptation to cold environments, yet not significantly stronger compared to their diploid relatives.

P.0626 Effect of glacier melting on the genetic structure and differentiation of Macrocystis pyrifera in the Patagonian Andes, Chile

Diana Coral-Santacruz[1,2], Máximo Gonzales[3], Nicolas Segovia[1,4], Pilar A. Haye[1,4], Andrés Mansilla[5,6]

1 Laboratorio de Diversidad Marina, Departamento de Biología Marina, Facultad de Ciencias del Mar, Universidad Católica del Norte, Coquimbo, Chile. 2 Doctorado en Biología y Ecología Aplicada, Universidad Católica del Norte, Coquimbo, Chile. 3 Centro de Estudios de Zonas Áridas, La Serena, Chile. 4 Instituto Milenio en Socio-Ecología Costera, Coquimbo, Chile. 5 Laboratorio de Ecosistemas Marinos Antárticos y Subantárticos, Departamento de Ciencias y Recursos Naturales, Universidad de Magallanes, Punta Arenas, Chile. 6 Cape Horn International Center, Universidad de Magallanes, Punta Arenas, Chile.

During the Last Glacial Maximum (21,000 years ago), the **Patagonian Andes** (between 46° and 55°S) were covered in ice. Currently, this area presents heterogeneity of marine ecosystems with different habitats distributed among fjords, channels, and archipelagos, as a result of the advance and retreat of ice masses since the Quaternary. Chilean Patagonia represents 88% of the total glaciated area and harbors a great diversity of fauna and flora, including important endemisms, being declared a Biosphere Reserve for being a hotspot of cryptogam species. However, anthropogenic climate change has accelerated global warming, causing a significant increase in **glacier melting** (GM) since 1961, which has intensified in the last decade. In this study, the effect of GM on the genetic-environmental response in *Macrocystis pyrifera*, a brown macroalga that forms abundant biomass underwater forests, inhabiting protected and exposed zones of the subtidal rocky area, considered a key species and susceptible to environmental changes, was evaluated. Tissue samples were collected from the fronds of young individuals of *M. pyrifera* from six populations, three located in the Mountains Fjord (MF) (51°10′53″S, 73°17′08″W) and three in the Beagle Channel (BC)

(54º52’32”S, 68º08’11”W). Through massive sequencing using GBS, 2,444 SNPs dispersed throughout the genome of *M. pyrifera* were obtained and used for marine landscape genomics analysis. Adaptive divergence was detected among populations of M. pyrifera that are exposed to GM versus those populations not exposed to these conditions. At the genetic-population level, differences attributed to geographic distance (between MF and BC) and variations in salinity and turbidity, mainly in populations influenced by GM, were detected. These results suggest that *M. pyrifera* exhibits putative signals of local adaptation that have allowed it to persist in this changing environment.

P.0627 Impact of mining activities on the genomic diversity of black spruce (Picea mariana) in Arctic and Sub-Arctic ecosystems

Mingming Cui[1], Juan Carlos Villarreal Aguilar[2], Ilga Mercedes Porth[1], Damase P. Khasa[1]

1 Département des sciences du bois et de la forêt, Lavel University, Quebec, Canada. 2 Département de Biologie, Lavel University, Quebec, Canada.

The Ecogenomics of Mining Areas for Sustainable Canadian North (GENOSCAN) project aims to explore the ecological consequences of mining activities, compounded by climate change, on the soil-plant microbiomes within Arctic and sub-Arctic ecosystems. This study focuses on the genomic analyses of black spruce (Picea mariana) populations in Northern Quebec, employing advanced omics tools to assess genetic variation under environmental stress. Utilizing a double-digested genotyping-by-sequencing (GBS) approach on the NovaSeq 6000 platform, we analyzed 268 samples from two distinct populations, Schefferville and Fermont, each under natural and mine-impacted conditions. With approximately 15 individuals from 10 sites per population, including both natural and mine-impacted sites, this comprehensive dataset provides a unique insight into the effects of mining on plant genetic diversity in northern ecosystems. The goal of this investigation is to elucidate the genomic alterations in black spruce as a response to mining activities, thus contributing to the understanding of environmental resilience and adaptation strategies in these vital but vulnerable ecosystems. Preliminary results are pending, promising to offer significant contributions to the field of conservation genomics and sustainable management practices.

P.0628 Genetic and morphological investigation of seed shattering in common buckwheat (Fagopyrum esculentum).

Gunko Elizaveta M.[1], Logacheva Maria D.[1,2], Fesenko Alexey N.[3], Fesenko Ivan N.[3]

1 Skolkovo Institute of Science and Technology, Moscow, Russia. 2 IITP RAS, Moscow, Russia. 3 All-Russian Research Institute of Leguminous and Cereal Crops, Orel, Russia.

Seed shattering is an important mechanism serving to disperse seeds far from the mother plant. In domesticated cultivars however this trait is unfavorable because it leads to the loss of yield. As well as many other agriculturally important traits, it underwent selection independently in different species, being the part of the domestication syndrome. The subject of our study is common buckwheat (*Fagopyrum esculentum*), an orphan crop from the family *Polygonaceae*. While nearly all cultivated varieties of buckwheat are non-shattering, shattering habit is retained in wild ancestor, *F. esculentum* ssp. ancestrale. Despite being an important trait for breeding, seed shattering in buckwheat is poorly studied. We studied the processes which happen in the pedicels during abscission from anatomical and genetic point of view. Using histological sectioning of pedicels we characterized abscission zone (AZ) in *F. esculentum* ssp. ancestrale. Comparative transcriptome analysis of shattering and non-shattering buckwheat samples using RNA-seq allowed us to describe the dynamics of AZ development. We found that abscissic acid (ABA) response genes are important contributors to this process at early steps; later steps are characterized by the involvement of cell wall modifying enzymes. Also we have performed bulk segregate analysis to locate the genomic region which contains the gene responsible for seed shattering. The most plausible candidate to be a regulator of fruit abscission in buckwheat is JOINTLESS, which was previously described in tomato. Its ortholog in buckwheat is located in the associated region.

P.0629 Genetic architecture of ecological divergence between Oryza rufipogon and O. nivara

Qing-Lin Meng[1,2], Cheng-Gen Qiang[1,2], Ji-Long Li[1,2], Song Ge[1,2]

1 Institute of Botany, Chinese Academy of Sciences, Beijing, China. 2 University of Chinese Academy of Sciences, Beijing, China.

Ecological divergence due to habitat difference plays a prominent role in the formation of new species but the genetic architecture during ecological speciation and the mechanism underlying phenotypic divergence remain less understood. Two wild ancestors of rice (*O. rufipogon* and *O. nivara*) are a progenitor-derivative species pair with ecological divergence and provide a unique system for studying ecological adaptation/speciation. Here, we constructed a high-resolution linkage map and conducted a quantitative trait locus (QTL) analysis of 19 phenotypic traits using an F_2 population generated from a cross between the two *Oryza* species. We identified 113 QTLs associated with interspecific divergence of 16 quantitative traits, with effect sizes ranging from 1.61% to 34.1% in terms of the percentage of variation explained (PVE). The distribution of effect sizes of QTLs followed a negative exponential, suggesting that a few genes of large effect and many genes of small effect were responsible for the phenotypic divergence. We observed 18 clusters of QTLs (QTL hotspots) on 11 chromosomes, significantly more than that expected by chance, demonstrating the importance of coinheritance of loci/genes in ecological adaptation/speciation. Analysis of effect direction and *v*-test statistics revealed that interspecific differentiation of most traits was driven by divergent natural selection, supporting the argument that ecological adaptation/speciation would proceed rapidly under coordinated selection on multiple traits. Our findings provide new insights into the understanding of genetic architecture of ecological adaptation and speciation in plants and helps effective manipulation of specific genes or gene cluster in rice breeding.

P.0630 Population genomics of a cosmopolitan weed

Lucas M. S.[1,2], Hensen I. [1,2], Barratt C. D. [1], Durka W.[1,3], Nagy D. U.[2], Onstein R. E. [1,4], Rosche C. B. [1,2]Lucas M. S.[1,2], Hensen I. [1,2], Barratt C. D.[1], Durka W.[1,3], Nagy D. U.[2], Onstein R. E.[1,4], Rosche C. B. [1,2]

1 German Centre for Integrative Biodiversity Research, Germany. 2 Martin Luther University Halle-Wittenberg, Germany. 3 Helmholtz Center for Environmental Research, Germany. 4 Naturalis Biodiversity Center, Netherlands.

Understanding genetic mechanisms of high throughput data facilitates landscape genomic approaches to infer how dispersal is controlled by adaptive vs. non-adaptive drivers of gene flow. Invasive plant species are suitable study models because non-native populations are often prone to rapid genomic changes as a result of colonizing a novel range. However, many studies on invasive plants compared only a few populations in large distributions, underestimating variation within each range, and restricting their ability to predict the native source region and the identification of drivers of gene flow. We explore the genomic structure of 109 native and 183 non-native populations of *Conyza canadensis* across the Northern Hemisphere using ddRADseq. *Conyza canadensis* is an interesting model to investigate global gene dispersal because it is a successful invader with a cosmopolitan distribution and an economically significant agricultural weed. We test the hypothesis that an interplay between environmental gradients and non-adaptive, demographic processes dictates its global genomic structure. Results suggest strong differentiation among populations and low variation within populations. We also found pronounced differentiation between the genomic structures of native vs. non-native populations. Partial Mantel tests showed a significant correlation between genetic distances and both spatial and climatic distances of the populations. However, isolation by environment was more pronounced in the native ranges whereas isolation by distance was predominant in the non-native ranges. Furthermore, clustering analysis using admixture coefficients shed light on how population history dictates biotic interactions across large spatio-environmental scales. Our results suggest that high selfing rates determine the global genomic structure. Gene flow among native populations is controlled by functional connectivity whereas non-deterministic dispersal probabilities drive genetic differentiation in the non-native ranges. Upcoming analyses will be presented at IBC 2024 including gene flow to illustrate the magnitude of relative migration rates and the clustering of similar sampled areas.

P.0631 Genomic signatures of adaptation in English yew (Taxus baccata L.) at different spatial scales

Thomas Francisco[1], Santiago C. González-Martínez[1], Miquel Riba[2,8], Katharina B. Budde[3], Marco Heurich[4], Sara Pinosio[5], Giovanni G. Vendramin[5], Marjana Westergren[6], Stephen Cavers[7], Maria Mayol[2,8]

1 INRAE, Univ. Bordeaux, BIOGECO, Cestas, France. 2 Univ. Autònoma Barcelona, Cerdanyola del Vallès, Spain. 3 Northwest German Forest Research Institute, Münden, Wildlife Ecology and Conservation Biology, Faculty of Environment and Natural Resources, University of Freiburg, Freiburg, Germany. 5 Institute of Biosciences and Bioresources IBBR-CNR, Sesto Fiorentino, Italy. 6 Slovenian Forestry Institute, Ljubljana, Slovenia. 7 UK Centre for Ecology & Hydrology, Penicuik, Midlothian, UK. 8 CREAF, Cerdanyola del Vallès, Spain.

Studies on how tree species adapt to major environmental drivers have acquired great relevance in the last years. This has been fostered by increasing societal demands to produce sound forest management and conservation plans in the context of climate change. However, most of the studies involve widespread species of economic value, which have substantial gene flow among populations and therefore large effective population sizes. The importance and scale of local adaptation in non-model tree species with distinctive life-history traits and usually occurring as small and isolated populations, has received comparatively less attention, despite its relevance for conservation. English yew (*Taxus baccata* L.) is a long-lived tree native to Eurasian temperate and Mediterranean forests from North Africa to Scandinavia, and from the Iberian Peninsula to the Caspian Sea. Despite its wide range, the species is typically distributed in small stands and/or isolated populations. As a result, genetic diversity in English yew is highly structured, both at the local and the species-wide scales. A high degree of environmental heterogeneity within the species' range, together with reduced gene flow among populations, seems to have promoted adaptation to local environments. This is evident in phenotypic variability in a common garden and climate-associated SNPs from several candidate genes. Here, we combine genomic and phenotypic data to provide novel evidence regarding adaptation in this iconic tree. We characterized variation at 1,077 candidate genes (~12,000 SNPs) in 40 populations (~600 trees) covering an extensive environmental gradient in Europe. We used this data to test how admixture between previously identified divergent lineages affects the adaptive potential of populations. Finally, at the Iberian Peninsula scale, based on a sampling of 33 populations (341 trees) and ~8,000 SNPs, we searched for associations between genetic polymorphisms and phenotypic variation found in key leaf functional traits.

S.073. GEOPHYTIC MONOCOTS: TAXONOMY AND THE EVOLUTION OF SUCCULENCE

P.0632 Overexpression of ABA receptor PYL1_5m enhances drought tolerance in Nicotiana benthamiana through agonist combinations

Reyes Mora[1], Constanza Martin-Vasquez[1], Jordi Sevilla[2], Pedro L. Rodríguez[1].

1 Instituto de Biología Molecular y Celular de Plantas (CSIC/UPV), Valencia, Spain. 2 Unidad Mixta "Infección y Salud Pública" FISABIO-Universitat de València (I2SysBio), Valencia, Spain.

Climate change and global warming are imposing severe challenges on agricultural productivity. Escalating temperatures and increased drought incidence are major constraints on crop yields. Plants respond to abiotic stress, particularly drought, by orchestrating adaptive mechanisms through the abscisic acid (ABA) hormone, enhancing survival and productivity in water-stressed environments.

The PYR/PYL/RCAR receptor family and the type 2C phosphatase (PP2C) subfamily mediate the ABA response. Targeting ABA signaling presents a promising avenue in plant biotechnology to alleviate the adverse effects of drought on crops. This includes the development of chemical compounds mimicking ABA action and genetic strategies, such as the constitutive activation of ABA-mediated plant responses via ABA receptor overexpression. This study focuses on the overexpression of the ABA receptor PYL1^{5m} in *Nicotiana benthamiana*, assessing drought response using innovative agonist molecules, iSB09 and X1. The synergistic combination of these agonists significantly enhances water use efficiency in agriculture. Physiological, photosynthetic, and gene expression parameters were meticulously measured to unravel the intricate mechanisms underlying these interventions. Our findings contribute to advancing the fundamental understanding of plant responses to water stress and hold practical implications for the development of more resilient and resistant crops. This innovative perspective contributes to the ongoing efforts to create crops capable of withstanding the challenges posed by global climate change and ensuring global food security.

P.0633 Artificial Intelligence in plant genomics: assessing mutational effects beyond model organisms

Eva Pardo Otero[1], Verónica Bolón Canedo[2], Rosalía Piñeiro Portela[3]

1 Evolutionary Biology Research Group, Center of Information and Communication Technologies, University of A Coruña, A Coruña, Spain. 2 Laboratory for Research and Development in Artificial Intelligence, Center of Information and Communication Technologies, University of A Coruña, A Coruña, Spain. 3 Evolutionary Biology Research Group, Interdisciplinary Centre of Chemistry and Biology, University of A Coruña, A Coruña, Spain.

In plants, the study of the genomic basis of adaptation has mostly focused on the identification of favourable genetic variants. However, the role played by deleterious mutations is less explored. The accumulation of unfavourable mutations leads to a genetic load that can reduce fitness. In this context, predicting the mutational effect is a significant step and, given the increasing availability of plant genomic data, the application of computational methods becomes crucial. In recent years, several tools have been developed with a clear inclination towards the integration of artificial intelligence techniques, focusing on human variants or model organisms without a standardized methodology. To test their performance in plants and compare the effectiveness of different methods, we applied the most promising tools in a curated diverse dataset of plant variants, annotated with their effect based on experimental evidence. This will provide insight into the extent to which artificial intelligence designed for human variants or model species can be extrapolated to the genomic context of plants, enabling an assessment of whether its adoption should be further explored in the plant community.

P.0634 The genetic architecture of some phenological and reproduction-related morphological traits in Chouardia litardierei (Hyacinthaceae) as revelaed by GWAS

Sara Laura Šarančić [1], Nikolina Pleić [2,3], Krešimir Križanović [4], Ivan Radosavljević [1]

1 Department of Biology, Faculty of Science, University of Zagreb, Zagreb, Croatia. 2 Department of Medical Biology, School of Medicine, University of Split, Split, Croatia. 3 University of Applied Sciences ASPIRA, Split, Croatia. 4 Department of Electronic Systems and Information Processing, Faculty of Electrical Engineering and Computing, University of Zagreb, Zagreb, Croatia.

Chouardia litardierei (Hyacinthaceae) is a bulbous, perennial species of the western parts of the Balkan Peninsula. It is characterized by a pronounced ecological plasticity since its populations are distributed across contrasting habitat types: karst poljes, wet meadows near the seashore, and dry mountain slopes. Thus, *C. litardierei* presents a valuable model for addressing one of the central questions of evolutionary biology: what genomic mechanisms underlie local adaptation and ecological divergence? Here we present the results of a genome-wide association study (GWAS) that aimed at elucidating the genetic architecture of some complex traits in studied species. For this purpose, we set the common garden experiment with 214 individuals from nine selected populations, three representing each assumed ecotype. We performed comprehensive morphometric and phenological analyses and genotyped all individuals using a genotyping-by-sequencing approach. Finally, we combined all the obtained results in a comprehensive study to characterize the genotype-phenotype relations of selected traits. For the analysis, we used 24,660 SNPs, five reproduction-related morphological, and five phenological traits. All traits were considered polygenic, and GWAS analyses were performed assuming an additive genetic model. For each association analysis, we considered two different statistical approaches: the frequentist single-locus models and Bayesian multi-locus models. Within the single-locus models, for each trait, we fitted a standard linear mixed model (LMM) in GEMMA, as well as a Poisson linear mixed model in GMMAT for traits that represented count data, to correctly model the trait's distribution. Within the multi-locus models, we fitted a Bayesian sparse linear mixed model (BSLMM) and a latent Dirichlet Process Regression (DPR) model for each trait. Results were visualized using Manhattan and QQ plots. Multiple candidate loci were detected for different traits, and the results are being discussed.

P.0635 Genome-environment association study uncovers loci associated with local adaptation in Chouardia litardierei (Hyacinthaceae)

Sara Laura Šarančić[1], Damjan Mitić[1], Krešimir Križanović[2], Ivan Radosavljević[1]

1 Department of Biology, Faculty of Science, University of Zagreb, Zagreb, Croatia. 2 Department of Electronic Systems and Information Processing, Faculty of Electrical Engineering and Computing, University of Zagreb, Zagreb, Croatia.

Environmental heterogeneity is considered to be one of the major stimuli of the speciation process. By purging genes maladapted to specific environments and supporting the ones that underlay the well-adapted traits, natural selection enables adaptive divergence as a crucial step in lineages' differentiation. *Chouardia litardierei* (Hyacinthaceae) is a bulbous perennial monocot species that occupies contrasting habitats. Its populations occupy wet meadows in coastal areas of the eastern Adriatic, periodically flooded karst poljes across the Dinaric Alps, and rocky and arid slopes of limestone and dolomite mountains in southern parts of its distribution range, thus forming three distinct ecotypes. Although morphologically hardly distinguishable, they thrive in highly contrasting climatic and soil environments. To investigate the genomic background of their local adaptation, we performed a comprehensive genome-environment association analysis. After sampling 33 selected populations across the entire distribution range, sequencing of 129 samples following the ddRAD-seq approach was performed. A set of 8,357 SNPs was obtained and used in several different approaches with the goal of detecting loci under possible selection. Finally, we annotated recognized loci against the available *C. litardierei* draft genome and online databases.

P.0636 Conservation genomics of the narrow endemic Zoysi's harebell (Favratia zoysii Feer)

Garima Singh[1], Marco Canella[1], Sara Natale[1], Nicoletta La Rocca[1], Alessandro Alboresi[1], Barbara Baldan[1], Špela Pungaršek[2], Francesco dal Grande[1]

1 University of Padova, Padova, Italy. 2 The Slovenian Museum of Natural History, ljubljana Slovenia.

Alpine plants with small, disjunct populations are among the most vulnerable to extinction due to climate change. In fact, under the global change scenario, it is predicted that several alpine species may decline and be replaced by those from lower elevation through upward range extension. Such species therefore require immediate efforts for assessing their fitness and vulnerability to climate change to plan adequate biodiversity management and recovery. Here we studied *Favratia zoysii*, a narrow endemic chasmophyte plant of South-east Alps to evaluate its adaptive potential and conservation status. Briefly, after obtaining a high-quality reference genome, we implemented a low-coverage whole genome resequencing approach on 150 individuals from the entire distribution range. We found that the *F. zoysii* populations show signatures of genetic vulnerability and characteristics of declining populations. We propose a road map to management and recovery for this species that could be extended to alpine endemics having small population sizes.

P.0637 Population genomics reveals the evolutionary history of climate adaptation in Japanese Arabidopsis halleri

Ryo Suda[1], Shosei Kubota[2], Shin-Ichi Morinaga[3], Takashi Tsuchimatsu[1]

1 Department of Biological Sciences, The University of Tokyo, Tokyo, Japan. 2 Fasmac Co., Ltd., Kanagawa, Japan 3 Department of Natural & Environmental Science, Teikyo University of Science, Tokyo, Japan.

Plants widely distributed in the climatically diverse Japanese archipelago can provide insights into the mechanisms of local adaptation. *Arabidopsis halleri* subsp. *Gemmifera* is ideal plants for analyzing the genetic background of local adaptation, as it is distributed widely across Japan and is closely related to the model plant *A. thaliana*. Although previous studies have reported various morphological and ecological variations in wild populations of this species, comprehensive analysis of its evolutionary history and genetic basis of adaptation has been limited. This study aims to understand geographical differentiation and climate adaptation of Japanese *A. halleri*. We analyzed whole genome resequence data from 141 wild strains across the archipelago to elucidate population structure, evolutionary history among subpopulations, genomic regions showing correlations with environmental gradients or selection signatures, and potential distribution areas based on climate variables. We found clear geographical differentiation, classifying individuals into four subpopulations: Northern Japan (NJ), Central Japan (CJ), Kansai Region (KR), and Western Japan (WJ). Population demographic analyses suggested that NJ population first diverged and that all differentiations occurred during the Last Glacial Period (LGP). Signatures of selection were enriched in the genomic regions correlated with higher temperatures in WJ and KR populations, as well as with lower precipitation in CJ and NJ populations. These genomic regions included genes related to high-temperature and stress responses, with contrasting allelic distributions among the regions. Furthermore, the distribution areas during the LGP were estimated to be the lowland plains. These findings indicate that Japanese *A. halleri* expanded its distribution during the LGP and adapted to warmer climates in the lowlands of WJ and KR following the postglacial climate change.

P.0638 Exploring adaptive roles of terpene volatiles in the diversification of plant-pollinator interactions in Asarum sect. Herotropa

Anna K. Valchanova[1,2], Satoshi Kakishima[3], Kanako Sekimoto[4], Yudai Okuyama[2]

1 University of Tokyo, Tokyo, Japan. 2 Tsukuba Botanical Garden, National Museum of Nature and Science, Tsukuba, Japan. 3 Mt. Fuji Institute for Nature and Biology, Showa University, Fujiyoshida, Japan. 4 Yokohama City University, Yokohama, Japan.

The genus *Asarum* sect. *Heterotropa* (Aristolochiaceae) is highly diversified across the Japanese archipelago and exhibits remarkable variation in floral phenotypes, especially floral scent. This is thought to be an adaptive mechanism to attract local pollinators, by oviposition-site mimicry. However, the pollinators of most species remain unknown. Terpenes make up a significant component of the floral scents, and their expression across the phylogeny is highly variable. This study investigates how terpene floral volatiles can function as an adaptive trait by facilitating plant-pollinator interactions, and their evolutionary significance. To establish the link between the terpene volatiles and the pollinators, we characterised the floral scent profiles of over 30 *Heterotropa* species using gas chromatography-mass spectrometry (GC-MS), from which we found that terpene content varies significantly. We are collecting pollination data by time lapse photography and identification of eggs laid inside flowers sampled from field sites around Japan. We have tentatively identified dipteran pollinators for three *Heterotropa* species (Phoridae and Mycetophilidae). Preliminary data from other species, including terpene-rich species, suggests that *Heterotropa* rely principally on species-specific dipterans for pollination, and that there may be a link between terpenes and certain Phoridae species. To determine the evolutionary significance of the terpene volatiles, we should characterise the genetic basis of terpene emission. Therefore, we identified candidate terpene synthase genes from the floral transcriptomes of terpene-rich species. We then isolated and characterised their function by heterologous expression in *E. coli*, followed by an enzymatic assay with the crude protein extract. One gene, *TPS10B*, showed unique monoterpene synthase activity, producing volatiles which correspond to the floral scent profiles of the *Heterotropa* species in which it is highly expressed. Having identified*TPS10B*as one key component of the terpene genotype, we are currently characterising the other candidate genes, and will then test for evidence of natural selection.

P.0639 Cytotaxonomy of the Cape-pondweed family (Aponogetonaceae) in India: scopes and limitations

Rupali N. Chougule[1], Shrirang R. Yadav[1], Manoj M. Lekhak[1]

1 Shivaji University, Kolhapur, India.

Aponogeton L.f. (Alismatales: Aponogetonaceae) is an aquatic tuberous plant distributed mainly in tropical and subtropical regions of the Old World. It comprises about 60 species worldwide whereas in India there are ten species. Cytogenetical studies on the family are far from complete. The basic chromosome number $x = 8$ has been reported for the genus. Chromosomes are usually small (0.5-2.5 µm long) and have a strong tendency to stick together that makes analysis of even the best metaphase spreads difficult. Cytogenetical studies on ten species revealed the somatic chromosome numbers of $2n = 26$, 30, 32, 40, 42, 44, 56, 80, 84 and 86. *Aponogeton satarensis* had the lowest chromosome number, i.e. $2n = 26$ and *A. undulatus* the highest chromosome number, i.e. $2n = 86$. *A. satarensis* female plants also showed triploidy ($2n = 3x = 39$) and did not set seeds. Karyotype was represented by metacentric (m) and submetacentric chromosomes (sm). Polysomaty was reported in *A. microphyllus* with root-tip cells showing $2n = 40$, 42 and 44 chromosomes. Species with low ploidy ($2n = 26$-42) reproduced sexually and exhibited normal meiosis. *A. bruggenii* ($2n = 56$) and *A. undulatus* ($2n = 86$) with high ploidy were sterile and propagated vegetatively. Meiosis in these species was abnormal and anomalies like bridges, laggards, precocious separation, stickiness, ring formation, etc. were frequent. Pollen viability ranged from 88% to 99% except for *A. undulatus* which had a pollen viability of 30%. Our findings suggest that *Aponogeton* is a polybasic genus and thorough investigations are needed to understand chromosomal evolution.

P.0640 Complete plastid genome of Iris orchioides and comparative analysis with 19 Iris plastomes

Tae-Young Choi[1], Soo-Rang Lee[1]

1 Department of Biology Education, Chosun University, Gwangju, South Korea.

Iris is a cosmopolitan genus comprising approximately 280 species distributed throughout the Northern Hemisphere. Although *Iris* is the most diverse group in the Iridaceae, the number of taxa is debatable owing to various taxonomic issues. Plastid genomes have been widely used for phylogenetic research in plants; however, only limited number of plastid DNA markers are available for phylogenetic study of the *Iris*. To understand the genomic features of plastids within the genus, including its structural and genetic variation, we newly sequenced and analyzed the complete plastid genome of *I. orchioides* and compared it with those of 19 other *Iris* taxa. Potential plastid markers for phylogenetic research were identified by computing the sequence divergence and phylogenetic informativeness. We then tested the utility of the markers with the phylogenies inferred from the markers and whole-plastome data. The average size of the plastid genome was 152,299 bp, and the overall genomic content and organization were nearly identical among the 19*Iris* taxa, except for minor variations in the inverted repeats. We identified 5 highly informative regions (*rpoC2, ycf1, matK, rpoB-trnC* IGS, and *petA-psbJ* IGS) and inferred a phylogeny from the regions. Notably, the phylogeny was mostly consistent with the phylogeny reconstructed from the whole plastome data. Our results suggested that the 5 selected regions may be used as an alternative to the whole plastome data particularly for molecular diagnoses between closely related *Iris* taxa at low cost.

S.074. GLOBAL CHANGE AND EVOLUTIONARY ADAPTATION OF PLANTS IN COASTAL AREAS

P.0641 The effects of urbanization on plant diversity in Florida Gulf Coast salt marshes

Bethany Burns[1], Kelsey Bonini[1], Kyle A. Keefer[1], Erica Molnar[1], Andrew M. Kramer[1], Christina L. Richards[1,2]

1 University of South Florida, Tampa, USA. 2 University of Tübingen, Tübingen, Germany.

The Gulf Coast of Florida has continuously been growing in human population, especially directly on the coast. One of the dominant intertidal habitats facing threats along this coast is salt marshes. Plant diversity is threatened by human activities however the effects of current and future urbanization on plant biodiversity in salt marshes are not well known. We surveyed plant species at six conservation parks around Tampa Bay in Florida to determine the diversity of coastal plant communities at each location. We then categorized the sites into low and high surrounding urbanization using the ArcGIS Human Footprint Index. We found a total of 18 species among the sites, including grasses, succulents, and mangroves. We found a larger variance in Simpson's Diversity Index within sites than between sites however, the high urbanization sites had more variation within the sites than the low urbanization sites. The low urbanization sites had much higher abundances of coastal grass which decreased the Simpsons Diversity Index due to its sensitivity to large abundances. This finding may indicate that the high urbanization sites have more variation in diversity due to lower amounts of coastal grasses. Coastal grasses play an important role in ground stabilization and provide habitat for many organisms that other plant species cannot replace ecologically. Thus, our results suggest that species diversity as a whole may not be the best indicator to quantify the effects of urbanization and instead conservation efforts should focus on key species.

P.0642 Seawater effect on the development of plant species from Mediterranean coastal dunes

Marcello Dante Cerrato[1,3], Iván Cortés-Fernández[1], Pere M. Mir-Rosselló[1,3], Arnau Ribas-Serra[1], Carles Cardona[1,2], Cyril Douthe[3], Jaume Flexas[3], Lorenzo Gil[1]

1 Interdisciplinary Ecology Group, Department of Biology, University of the Balearic Islands, Palma, Spain. 2 Centre Forestal de les Illes Balears, Institut Balear de la Natura, Palma, Spain 3 Research Group On Plant Biology Under Mediterranean Conditions, Departament de Biologia, Universitat de les Illes Balears-Agro-Environmental and Water Economics Institute, Palma, Spain.

The encroaching influence of seawater poses an escalating threat to coastal regions. Dune ecosystems serve as pivotal barriers between seawater and inland environments, holding immense significance. Understanding the response of dune species to salinity is of key importance in anticipating dune evolution amidst heightened coastal salinity scenarios. This study investigates the response of Mediterranean dune plant species to salinity-induced stress. Over a 180-day period, seven Mediterranean coastal dune species alongside a halophytic outlier were cultivated under both control conditions and salt-exposed settings (20% seawater). Assessments of gas exchange, leaf fluorescence response, and biomass production were conducted every 60 days. Utilizing various ratios, indices, and resemblance analyses, the study sought to delineate similarities and tolerance discrepancies among these species. The primary outcomes indicate distinct biomass and physiological traits for dune species, regardless of their position within the dune system, under both control and salt-exposed conditions. Species were classified into fast and slow growers, with the former predominantly inhabiting embryonic dunes. Water relations emerged as critical during initial developmental stages, while assimilation and biomass-related parameters gained prominence in later stages. Despite salinity exposure, allocation patterns remained unaffected, though increased physiological resemblance among species was noted. Species that evade stress and those adept at coping with it were identified. While salinity disproportionately impacted biomass in fast-growing species, lower salinity tolerance was observed in two slow-growing, stress-coping taxa based on the ETR/An ratio. This study underscores the intricate nature of dune systems, unveiling diverse responses to salinity stress. Anticipated effects of salinity stress are likely to shape dune habitats based on specific species compositions, rather than only their location within the dune system or presence on a specific phytosociological plant community.

P.0643 Abundance of beach litter in coastal habitats and its impact on psammophilous plant communities

Giulia Calderisi[1], Joana Cursach[2], Donatella Cogoni[1], Giuseppe Fenu[1]

1 University of Cagliari, Cagliari, Italy. 2 University of Balearic Islands, Palma, Spain.

Beach litter (hereafter BL) is a serious issue that affects coastal ecosystems and psammophilous plant communities. In fact, different plant species can catch BL, determining variations in its distribution across the dune ecosystem. In this general context, the aims were to investigate the composition and distribution of BL across dune habitats and the effect of summer tourism and proximity to inhabited areas on the distribution and composition of BL. To do this, we selected 16 beaches in Mallorca and Sardinia (western Mediterranean Basin), divided into two distinct groups: (i) beaches near inhabited areas and (ii) beaches far from inhabited areas. We devised a monitoring plan that includes two surveys, before and after the summer tourist season, using transects randomly set in the dune system and considering all consecutive plots (4 m2 in size) present within each transect. For each plot, we estimated the coverage percentage of each plant species using the Braun-Blanquet index, and we took a photo to measure the surface-area occupied by each object using ImageJ. Besides, we used the Clean-Coast Index (CCI) to assess the cleanliness of the beaches. Our results indicated that plastic was the most common waste collected on the investigated beaches. Surprisingly, beaches near inhabited areas appeared to have less BL than beaches farther away. The CCI's analysis revealed that six beaches far from inhabited areas were extremely dirty (only two were moderately clean), whereas three beaches near inhabited areas were moderately clean, three were dirty, and only two were extremely dirty. Furthermore, in the two groups of beaches, the vegetated zone contained more BL than the aphytoic zone. Overall, a long-term monitoring plan is crucial for obtaining comprehensive data on this new ecological component, which can aid in developing sustainable management strategies for this fragile ecosystem.

P.0644 Crithmum maritimum: biological activities and metabolic diversity along Mediterranean and French Brittany coasts

Killian Auzende[1], Clément Lemoine[2], Xavier Dauvergne[1], Christian Magné[1]

1 Laboratoire Geoarchitecture, Brest University, Brest, France. 2 Evonik Advanced Botanicals, Parçay-Melay, France.

Plants have been a source of medicines for thousands of years and phytoproducts are widely used in the food industry, nutraceuticals, and medicine. The latest trend of returning to natural sources for health has generated development in the recovery of bioactive components from plants. For instance, the antioxidant potential of plants has received a great deal of attention for the last two decades. In that context, halophytes represent a renewable source of bioactive molecules. Recent works showed that they contain high levels of secondary metabolites which are responsible for many biological effects. *Crithmum maritimum* L., commonly known as sea fennel or rock samphire, is a widespread perennial halophyte which grows along the coastal areas of the Mediterranean Sea and of the Pacific and Atlantic oceans. The PRIMA-SEAFENNEL4MED project aims to develop a new sustainable cultivation system for sea fennel. In this context, we have characterized the metabolites and antioxidant activities of different populations of C. maritimum (Croatia, France, Italy, Tunisia, Turkey). Metabolites were extracted with ethanol 30% (v/v) and fractionated by chromatography. These metabolites were identified and quantified by nuclear magnetic resonance (NMR). Antioxidant capacity was evaluated using DDPH and FRAP assays on whole extracts and fractionated extracts. Metabolic composition and antioxidant activity revealed major differences between *C. maritimum* populations. In order to explain these differences, greenhouse cultures were carried out to assess the responses of different populations to salt stress.

P.0645 Germination ecology of a range-restricted species from coastal dune

Antoni Josep Far[1], Marcello Dante Cerrato[1], Carles Cardona[1,2], Llorenç Gil[1], Joana Cursach[1]

1 Department of Biology, University of Balearic Islands, Palma, Spain. 2 Centre Forestal de les Illes Balears, Institut Balear de la Natura, Palma, Spain.

Understanding germination ecology of plant species is crucial, especially for annual species with limited distribution. This study focuses on the germination ecology of *Silene migjornensis*, an endemic annual species of Mallorca (Balearic Islands, western Mediterranean Basin) that occurs solely within the Es Trenc-Salobrar de Campos Maritime-Terrestrial Natural Park's white dunes. Controlled germination experiments were conducted to study (i) germination requirements (seed age, photoperiod and temperature) and (ii) salinity effects (NaCl, MgCl$_2$, MgSO$_4$ and Na$_2$SO$_4$ at concentrations ranging from 0.1 to 0.4 -M) on seed germination. Besides, 50 soil cores (785 cm^3 each) collected near *S. migjornensis* plants were monitored weekly for seed bank evaluation. Results revealed negligible germination within five months from seed collection, moderate germination (40-60%) after six months, and optimal germination (c. 80%) after seven months onwards. Artificial aestivation at 40ºC failed to expedite germination, causing reduced germination and increased seed death after nine weeks of heat treatment. *Silene migjornensis* exhibited strong photoinhibition, with no germination under light exposure. In darkness, optimal temperature ranged from 16 to 20 ºC, with moderate germination (40-70%) at lower temperatures (5-14 ºC) and lower germination (20%) at higher temperatures (23 ºC). In optimal conditions, seed germination occurred within six days, with a mean T$_{50}$ of 1.85 (±0.11) days. Salinty significantly inhibited seed germination, with moderate reductions at lowest concentration and notable reduction starting at 0.2 M. In soil cores, number of emerged seedlings during the first three months was very variable, ranging from 0 (32% of cores) to >20 (4% of cores) with a mean value of3.96 (±0.84). Most seedling emergence ocurred in the first week (12.5-100%). In conclusion, *S. migjornensis* has restricted salinity tolerance, coupled with significant photoinhibition and morphophysiological dormancy, which guarantees rapid autumn germination when optimal conditions occur.

P.0646 Current situation of Stachys maritima Gouan in Spain: the need to create an international network of research on the species

Carles Barriocanal[1], Jordi López-Pujol[2], Xavier Sanjuan[3], GemmaDíaz-Martínez[1], Cristina Durà-Lahoz[1]

1 University of Barcelona, Barcelona, Spain. 2 Botanical Institute of Barcelona (CSIC-CMCNB), Barcelona, Spain. 3 Corps of Rural Agents of the Generalitat de Catalunya in Baix Empordà, Girona, Spain.

As its name suggests, *Stachys maritima* Gouan (Lamiaceae) is often found in coastal areas, particularly in sandy habitats along the coasts of the Mediterranean region. In its native habitats, *Stachys maritima* plays a role in stabilizing coastal dunes and provides habitat and food for various wildlife, including pollinators such as bees and butterflies. The species has the ability to withstand the challenging conditions of coastal environments, such as salt spray, sandy soils, and high winds. Its gray-green leaves and deep root system help it adapt to these conditions by minimizing water loss and stabilizing the soil. Unfortunately, most of the sandy beaches of the Mediterranean region have been deeply transformed for human use, such as the tourist industry, which has profoundly affected its populations. Nowadays, the species is protected in most of its range, but not uniformly and with different protection statuses. In Spain, despite being considered "endangered" (EN) in the most updated (2010) Red List of Spanish Vascular Flora, the few remaining populations—all fragmented and having very small population size—show genetic erosion, and there are no effective conservation measures. All populations are located in small patches in the Costa Brava region (Girona province) and basic monitoring has not been continuous over time. We present the update of the *Stachys mariti-*

ma population in its Spanish range and discuss the need to tackle a network of research on the species along its whole distribution range.

P.0647 Storms on the Western Black Sea shore: an opportunity for long-distance dispersion of coastal dunes psammophytes?

Andreea Sandu[1], Ciprian C. Mânzu[1], Maria M. Zamfirache[1], Alina G. Cîșlariu[2]

1 Faculty of Biology, Alexandru Ioan Cuza University of Iași, Iași, Romania. 2 Department of Botany and Microbiology, Faculty of Biology, University of Bucharest, Bucharest, Romania.

Coastal areas are considered to be among the planet's most dynamic yet vulnerable environments, the shape of the sand dunes being typically modeled by two sets of forces: the relatively constant action of wind and waves, and the disturbances caused by infrequent but powerful storms. These meteorological events, whether extreme or not, affect the plant communities, but also can play an important role in the long-distance dispersal of some psammophytes. The action of waves and wind can expose, uproot, break apart into pieces and spread plant fragments, whole plants or seeds through sea water. Then, depending on the resilience of the plant to seawater immersion, the time of immersion, the temperature of the water, the type of fragment transported and the suitability of the new habitat, new populations can be established. This study aimed to assess the resilience to seawater and the ability of long-distance dispersion by seawater of three psammophytes: *Convolvulus persicus*, *Alyssum borzaeanum* and *Silene thymifolia*. The experiments tested the viability of vegetative fragments and the reproductive capacity of seeds under different exposure periods (5, 10 and 15 days) and temperature conditions: 4°C (average surface seawater temperature during winter and early spring when storms on the Black Sea Coast occur), 13°C (average surface seawater temperature) and 23°C (average summer surface seawater temperature). The increase of both seawater temperature and the exposure time had a significant negative influence on the viability of the vegetative fragments and on germination capacity. After exposure to seawater, *Convolvulus persicus* and *Silene thymifolia* are able to establish new populations through vegetative fragments or seeds, whilst in case of *Alyssum borzaeanum* no vegetative regeneration was observed, relying only on seeds for dispersal and propagation.

P.0648 Local adaptation between coastal and inland populations of the endemic Brazilian orchid Epidendrum fulgens Brongn.

Thales M. de Lima[1,2,*], Simone F. da Silva[1], Rafael Vasconcelos Ribeiro[1], Julia Sanchéz-Vila[3,4], Fábio Pinheiro[1]

*1 Universidade Estadual de Campinas, Departamento de Biologia Vegetal, Instituto de Biologia, Campinas, Brazil. 2 Current adress: Royal Botanic Garden Edinburgh, Edinburgh, Scotland, United Kingdom. 3 Organisms and Environment Division, Cardiff School of Biosciences, Cardiff University, Sir Martin Evans Building, Cardiff, United Kingdom. 4 Departamento de Bioloxía Funcional, Facultade de Bioloxía, Universidade de Santiago de Compostela, Santiago de Compostela, Spain. *Email: tdelima@rbge.org.uk*

Few studies on local adaptation in plants investigate in depth which environmental factors generate the selective pressures that lead to the evolution of this phenomenon. We analyzed local adaptation between coastal and inland populations of *Epidendrum fulgens* Brongn., an orchid species endemic to Brazil. The hypothesis tested is that coastal plants would be more resistant to salt in the form of salt spray. To do this, we carried out an experiment in a greenhouse, exposing 96 plants – two populations from each region – to salt spray for 60 days. Plant performance was evaluated by measuring maximum PSII yield (F_v/F_m), leaf expansion rate, osmotic potential (OP), relative water content (RWC), leaf chlorophyll index, leaf concentration of Na^+ and relative growth rate (RGR). In both groups, OP, RWC and chlorophyll index were not affected by salt. In sprayed plants, leaf expansion rate, RGR and F_v/F_m were lower, but the reduction was similar between groups. Furthermore, plants sprayed with salt had leaves with Na^+ concentrations approximately 3 times higher than control plants. On the other hand, coastal plants had lower foliar Na^+ concentration than inland plants in both control and treatment conditions. Overall, both groups were considerably resistant to salt. The difference in Na^+ concentration between coastal and inland plants could suggest that those on the coast are better adapted to salt, preventing its absorption by the leaves. However, this difference in absorption does not appear to provide an advantage to coastal plants as leaf expansion rate, RGR and F_v/F_m of coastal and inland plants were equally affected by salt. Therefore, taken together, the physiological data do not demonstrate local adaptation of coastal plants to salt spray.

P.0649 Recovery and Conservation Plan for the species of dunes, sandbanks and coastal cliffs in Andalusia.

Fernando Sanz[1], Hedwig Schwarzer[2], Miguel Arrufat[2], Laura Fernández[2], Guillermo Ceballos[1], Working team of the Recovery, Conservation Plan for the species of dunes, sandbanks and coastal cliffs in Andalusia[2]

1 Consejería de Sostenibilidad, Medio Ambiente y Economía Azul, Junta de Andalucía, Spain. 2 Agencia de Medio Ambiente y Agua de Andalucía, Junta de Andalucía, Spain.

Recovery and Conservation Plan for the species of Dunes, Sandbanks and Coastal Cliffs in Andalusia (hereinafter, Dunes Plan), approved by Agreement of March 13, 2012, of the Governing Council, establishes protection measures for 35 species of flora and 1 of invertebrate fauna, as well as measures for the conservation of the ecosystems that host them, especially pine forests, juniper groves, cork oak groves and coastal wild olive groves. The Dunes Plan includes 10 lines of action: 1. Cataloguing. The aim of this line is to determine the criteria to establish when a species should be re-evaluated.; 2. Habitat management. This includes measures aimed at improving the territories.; 3. Population management. To achieve the persistence of the different population nuclei.; 4. Ex situ conservation measures. Aimed at conserving the greatest genetic variability of the populations and to develop protocols related to the reproduction of the species for reintroductions and population reinforcements.; 5. Monitoring. Both to know the status of each of the species and to be able to detect the threats that affect them and how the actions carried out are working.; 6. Research. In collaboration with research groups.; 7. Dissemination and communication. To publicize the plan and its progress.; 8. Education and awareness. To get society to recognize the importance and become involved in the conservation of species associated with dunes, cliffs and coastal sandbanks.; 9. Social participation. To achieve the participation of the sectors that could be involved in the execution of the Plan.; 10. Cooperation and coordination. This line of work seeks the connection between the different national and international projects aimed at species associated with dunes, cliffs and coastal sandbanks. This paper presents the most significant advances in some of these lines of work.

P.0650 Community phytochemistry of Japan's mangrove guild: ecological and evolutionary patterns

Katharine M. Saunders[1], Helene F. Bee[1], Callum J. Hudson[1], Amy H. Morrell[1], David W. Armitage[1]

1 Okinawa Institute of Science and Technology Graduate University, Onna, Japan.

Relative to other traits, comparative studies of metabolic traits in plant guilds remain scarce, yet hold promise as a nexus for clarifying the joint effects of evolutionary and environmental factors shaping community assembly and geographic distributions. To better understand roles of ecological and evolutionary factors contributing to the phytochemistry of plant communities, we quantified the joint influences of geography, local scale environmental gradients, and evolutionary history on the evolutionarily diverse mangrove guild of the Ryukyu Archipelago in Southwest Japan. We collected leaf samples from mangrove trees, non-mangrove associates, and terrestrial trees from Okinawa-jima, Ishigaki-jima, and Iriomote-jima islands and performed untargeted metabolomics using liquid chromatography mass spectrometry and nuclear magnetic resonance spectroscopy to characterize the bulk phytochemical traits of our focal taxa. We encountered a strong phylogenetic signal in mangrove metabolomes that was more pronounced than those of geographic or environmental gradients. Mangrove secondary chemical profiles were clustered independent of family, hinting at potential parallel evolution of metabolic traits during a shift to the mangrove habit. Further analysis also revealed various compounds, including some important secondary metabolic pathways, that were reliably differentially expressed across a local salinity gradient. Our results are a first step toward integrating phytochemistry into the evolutionary ecology of mangroves. Future work will use this community metabolomic approach to investigate mechanisms of climate-driven range shifts and parallel evolution in this unique and important guild.

P.0651 The influence of macroclimatic drivers on the macrophyte phylogenetic diversity in South African estuaries

Dimitri A. Veldkornet[1]

1 Department of Plant Sciences, Faculty of Natural and Agricultural Sciences, Bloemfontein, South Africa.

The geographical distribution of plants is influenced by macroclimate and dispersal limitations, which have led to lineage isolation and subsequent diversification within and across various environmental gradients. Macroclimatic variables in coastal wetlands influence plant species and lineages across biogeographical boundaries. This study aimed to determine the influence of macroclimatic variables on species and phylogenetic richness in South African estuaries. Open-source chloroplast DNA barcoding sequences, species distribution and climatic data layers were used to determine the relationship between species richness, MPD, MNTD and each bioclimatic variable. Temperate species richness and phylogenetic diversity were positively correlated with temperature bioclimatic variables whereas subtropical and tropical species were associated with increased precipitation. Phylogenetic niche conservatism is evident in malvids and rosids which are restricted to tropical and subtropical regions due to their physiological adaptations to tropical climates. Caryophyllales was mostly associated with temperate regions. Poales and Alismatales showed wide distributions that are likely attributed to traits related to wind pollination and hydrochory, rapid, clonal, and high reproductive output, tolerance to stressful conditions, and intraspecific genetic diversity. The findings highlight the importance of considering macroclimate and phylogenetic factors in understanding the distribution and diversity of coastal wetland plants.

S.075. GLOBAL CONSERVATION CONSORTIA: INTEGRATED PLANT CONSERVATION ON A GLOBAL SCALE

P.0652 A task force for extinct-in-the-wild species

Thomas Abeli[1,12], Sarah E. Dalrymple[2,12], John G. Ewen[3,12], Tania C. Gilbert,[4,5,12], Carolyn J. Hogg[6,12], Natasha A. Lloyd[7,12], Axel Moehrenschlager[7,8,12], Jon Paul Rodriguez[9,10,12], Paul P. Smith[11,12]

1 Department of Science, University of Roma Tre, Roma, Italy. 2 School of Biological and Environmental Sciences, Liverpool John Moores University, Liverpool, UK. 3 Institute of Zoology, Zoological Society of London, London, UK. 4 Marwell Wildlife, Hampshire, UK. 5 School of Biological Sciences, University of Southampton, Southampton, UK. 6 Faculty of Science, School of Life and Environmental Sciences, The University of Sydney, Sydney, Australia. 7 Wilder Institute / Calgary Zoo, Calgary, Canada. 8 Department of Biological Sciences, University of Calgary, Canada 9 IUCN Species Survival Commission, Caracas, Venezuela. 10 Instituto Venezolano de Investigaciones Científicas, and Provita, Caracas, Venezuela. 11 Botanic Gardens Conservation International, Surrey, UK. 12 IUCN SSC Conservation Translocation Specialist Group, Calgary, Canada.

Of the 157,190 species listed under the IUCN Red List, 44,000 are classified as threated but only 84 species are listed as Extinct in the Wild (EW). Species that only exist in ex situ populations in zoos, aquaria, botanic gardens, private collections, and seedbanks. Long-term human care is risky. Most EW species are in a precarious state because they were founded by a small number of individuals, have small/poorly integrated populations, and are held by a small number of institutions. Of the 95 that have entered this space since 1950, we've lost (11) approximately as many as we have reintroduced in the wild (12). There are various **options for EW species recovery, but poor attention has been given to this group of taxa.** A IUCN/SSC Conservation Translocation Specialist Group Taskforce for Extinct in the Wild Species has been created, to inform, promote and advise the long-term recovery in the wild of EW taxa through a four Rs strategy: -Rescue species close to extinction into ex situ care; -Revitalise existing ex situ populations (increase their size, ensure they are well managed across more institutions. Store plant species in seed banks where possible); -Release EW species back to the wild, including using introductions or assisted colonisations for species where habitat/climate is no longer viable; -Reinforce and manage the wild populations that we have established. The Task Force has promoted a motion supporting reestablishment of EW species by 2030 at the 2021 IUCN World Conservation Congress and members of the task force have been involved in the rediscovery and reassessment of *Nymphaea thermarum*in Rwanda and in the delisting from EW to Endangered (EN) of the Scimitar-Horned Oryx in December 2023.

P.0653 Threatened C4 plant species and their habitats of conservation concern in Armenia

Anna Asatryan[1], Mehdi Dehghani[2], Hripsik Qosyan[1], Razmik Papikyan[1], Yekaterina Shcherbakova[1], Alexander Rudov[1,3]

1 Institute of Botany after A.L. Takhtajyan NAS, Republic of Armenia. 2 University of Zabol, Islamic Republic of Iran. 3 University of Tehran, Tehran, Islamic Republic of Iran.

Armenia is a mountainous country a with rich flora and remarkable diversity of habitats. The country's C_4 flora is of particular interest and importance for conservation. It includes about 94 plant species, 10 of which are threatened and included in the Red Data Book of Armenia. They are mainly found in the semidesert belt: mountain plateaus and foothills of mountain ranges at about 400 – 1300 m above sea level. Historically these areas have been sensibly affected by human activity and because of habitat destruction only small fragments of aboriginal vegetation survived. Some of the threatened C_4 plant species play a forming and/or dominant role in plant communities, others occur with single specimens, but all are threatened because of restricted area of occupancy and continuous influence of agricultural, recreational and construction activities. At least 10 C_3 plant species are found at the same habitats where the threatened C_4 species occur – mainly found on sands, clay, gypsum and saline soils, they include also riverine areas, rocks and screes in deep gorges. In spring – autumn of 2023 during fieldwork aimed at research of extremophile plants and their habitats in Armenia we collected data on distribution, ecology and condition of threatened C_4 plant species. Their habitats of conservation concern have been studied too. New populations of the target species have been found, the habitats were described and seeds of both rare C_4 and C_3 species were collected for ex-situ conservation and creation of a model biotope in Yerevan Botanical Garden. A very small part of the areas with presence of threatened C4 species overlaps state protected areas. One of the main goals of the ongoing project is to collect data and to prepare recommendations for conservation and monitoring of these ecosystems.

P.0654 Dr H. K. Baruah Regional Botanical Resource Centre of Gauhati University, Assam, India: Scope for integrating research, germplasm conservation, environmental education and public recreation

Buragohain R.[1,*], Tanti B.[1]

*1 Regional Botanical Resource Centre. Department of Botany, Gauhati University. Assam, India. *rubul10@gauhati.ac.in*

The Gauhati University Botanical Garden is one of the largest and oldest Botanical Gardens of the North East India in particular and the country in general. The Garden was developed with an objective to study the rich and diverse flora of N.E. India and to conserve the rare, endangered and threaten plant species of the region and at present, it is spread over an area of ca 62 acres situated in the hills and valleys of Jalukbari hills within the university campus at an altitude ranging from 213 to 247 ft msl. Total 210 trees, 56 shrubs, 120 herbs species have been recorded so far. Out of all these 56 species are medicinal. During individual tree count we found highest no of *Caryota urens* with 130 trees followed by *Milletia pinnata* with 58, *Putranjiva roxburghii* with 28, *Lagerstroemia speciosa* with 27 and *Monoon longifolium* with 25 recorded. The highest species belongs to Fabaceae with 12 and Moraceae with 8 shows maximum number of species. About 15 species are conserved which are under threaten category. Along with the plant diversity the centre has ca.120 birds, ca.150 butterflies and ca.25 snakes are also remarkable in this centre which varies from season to seasons.

P.0655 How do we achieve sustainable management of non-timber forest products? A typology of recommended management targets

Michael A. Coe[1], Irene Teixidor-Toneu[2,]

1 IMBE, Aix Marseille Univ, IRD, Marseille, Franc.e 2 IMBE, Aix Marseille Univ, Avignon Univ, CNRS, IRD, Marseille, France.

Non-timber forest product (NTFP) harvesting contributes to local livelihoods and subsistence strategies for Indigenous peoples and local communities (IPLC) worldwide. NTFP have been managed by IPLC for thousands of years and often serve as primary sources of food, medicine, and income for millions of people around the globe. Over the last three decades, a growing number of studies by applied ecologists and ethnoecologists have used quantitative tools to measure the impacts of NTFP harvest on the demography of wild plant populations including matrix projection and integral projection models, elasticity analyses, and life table response experiments. In some cases, these harvest impact assessments also incorporate harvester decision making guided by local ecological knowledge (LEK). While these studies often define sustainable harvest limits and recommend sound management strategies useful for conservation and restoration efforts of NTFP populations, few conservation managers and restoration efforts have incorporated these suggestions in developing management plans or in guiding restoration efforts. Further, LEK and knowledge holders have often been overlooked, under-emphasized, ignored, or used marginally and unconsciously in informing species conservation management decisions. We provide a global synthesis of NTFP management strategies informed by ecologists' assessments of the effect of harvest and IPLC harvester decision making. This generalized typology for NTFP plant species across species' life-form, life-history, organs harvested, and ecological system will facilitate access to disciplinary, inter-, and trans-disciplinary knowledge for conservation and restoration efforts. We also assess whether there is evidence that the proposed IPLC and scientific management strategies result in conservation of NTFP plant populations and community wellbeing.

P.0656 Strengthening the population of the threatened mangrove Pelliciera benthamii through ex situ and in situ conservation strategies

Maria Paula Contreras[1], Camila Rueda[2]

1 Horticulture and Science Department, Cartagena Botanical Garden, Colombia. 2 Universidad de los Andes, Bogotá DC, Colombia.

Although not evaluated by the IUCN, *Pelliciera benthamii* (Triana & Planch.) Cornejo, is likely the most threatened of the mangrove species present in the Colombian Caribbean region due to its limited distribution and severe threats to its ecosystem caused by expansion in construction and unsustainable economic activities. Conservation activities are needed at a broad front, including research, education, in-situ and ex-situ conservation and ecosystem protection. Piñuelo, *P. benthamii*, a segregated species from *Pelliciera rhizophorae* Triana & Planch, is a mangrove species restricted to small populations in the Panamanian Pacific and the Colombian Caribbean. *P. rhizophorae* was listed as vulnerable by the IUCN due to isolated populations, reduced range, and decline in habitat quality. We are re-assessing *P. benthamii*, and its conservation status will most likely change from vulnerable to endangered. The Cartagena Botanical Garden's science and horticulture teams have worked together to strengthen the population of *P. benthamii* in the Colombian Caribbean region. We identified three localities for seed collection near Cartagena, where we made phenological annotations and the recognition of potential planting areas. To accomplish mangrove conservation, we established propagation protocols and nursery line guides and submitted a new

Red List assessment for *P. benthamii*. Additionally, we have propagated other mangrove species, as it may be beneficial that restoration initiatives focus on ecosystem restoration rather than planting individual species. In addition to *in-situ* initiatives, we will strengthen *ex-situ* through the establishment of a new living collection of mangrove species in the Cartagena Botanical Garden, and installation of educational displays to educate visitors about this important ecosystem. We aim to increase the information regarding propagation strategies and conservation actions to provide input for future restoration and protection initiatives.

P.0657 Description of pistillate flowers and conservation status of two Mollinedia species (Monimiaceae) from Brazilian Atlantic Forest

Letícia Guimarães Barbosa[1,2], Patrícia da Rosa[3,4], Danilo Alvarenga Zavatin[1,2], Joelcio Freitas[2,5], José Augusto de Andrade Souto Maior[2], Elton J. de Lírio[1,2]

1 Universidade de São Paulo, São Paulo, Brazil. 2 Conservação de Espécies Ameaçadas da Mata Atlântica (CEAMA), São Paulo, Brazil. 3 Universidade Estadual do Rio de Janeiro, Rio de Janeiro, Brazil. 4 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 5 Instituto Nacional da Mata Atlântica, Santa Terresa, Brazil.

Mollinedia ruschii and *Mollinedia dolichotricha* are endemic to the Atlantic Forest. Both species were described in the last decade based on staminate flowers and fruits. *Mollinedia ruschii* is microendemic and occurs in two Protected Areas in Santa Teresa, in Espírito Santo state (ES), and was assessed as Critically Endangered (CR). *Mollinedia dolichotricha* also occurs in ES and the states of Bahia and Minas Gerais, having been assessed as Endangered (EN). Recently, during fieldwork, members of CEAMA found previously unknown pistillate individuals of both species, which were collected and photographed. Furthermore, new individuals and threats were recorded for both species. The study aimed to reassess the risk of extinction based on IUCN criteria and carry out the redescription of the species, including the description of the pistillate flowers and new characteristics of the fruit of *M. ruschii*. Twelve new individuals of *M. ruschii* and six of *M. dolichotricha* were found. For both species, the first pistillate individual was found, which allowed the description of the pistillate flower. In addition, for *M. ruschii*, it was possible to observe in loco morphological characteristics of fresh fruits such as color and shape, also unknown until then. The extinction risk reassessment showed a change in the criteria for both species, but the risk category was maintained. *Mollinedia ruschii* has been categorised as CR, B1ab(i,ii,iii,v); C2a(i); D, while *M. dolichotricha* was reassessed as EN, B2 ab(ii,iii,v). The new data on the morphology of the flowers and fruits of the species are essential to establish comparisons between other species within the genus, facilitating the development of new identification keys, morphological phylogenies, and character evolution. Despite discovering new individuals for the species, the extinction risk reassessment revealed that both are still at high risk of extinction; therefore, protective measures are necessary for the species.

P.0658 Effect of climate change on the spatial distribution of plant endemism in the coastal Mediterranean strip in Egypt

Mohamed M. El-Khalafy[1], Kamal H. Shaltout[2], Marwa w. Halmy[3], Heba Bedair[2]

1 Botany and Microbiology Department, Faculty of Science, Kafrelsheikh University, Kafr El-sheikh, Egypt. 2 Botany and Microbiology Department, Faculty of Science, Tanta University, Tanta, Egypt. 3 Department of Environmental Sciences, Faculty of Science, Alexandria University, Alexandria, Egypt.

The Mediterranean region is characterized by a heavy endemism of plant diversity, where the majority of its species are narrow endemic species. The distribution of these endemic plants in Egypt has declined significantly over the previous century across its geographical region. This decrease is related to changes in natural resources, such as water and foraging site capacity, due to continuous climate change. In addition, human impacts (urbanization and tourism) are effective threats that impacted these taxa. The mediterranean coastal strip in Egypt includes 15 endemic plants. We used species distribution models (SDMs) to study plant endemism reaction to projected climate change over the next few decades in the

Mediterranean region in Egypt. To reduce uncertainty and bias in our SDM predictions, we fitted ensemble SDMs with freshly developed climatic data based on more accurate climate models and diverse dispersal scenarios. Furthermore, our models anticipated that the distribution range of plant endemism would drop by more than 20 % during the next few decades. Our findings advocate for immediate conservation action of reintroduction and in-situ conservation planning for these endemic taxa.

P.0659 The cycads collection at the Marimurtra Botanical Garden a resource for ex situ conservation.

Iván Soto[1], Jordi Fàbregas[1], Anna Sans[1], Carles Burguera[1], Pere Fraga[1,2]

1 Jardí Botànic Marimurtra, Fundació Privada Carl Faust, Blanes, Spain. 2 Institut Menorquí d'Estudis, Maó, Spain

One of the main functions of botanical gardens is the ex-situ conservation of threatened plants in the wild, so those populations in cultivation can be a resource for the reintroduction or reinforcement of existing populations. Cycads have been present in the Marimurtra Botanical Garden since its foundation, now 100 years ago. Its microclimatic conditions make it possible to grow many of these plants outdoors. This open-air cultivation allows individuals to be shown in more natural conditions and their development is better. In recent years the collection of these plants has significantly increased thanks to the dedication of the gardeners and technical staff. An important part of the new additions has been thanks to the exchange with other collections, both public and private. Today, a significant number of individuals have already reached sexual maturity and are active reproducers, this has allowed to increase the operations of exchange of reproductive material. This activity serves both to increase taxonomic diversity and to improve genetic diversity, so the collection could be more useful for ex-situ conservation. Currently, the cycads collection of Marimurtra consists of 117 taxa, the distribution by genera is as follows: *Ceratozamia*, 6; *Cycas*, 30; *Dion*, 16; *Encephalartros*, 43; *Lepidozamia*, 1; *Macrozamia*, 14; *Stangeria*, 1; *Zamia*, 6. Cycads are of special conservation interest due to the threatened situation in which are many of the species. According to the latest assessment carried out by the IUCN, the threat levels of cultivated taxa are as follows: VU, 22; EN, 19; CR, 8. All this makes the cycads collection of Marimurtra an ex-situ resource to be considered for the conservation of this important taxonomic group.

P.0660 Overview of the database on conservation actions on threatened plant species in Europe

Maja Lazarević[1*], Boštjan Surina[2], Sandrine Godefroid[3], Andreas Ensslin[4], Justyna Wiland-Szymańska[5], Marcin Klisz[6], Joaquim Santos[7], Sílvia Castro[7]

*1 University of Belgrade, Faculty of Biology, Belgrade, Serbia. 2 University of Primorska, Faculty of Mathematics, Natural Sciences and Information Technologies, Koper, Slovenia, Natural History Museum Rijeka, Rijeka, Croatia. 3 Meise Botanic Garden, Meise, Belgium. 4 Conservatory and Botanic Garden of the City of Geneva, Geneva, Switzerland. 5 Adam Mickiewicz University, Faculty of Biology & Botanical Garden, Poznań, Poland. 6 Forest Research Institute, Dendrolab IBL, Raszyn, Poland. 7 University of Coimbra, Coimbra, Portugal.*majat@bio.bg.ac.rs*

At a time when the state of biodiversity is constantly deteriorating, the Database on Conservation Actions on threatened plant species and institutions dealing with plant conservation represents a valuable source of information about plant conservation activities in Europe from the year 2000 until today. Defining conservation actions as specific activities undertaken to help a threatened plant species survive, the main aim of this initiative is to provide conservation practitioners and stakeholders of different backgrounds with information about past and ongoing conservation actions, enabling the easy and free exchange of knowledge and experience among them. The Database currently hosts information about c. 3,500 conservation actions from 32 European countries, about more than 900 taxa belonging to almost 100 plant families. For each of them, various data are available such as basic information about the locations where the activities took place, typology of involved institutions, financial structure, information about the species and its conservation status, details about the implemented *in situ* and *ex situ* conservation measures, as well as about monitoring and success evaluation. The Database can be collaboratively updated in the future, providing the opportunity for monitoring the plant conservation activities throughout Europe in the long run, and contributing to the promotion of best practices for the benefit of all stakeholders and biodiversity conservation.

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P.0661 WANTED (alive): Pollinators and flower visitors of European threatened plants

Sara B. Lopes[1], Ana Afonso[1], Boštjan Surina[2,3], João Loureiro[1], Fatal attraction team, Sílvia Castro[1]

1 Centre for Functional Ecology, University of Coimbra, Coimbra, Portugal. 2 Natural History Museum Rijeka, Rijeka, Croatia. 3 FAMNIT, University of Primorska, Koper, Slovenia.

Developing integrated conservation programs requires a holistic approach. In the case of European threatened plants, considering that the majority are angiosperms that depend on animal pollinators to assure successful reproduction, information regarding their pollinators must be included. The main goal of this study is to compile data on pollinators/flower visitors of threatened European plants (CR, EN and VU) to assess the current situation and identify knowledge gaps. The information was obtained through bibliography revision and the compilation of data provided by several collaborators from different European countries, who have been responding to the call 'Fatal attraction: endangered plant's lovers'. Until now, we have compiled data for 16% of the European animal-pollinated threatened plant species and for 114 species considered threatened at the national and regional level. More than 2000 interactions were obtained, with information at the plant species level for 72% of them. Orchidaceae was the family with the most reported interactions. Regarding the identity of the flower visitors, almost a quarter of the interactions comprise species from the Order Diptera, followed by Hymenoptera. Preliminary results from the analysis of the interactions show that the species with the highest number of interactions reported is *Androsace brevis* (VU in Italy) with 150 interactions, being visited by 55 different insect species, followed by *Dianthus morisianus* (CR in Europe) with 120 interactions and visited by 14 insect species. In this poster, interaction networks between threatened plants and their floral visitors will be presented to evidence species interdependence and the most threatened interactions. Information gathered so far is valuable and should be integrated into conservation programs. However, the majority of species still lack sufficient information, requiring our attention and efforts to fill these knowledge gaps.

P.0662 Filling gaps for the evaluation of "Endangered Living Fossils" from the Mediterranean Basin

Enrique Maguilla[1], Mónica Míguez[1]

1 Departamento de Biología Molecular e Ingeniería Bioquímica, Universidad Pablo de Olavide, Sevilla, Spain.

Vargas et al. defined in 2020 the concept of "Endangered Living Fossils" (ELFs), aiming to preserve unique taxa from a phylogenetic perspective. ELFs must meet three requirements: (1) they must be scarce and have a restricted distribution; (2) evolutionarily well-differentiated lineages with low or no diversification rate; (3) the diversification origin must be ancient and predates drastic environmental changes associated with a specific geological epoch. Considering a species as an ELF adds a threat component, not intrinsic to the traditional concept of living fossil, helping to identify and preserve potentially threatened taxa. Vargas et al. studied six potential ELFs in the Iberian Peninsula, identifying nine other monospecific genera in the Mediterranean basin, excluded from the Iberian Peninsula, listed on red lists of threatened species, and thus, potential ELFs (*Crambella* (Brassicaceae), *Degenia* (Brassicaceae), *Horstrissea* (Apiaceae), *Kremeriella* (Brassicaceae), *Petagnaea* (Apiaceae), *Phitosia* (Asteraceae) *Pseudoridolfia* (Apiaceae), *Rytidocarpus* (Brassicaceae) and *Saccocalyx (Lamiaceae)).* The main objective of the proposed research is to confirm the consideration of these nine taxa from the Mediterranean region as ELFs, filling knowledge gaps regarding phylogenetic relationships, lineage dating, and demographic and diversity data on these species, at the time that we assess or re-assess the threat status for each taxon. A combination of traditional Sanger sequencing, phylogenomics based on Hyb-seq and the use of RADseq for demographic studies, combined with results from niche distribution modelling, dating analyses and the effort for the estimation of extinction probability in a near future, are the backbone of the project, hoping to obtain strong results contributing to the knowledge of the study species and related ones, at the time that it helps to preserve these unique taxa. Additionally, phylogenetic reconstructions will be explored to detect long branches with taxa that, although currently not classified under any threat category, may be evolutionary and conservational significant.

P.0663 Drivers of vascular epiphyte assemblages across the Neotropics

Glenda Mendieta-Leiva[1], Flavio N. Ramos[2], João P. C. Elias[2], Gerhard Zotz[3,4], Margoth Acuña-Tarazona[5], Francine Seehaber Alvim[6], Daniel E. F. Barbosa[6], Geicilaine A. Basílio[7], Sven P. Batke[8], Ana María Benavides[9], Christopher T. Blum[10], Carlos R. Boelter[11], Pedro H. S. Brancalion[12], María Judith Carmona[13], Luciana P. Carvalho[6], Edilia de la Rosa-Manzano[14], Helena J. R. Einzmann[3], Manuel Fernández[15], Samyra G. Furtado[6], André L. de Gasper[16], Valeria Guzmán-Jacob[17], Peter Hietz[18], Mariana V. Irume[11], Derio Antonio Jiménez-López[19], Michael Kessler[20], Holger Kreft[17,21], Thorsten Krömer[22], Giesta Maria O. Machado[16], Nayely Martínez-Meléndez[19], Pedro Luiz S. S. Martins[6], Rodrigo de Macêdo Mello[23], Alex F. Mendes[12], Luiz Menini Neto[6], Sara R. Mortara[24,25], Camila Nardy[2], Rodolfo de Paula Oliveira[3,26], Ana Clara A. Pereira[6], Luis Pillaca[27], Adriano C. Quaresma[28], Calixto Rodríguez Quiel[29], Edier Soto Medina[30], Amanda Taylor[17], Michael S. Vega[31], Márcio S. Werneck[32], Florian A. Werner[33], Jan H. D. Wolf[34], Charles E. Zartman[11], Daniel Zuleta[35], Borja Jiménez-Alfaro[36]

1 Faculty of Geography, University of Marburg, Marburg, Germany. 2 Universidade Federal de Alfenas, Alfenas, Brazil. 3 Institute of Biology and Environmental Sciences, University of Oldenburg, Oldenburg, Germany. 4 Smithsonian Tropical Research Institute, Panamá, República de Panamá. 5 Instituto de Ecología A.C., Xalapa, México. 6 Universidade Federal de Juiz de Fora, Juiz de Fora, Brazil. 7 Centro de Ensino Superior de Juiz de Fora, Juiz de Fora, Brazil 8 Department of Biology, Edge Hill University, UK. 9 Jardín Botánico de Medellín, Antioquia, Colombia 10 Universidade Federal do Paraná, Paraná, Brazil. 11 Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil. 12 Universidade de São Paulo, São Paulo, Brazil 13 Universidad de Antioquia, Antioquia, Colombia. 14 Autonomous University of Tamaulipas, Tamaulipas, Mexico. 15 SUMPA S.A.C, Lima, Peru 16 Universidade Regional de Blumenau, Santa Catarina, Brazil. 17 Biodiversity, Macroecology and Biogeography, University of Göttingen, Göttingen, Germany. 18 University of Natural Resources and Life Sciences, Vienna, Austria. 19 El Colegio de la Frontera Sur (ECOSUR), Chiapas, Mexico. 20 Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland. 21 Centre of Biodiversity and Sustainable Land Use (CBL), University of Göttingen, Göttingen, Germany. 22 Universidad Veracruzana, Veracruz, México 23 Universidade Federal de Lavras, Lavras, Brazil. 24I nstituto de Pesquisas Jardim Botânico do Rio de Janeiro (JBRJ), Rio de Janeiro, Brazil. 25I nstituto Nacional da Mata Atlântica (INMA), Santa Teresa, Brazil. 26 Universidade de Brasilia, Brasilia, Brazil. 27 Departamento de Ecología, Museo de Historia Natural de la Universidad Nacional Mayor de San Marcos, Lima, Perú. 28 Working group Ecology, Monitoring and Sustainable Use of Wetlands (MAUA), Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil. 29 Programa de Maestría en Biología Vegetal, Universidad Autónoma de Chiriquí, David, Panama 30 Universidad del Valle, Cali, Colombia. 31 Jardín Botánico "Octavio Velarde Núñez", Universidad Nacional Agraria La Molina, Lima, Perú 32 Universidade Federal do ABC, São Paulo, Brazil 33 Gesellschaft für Internationale Zusammenarbeit (GIZ), Bonn, Germany. 34 Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, The Netherlands. 35 ForestGEO, Smithsonian Institution, Washington, DC, USA. 36 Biodiversity Research Institute (CSIC/UO/PA), Mieres, Spain.

Vascular epiphytes grow non-parasitically on other plants, mainly in tropical forest canopies, constituting about 10% of the world's vascular plant diversity and up to 39% in the Neotropics. They provide critical ecosystemic services and add complexity to forest canopies. Factors determining their distribution, including adaptations to low water availability and low temperatures, may act together. While global patterns of epiphyte richness mirror latitudinal diversity gradients, epiphyte richness decreases three times faster with increasing latitude compared to terrestrial plants, with a mid-elevation bulge observed. Despite recent global studies, regional heterogeneity's role in epiphyte diversity remains poorly understood due to predominantly local research. No comprehensive assessments of species richness and abundance exist at regional or continental scales. Understanding biodiversity mechanisms is crucial, particularly in global change scenarios. We aim to assess drivers of Neotropical epiphyte diversity using a new database encompassing data from approximately 9,000 host trees, 150,000 epiphyte individuals, and 1,500 species across 25 ecoregions. We'll evaluate elevational and latitudinal patterns using generalised additive and mixed-effect models, incorporating environmental, geographical, and historical predictors. We anticipate climatic variables related to precipitation and temperature to influence richness and abundance differently, with temperature favouring abundance and precipitation limiting richness.

P.0664 Systematics, natural history, and conservation of Erica (Ericaceae)

Michael D. Pirie[1], Anina Coetzee[2,3], Jaime Fagúndez[4,5], Félix Forest6, Seth Musker[7], E. Charles Nelson[8], Timotheus van der Niet[9], Fernando Ojeda[10]

1 University Museum, University of Bergen, Postboks Bergen, Norway. 2 FitzPatrick Institute of African Ornithology, DSI-NRF Centre of Excellence, University of Cape Town, Rondebosch, South Africa. 3 Conservation Management Department, Nelson Mandela University, George, South Africa. 4 Universidade da Coruña, BIOCOST research group, Centro Interdisciplinar de Química e Bioloxía (CICA), A Coruña, Spain. 5 Universidade da Coruña, Departamento de Bioloxía, Facultade de Ciencias, A Coruña, Spain. 6 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 7 Department of Biological Sciences, University of Cape Town, Rondebosch, South Africa. 8 Tippitiwitchet Cottage, Sutton, UK. 9 School of Life Sciences, University of KwaZulu-Natal, Scottsville, South Africa. 10 Departamento de Biología-IVAGRO, Universidad de Cádiz, Campus Río San Pedro, Spain.

Worldwide, a sobering proportion of plant species are threatened with extinction in the wild, and those that are naturally rare or have narrow distributions are particularly vulnerable. The flowering plant genus Erica is a prime example of challenges associated with conserving large, complex, plant groups, given its wide North-South disjunct distributions, and its numerous species concentrated in South Africa's spectacular Cape Floristic Region. The Erica research and conservation community is rallying to the call for a multi-disciplinary approach to these multifaceted challenges. We need to better understand, describe, and name species diversity, to enable accurate identification, and to understand the complexity of ecological interactions in the wild. We can then more effectively obtain and target funding for conservation efforts in natural habitats, and as a last resort, secure the most critically endangered species in seed banks and botanic gardens. In a topical collection of papers showcased in the Open Access journal PhytoKeys, we present a multi-disciplinary, maximally accessible resource representing the coming together of a substantial body of research on themes in nomenclature, taxonomy, phylogeny, ecology, and conservation of Erica species. As summarised in this poster, the themes are closely inter-dependent: by coordinating such an effort and ensuring that the results are maximally accessible we can provide a lasting resource and reference for future work, as well as a clear indication of where that work might lead to fill the most critical knowledge gaps. Acknowledgments: The collection will also serve to disseminate and honour the enormous contribution to Erica taxonomy of our longstanding collaborator E.G.H. (Ted) Oliver and his late wife Inge.

P.0665 Global data sources underestimate fern and lycophytes conservation priorities: The contribution of local sources of knowledge

Juan Reyes-Valentin1, Javian Gallardo-Valdivia[1], Paulette I. Naulin[1]

1 Universidad de Chile, Santiago, Chile.

Biosphere integrity recomposition is one of the main glocal challenges. The increasing functional and structural biodiversity affectation demands urgent conservation actions, which must set clear priorities for an effective conservation. Several approaches for the establishment of evidence-based conservation priorities have been created in recent years. Some of them are metrics that integrate species extinction risk and evolutionary information, through phylogenetic (*e.g.,* EDGE Index) or taxonomic data. Measurement of these metrics is sensitive to data quality, so the data source is a critical factor to consider. The study purpose was to evaluate the effect of local (LDS) and global data sources (GDS) in the establishment of species conservation priorities, using the ferns and lycophytes from Chile as study case. Species from both clades were reviewed in national catalogues and in the Catalogue of Life, along with their conservation status from the classification systems of the Chilean government department responsible for risk assessment and the International Union for the Conservation of Nature. The weighted taxonomic singularity of each species was calculated using the LDS and GDS data, to subsequently establish its conservation priority according to each of them. A total of 162 and 154 species were obtained from LDS and GDS, respectively. According to LDS, 12% of the ferns and lycophytes have a high priority and 19% a medium priority. In contrast, practically all species evaluated with GDS have a very low priority (99%). Furthermore, 20% of the species with high priority from LDS are not registered in GDS. The huge difference in species quantity in Near Threatened and Threatened categories explain the discrepancy between LDS and GDS priorities (101 and 0 respectively). The results highlight the importance of LDS for conservation priority setting. Coordination and data transfer between LDS and GDS should be strengthened to inform cross-scale conservation actions

P.0666 Investigating of the phenological growth stages in Iris hymenospatha in its natural habitat based on BBCH scale in two consecutive

Nasim Safari[1], Sajad Alipour[1]

1 Department of Horticultural Science, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, Iran.

The study of plant phenology helps to understand the plant biology, interrelationships of species, and the effect of climate change on life cycle of them. Additionally, the phenology data is used in various subjects such as agriculture, biology and botany. *Iris hymenospatha* B.Mathew & Wendelbo is one of the endangered and endemic species of Iran with ornamental and medicinal value. According to BBCH (Biologische Bundesanstalt, Bundessortenamt und CHemische Industrie) scale, from sprouting to winter rest, six main principal stages are described for sprouting, leaf development, flowering, fruit development, seed maturity and dormancy. This research was done from February 2020 to December 2022. Data on this study were collected every three days in the vegetative season and with a every thirty days during the dormant season. The results showed, sprouting was not the same in two consecutive years. In the first year, it occurred in the second decade of February, but in the second year, it happened about ten days later. In comparison to the second years, the leaves development occurred ten days earlier in the first year. In the first year, blooming occurred in the early of May but in the second year it occurred after 12 May. Also, seed maturity was recorded two weeks earlier in the first year (after middle May). The summer dormancy approximately occurred in late spring in two consecutive years. The results of t-test showed that there were significant differences in leaf number, plant height, flower length, and flower diameter in the first years in comparison with the second year ($P \leq P.5$). So, the analyses of the phenological stages of *Iris hymenospatha* provided better understanding of the climate change effect on the growth cycle of this vulnerable species and use these data for conservation projects.

P.0667 Plant Atlas 2020: Mapping changes in the distribution of the British and Irish flora

Kevin Walker[1], Pete Stroh[2], Tom Humphrey[3], Oli Pescott[4], Rich Burkmar[5]

1Botanical Society of Britain and Ireland, Harrogate, UK. 2 Botanical Society of Britain and Ireland, Cambridge University Botanic Garden, Cambridge, UK. 3 Botanical Society of Britain and Ireland, Wallingford, UK. 4 UKCEH Wallingford, Crowmarsh Gifford, UK. 5 UK Centre for Ecology & Hydrology, Bailrigg, Lancaster, UK.

In 2023 the BSBI published its third distribution atlas of the British and Irish flora based on fieldwork undertaken by almost 9,000 botanical recorders between the years 2000 and 2019. The findings were published as a two-volume book and on a dedicated website (plantatlas2020.org). The project covered around 3,500 taxa that had been recorded in the wild in Britain and Ireland; these comprised roughly equal numbers of native and non-native taxa and included many hybrids and infraspecific taxa. Species distributions were mapped as occurrence in 10 km x 10 km grid squares (hectads) and modelling to adjust for survey effort (Frescalo) was used to determine species trends over the long- and short-term (1930-2019, 1987-2019); whether increasing, stable or decreasing. Information published for each taxon included distribution maps, species captions, national status, species trends (long-and short-term), conservation status, phenology (leaf and flowering), altitudinal range and key references. The trend analysis identified over 50% of native species as having declined since the first atlas was published in 1962. The project was an outstanding success and the data produced will provide a vital evidence-base for conservation and research in the years ahead. The Atlas is perhaps unique in Europe, even world-wide in the detail and amount of information provided.

P.0668 Conservation challenges and priorities for Rafflesia species (Rafflesiaceae) in the Philippines

Adriane B. Tobias[1,2], Pastor L. Malabrigo Jr.[2,3,4], Lerma SJ. Maldia[2,5], Inocencio E. Buot Jr.[6], Chris Thorogood[7,8]

1 Graduate School, University of the Philippines Los Baños, Philippines. 2 Department of Forest Biological Sciences, University of the Philippines Los Baños, Philippines. 3 Museum of Natural History, University of the Philippines Los Baños, Philippines. 4 Land Grant Management Office, University of the Philippines Los Baños, Philippines. 5 Makiling Center for Mountain Ecosystems, University of the Philippines Los Baños, Philippines. 6 Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños, Philippines. 7 University of Oxford Botanic Garden, Rose Lane, Oxford, UK. 8 University of Oxford Department of Plant Sciences, Oxford, UK.

This paper presents the outcomes of a comprehensive study aimed at understanding the taxonomy, distribution, and conservation status of *Rafflesia* species in the Philippines. Through meticulous taxonomic review, field surveys, and data compilation, 16 *Rafflesia* species have been identified in the country, with the addition of a newly discovered species, *R. balatociana*. The IUCN Categories and Criteria assessment categorizes ten species as Critically Endangered, five as Endangered, and one as Vulnerable, emphasizing the urgent need for conservation actions. The study highlights various threats faced by *Rafflesia*, including deforestation driven by commodities, shifting agriculture, urbanization, illegal forest harvesting, and plantation establishment. Alarmingly, half of the recorded *Rafflesia* sites are located outside designated protected areas, underscoring the necessity for conservation efforts beyond protected areas. Even within protected areas, *Rafflesia* species face habitat degradation and tree cover loss. To ensure the sustainable conservation of these unique species, urgent actions are recommended to address the drivers of habitat loss, promote sustainable land-use practices, and establish more protected areas. Effective monitoring and collaboration among local communities, government agencies, and conservation organizations are vital for achieving positive conservation outcomes. Furthermore, strengthening legal frameworks and enforcement, habitat restoration efforts, regular monitoring, and raising awareness are identified as essential steps towards the recovery of *Rafflesia* species in the Philippines.

P.0669 An updated DNA barcoding tool for Aloe vera and CITES-restricted relatives

Yannick Woudstra[1,2], Paul Rees[1], Solofo Rakotoarisoa[3], Nina Rønsted[2,4], Caroline Howard[5], Olwen M. Grace[1]

1 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 2 Natural History Museum of Denmark, University of Copenhagen, Copenhagen, Denmark. 3 Royal Botanic Gardens, Kew, Kew, Madagascar Conservation Centre, Antananarivo, Madagascar. 4 National Tropical Botanic Garden, Kalaheo, Hawai'i, United States of America. 5 Wellcome Sanger Institute, Cambridge, United Kingdom.

DNA barcoding has revolutionised the identification of illegally traded material of endangered species as it overcomes the lack of resolution encountered with morphological identification. Unfortunately, in some recently evolved and highly diverse plant groups, such as the relatives of *Aloe vera*, the lack of interspecific sequence variation obtained with standardised markers compromises its efficacy. Here we present a new DNA barcoding tool using 189 nuclear markers, optimised for aloes (Asphodelaceae, Alooideae). We built a comprehensive sequence reference dataset from taxonomically verified source material covering >300 species of aloes, and validated this for identification through phylogenomic inference with anonymised samples. Ten CITES-regulated plants seized at London Heathrow Airport were subsequently identified to species level, including a critically endangered *Aloe* species from Madagascar. Other samples purchased commercially were confirmed to be the species they were advertised as. An accurate, reliable DNA barcoding method for aloe identification introduces new assurance to regulatory processes for valuable plants in trade.

S.076. GLOBAL MYRTACEAE SYSTEMATICS: PURE AND APPLIED PERSPECTIVES FOR MANAGING AND CONSERVING THE EARTH'S PLANT DIVERSITY

P.0670 Development of SSR markers for rare and endangered Myrtaceae species from the Brazilian Atlantic Forest

Ana Flávia Augustin[1,4,*], Duane F. Lima[1], Roberta Gargiulo[2], Valdir M. Stefenon[1], Fábio C. S. Vieira[3], Mayara Krasinki Caddah[1]

*1 Federal University of Santa Catarina, Florianopolis, Santa Catarina, Brazil. 2 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 3 University of Sao Paulo, Sao Paulo, Sao Paulo, Brazil. 4. *afaugustin@gmail.com.*

Understanding genetic diversity, especially in rare and/or threatened species, is extremely important for their long-term conservation. Microsatellite markers (or Simple Sequence Repeats – SSRs markers) have become an important tool in this kind of studies, as they are highly polymorphic, distributed throughout the genome and codominant, allowing to identify hetero- and homozygotes. Within the context of rare species, two recently described taxa of the Myrtaceae family were selected for this study: *Myrceugenia basicordata* F.C.S. Vieira, Molz & Sobral, and *Myrceugenia joinvillensis* F.C.S Vieira. Both of them are endemic to the southern Brazilian Atlantic Forest, occuring in regions close to major urban centers, with limited available biological information. Our objective was to describe genetic diversity in these two species by developing molecular SSRs markers, to support future studies in conservation genetics. To achieve this, individuals from all eight known populations of both species were collected. One individual of each species was sequenced through the Illumina platform. The search for SSR markers was conducted using specific software programmes, and the validation of the markers was performed in two stages: in a virtual environment and in laboratory. The sequencing resulted in 11,026,738 reads for *M. basicordata* and 15,862,298 for *M. joinvillensis,* with an average length of 100 base pairs per read. The search for SSR regions resulted in 184 *loci* for *M. basicordata* and 218 for *M. joinvillensis*. A total of 20 markers for each species were pre-selected *in silico*, most of them of di-, tri-, and pentanucleotides; 12 of which showed good amplification patterns in laboratory. This is the first SSR-focused work on *Myrceugenia* species. It is an important initial step for future population genetic characterization studies that will generate data that can be used in the long-term conservation of these and other species of the genera.

P.0671 Elucidating the origin and function of seminal structures in the polyploid specie Psidium cattleyanum Sabine (Myrteae, Myrtaceae)

Claudia Da Luz-Graña[1], Magdalena Vaio[1], Gabriela Speroni[1]

1 Departamento de Biología Vegetal, Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay.

A sexual or asexual (apomictic) seed is a mature ovule with seed-coat, nutritive tissue, and embryo. Embryo shape and seed-coat consistency have been used in taxonomic classifications of Myrtaceae. The few studies on Psidium cattleyanum have been carried out on mature seed, where the origin of each structure is not known. An ontogenetic analysis generates information that might contribute to the phylogeny of the family. The goal of this work is to describe the stages of the ontogenetic development of the embryo, endosperm, nucellus and seed coat in seeds produced by heptaploid plants of P. cattleyanum f. cattleyanum and octoploid plants of P. cattleyanum f. cattleyanum, to establish the origin of the seminal structures described at maturity for the species and to contribute to the taxonomic knowledge and reproductive biology of the species. Developing seeds, obtained from directed crosses between two octoploid and two heptaploid accessions of P. cattleyanum, were collected at 22, 29, 36, 43, 50, 57, and 67 days post-pollination. They were fixed in FAA and processed by the paraffin embedding technique. The seeds adopt a campylotropic form, with a 'C'-shaped interior. The embryo follows a globular, cordiform and torpedo-shaped development, to finally curve the hypocotyl-radicle axis and adopt a 'C' shape. The cotyledons, at maturity, are well developed and lie on the hypocotyl-radicle axis. The nucellus forms a hypostase and the nuclear endosperm persists in the mature seed. The seminal cover is formed by the external integument, which sarcotestal epidermis and mesotegument lignificated. The micropyle is surrounded by an operculum The seeds of P. cattleyanum are of the mesotestal-seed type, they present sarcotesta, hypostase, operculum and endosperm.

P.0672 Redescription and extinction risk reassessment of Plinia renatiana (Myrtaceae)

Heitor Lisboa da Fonseca[1], Amélia Carlos Tuler[2], Patricia da Rosa[3], Joelcio Freitas[4], Elton J. de Lírio[1]

1 Universidade de São Paulo, São Paulo, Brazil. 2 Universidade Federal de Roraima, Boa Vista, Roraima, Brazil. 3 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 4 Instituto Nacional da Mata Atlântica, Santa Teresa, Brazil.

Plinia renatiana is a species endemic to the state of Espírito Santo (ES) and has been assessed as endangered (EN). The species was described in the 1990s based on two samples from the municipality of Linhares, ES. Subsequently, other materials were identified as belonging to the species. However, this set of materials exhibits heterogeneous morphology, which raises doubts about the correct application of the name. Issues related to the taxon's circumscription and the need to reevaluate its conservation status in light of new data have been identified. Therefore, it was necessary to expand the species description by incorporating new field-collected data and analyzing a greater number of herbarium specimens. A comprehensive survey of all herbarium specimens of the species available in databases and in the herbaria RB, ESA, SP, CVRD, MBML, and SPF was conducted and the literature was reviewed. Field expeditions were also carried out in two subpopulations of the species. Based on the collected data, we have expanded the morphological description of species and reassessed its risk of extinction following IUCN guidelines. The redescription of *P. renatiana* provides more details about its morphology, contributing to more accurate identifications facilitating new records, and promoting new studies in the area. In addition to the morphological description, taxonomic comments, phenology, a distribution map, photographs, and illustrations are provided. In our reassessment, the species was categorized as EN (A2c; B1(i,iii,v) + 2ab(ii,iii,v)), with changes to the criteria used in the 2012 assessment, presenting three subpopulations in a fragmented population. Despite the review and inclusion of new data, the species has remained in the same threat category in which it was assessed more than a decade ago, underscoring the need for conservation efforts.

P.0673 Morphological diversity in Eugenia sect. Eugenia (Myrteae, Myrtaceae): approach to leaf venation patterns and floral colleters

Fiorella F. Mazine[1], Everton D. C. da Silva[1], Vinicius L. Denardi[1], Natália F. Mazzaro[1], Mariana A. B. da Silva[1], Adriano Maruyama[1], Mario Tommasiello[2], Karinne S. Valdemarin[2]

1 Universidade Federal de São Carlos, Sorocaba, Brazil. 2 Escola Superior de Agricultura "Luiz de Queiroz", Universidade de São Paulo, Piracicaba, Brazil.

With more than 1,100 species, *Eugenia* is one of the largest genera in angiosperms and currently circumscribes 11 sections. *Eugenia* sect. *Eugenia* encompasses 41 species, with Brazil recognized as the center of diversity of this section, with greater species diversity in the Atlantic Forest. *Eugenia uniflora* L. (popularly known as 'pitanga') is one of the species of this section. The species in this group stand out for the presence of long calyx lobes, leafy bracts (cataphylls) at the base of the racemes and pedicels and the central axis of the inflorescence that recovers vegetative development, a characteristic known as auxotelic inflorescence. Due to the remarkable uniformity in their morphology, the taxonomic analysis of this group faces considerable difficulties. The present study aimed to present a morphological characterization of the species of *E.* sect. *Eugenia* contemplating: 1) leaf venation patterns, 2) characterization of floral buds, and 3) characterization of colleters in floral parts. All data were obtained from herbaria specimens; the veins were analyzed using 2D X-ray images and the other structures with the naked eye or stereomicroscope. This study included an analysis of 31 species of the section. Regarding leaf venation, the results indicated a definition for 1st order leaf vein. This vein exhibited a variation in its course, varying between monopodial (in which the path is straight and does not undergo significant changes after the emergence of the secondary vein) and sympodial (characterized by the deviation caused by the divergence of the secondary vein). This distinction represented a useful attribute for categorizing species within the section. For the floral parts, the buds of all species of *E.* sect. *Eugenia* exhibited a partial fusion of the calyx lobes in the flower bud, pairs of sepals of equal size, and the presence of colleters in all reproductive structures. CAPES, CNPq, FAPESP.

P.0674 Taxonomic study of the widespread and very variable Eugenia punificifolia (Myrtaceae)

Janine D.O. Melo[1], Eve J. Lucas[2], Augusto G. de Oliveira[3], Nádia Roque[4]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Royal Botanic Gardens Kew, Richmond, UK. 3 Universidade Federal da Grande Dourados, Dourados, Brazil. 4 Universidade Federal da Bahia, Salvador, Brazil.

Eugenia P.Micheli ex L. (Myrtaceae), comprising ca. 1.200 species and with a Pantropical distribution, is the world's second largest genus in number of arboreal species. *Eugenia* is a taxonomically complex group due to the high morphological homogeneity between its species, leading to common misidentification throughout its history. *Eugenia* is subdivided into 11 sections, with exclusively Neotropical *Eugenia* sect. *Umbellatae* O.Berg being the most challenging, with ca. 600 species. The section is characterized by non-showy flowers and inflorescences fasciculate, glomerulous or umbellate, or short racemes. *Eugenia punicifolia* (Kunth) DC. has wide distribution (Cuba and North South America to Argentina) and broad morphological variation that is represented by 100 synonyms resulted from the publication of 'new species' usually based on morphological extremes. Until now, no detailed systematic study of *E. punicifolia* has been undertaken; this study addresses that gap. Synonyms and protologues of *E. punicifolia* were collated from literature and online platforms (Plants Of The World Online and Tropicos) and 33 nomenclatural types were analysed in person, the remaining were analysed from images accessible at Jstor, SpeciesLink and the Reflora Virtual Herbarium. All available specimens were used to collect comprehensive morphological and distribution datasets. As a result, 18 morphotypes were identified in *E. punicifolia*, these are geographically representative of the species and encompass variations in leaf shape (obovate, oblanceolate, oblong or elliptic), inflorescence architecture (solitary flowers, fascicle or short raceme), number of flowers per axil (2-6), floral bud and flower size, pedicel length and presence or absence of indumentum on leaves, hypanthium, sepals and staminal ring. Nomenclatural studies reveal that ca. 70 lectotypifications are required. Future steps will include a comparison of this baseline data with a phylogenomic hypothesis based on A353 targeted sequencing and ultimately an approach integrating macroecological considerations will likely be needed to separate taxonomically meaningful entities

S.077. GRAPEVINES (VITIS SPP.): A MODEL FOR MULTIDISCIPLINARY APPROACHES TO CONSERVING AND USING CROP WILD RELATIVES

P.0675 Bioclimatic characterization of Spanish heroic viticulture

Aitor Álvarez-Santacoloma[1], Giovanni Breogán Ferreiro-Lera[1], Ángel Penas[1] ,Sara del Río González[2]

1 University of Leon, León, Spain. 2 University of Leon, Mountain Livestock Institute CSIC-UNILEON, León, Spain.

The title of heroic viticulture was proposed in 1987, at which time the Center for Research, Safeguarding, Coordination and Valuation of Mountain Viticulture (CERVIM) was established, with the aim of preserving and promoting the traditional viticulture that is carried out in places whose orographic conditions cannot enable the mechanization of vineyard work. This organization has implemented a quality seal that certifies production from vines located in areas with tall slopes, therefore crops in terraces, as well as high landscape value. In Spain, there are five Protected Denominations of Origin (DOP), which are: Arribes del Duero, Canarias, Priorat, Ribeira Sacra and Vinos de Cangas. Using the bioclimatic classification system proposed by Rivas-Martínez *et al.* (2011), and other variables traditionally used in viticulture, the qualitative and quantitative bioclimatic characterization of the Spanish DOPs that have the heroic viticulture certification was carried out. For this, the CHELSA v.2.1 climate database was used for the period 1980-2018. The geographical information system (GIS) software ArcGIS Pro v.3.1.0, was used for the computation of the different bioclimatic parameters and indexes. Continentality Index, Annual Ombrothermic Index and Compensated Thermicity Index were selected as key bioclimatic predictors for vineyard characterization, in addition to others traditionally used. Therefore, the method proposed by Rivas-Martínez *et al.*, substantiated on the distribution of natural vegetation, can be applied in agronomic studies. The statistical analysis has been done using the IBM SPSS Statistics and RStudio software. The mean, maximum and minimum values were calculated for each of the analyzed environmental factors, as well as the interquartile range. Thus, allowing the definition of the suitable and optimal ranges for the survival of the vines in each of the denominations of origin was studied. References: Rivas-Martínez, S., Rivas, S. & Penas, A. (2011) "Worldwide bioclimatic classification system", *Global Geobotany*, 1(1), pp. 1-638.

P.0676 First genetic reserves of crop wild relatives in Spain

Elena Torres[1], Ada Molina[2], José M. Iriondo[2]

1 Dpto. Biotecnología-Biología Vegetal, Universidad Politécnica de Madrid, Spain. 2 Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, Spain.

Natural populations of crops and their wild relatives are a source of genetic diversity for plant breeders, whose main challenge is to develop varieties adapted to new scenarios resulting from climate change. Consequently, the conservation of these crop wild relatives (CWR) is of great importance for future food security, particularly in areas where they have developed unique properties. In this context, a pioneering pilot project in Spain led to the establishment of six genetic reserves in Sierra del Rincón Biosphere Reserve. Over three years, several activities were undertaken: 1) identification of priority CWR from the floristic inventory of the biosphere reserve; 2) localization of high CWR species richness spots in both public areas and fields managed by farmers; 3) census and habitat characterization of target populations; 4) interviews to understand the land uses and agricultural practices; 5) collection and *ex situ* conservation of seeds; 6) training for professionals working in the territory; and 7) communication and citizen participation. As a result, the selected areas, which include a livestock trail, a public-private educational farm, and four private farms, cover an area of 6.9 ha and provide habitat for 38 CWR populations. The main risks identified are related to changes in land use or management, such as an increase of the livestock load or cultivated area, mowing before seed dispersal, land abandonment, etc. Based on the information gathered, a management plan was prepared for each genetic reserve in collaboration with the land managers. These plans, which are the guidelines for the long-term conservation of the populations, will be reviewed every five years at the time of the monitoring of the genetic reserves. Providing continued technical support to participants is also an important task. Taking this project as a model, five additional genetic reserves are currently in progress in Salamanca, León, and Cáceres.

P.0677 The official strategy of Spain for the conservation and use of crop wild relatives

Elena Torres[1], Ada Molina[2], María Luisa Rubio Teso[2], Clara Álvarez Muñiz[2], Lucía de la Rosa[3], Esther Pajares[4], Javier Tardío[5], Luis Guasch[3], José M. Iriondo[2]

1 Dpto. Biotecnología-Biología Vegetal, Universidad Politécnica de Madrid, Madrid, Spain. 2 Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, Móstoles, Spain. 3 Centro de Recursos Fitogenéticos y Agricultura Sostenible, Alcalá de Henares, Spain. 4 Subdirección General de Medios de Producción Agrícola y Oficina Española de Variedades Vegetales, Madrid, Spain. 5 Instituto Madrileño de Investigación y Desarrollo Rural, Agrario y Alimentario, Alcalá de Henares, Spain.

Crop wild relatives (CWR), which include crop ancestors and other closely related species, have been specifically targeted for conservation both by the Convention on Biological Diversity (Aichi Target 13) and the Sustainable Development Goals (SDG Target 2.5). Compared with commercial cultivars, CWR have faced natural challenges for thousands of years and maintain a much higher level of genetic diversity. Thus, they can be used as a source of genes to improve crop adaptability in the current context of climate change. Given the importance of CWR for food security and sustainable agriculture, the Spanish Ministry of Agriculture approved a national strategy in 2022 to preserve this group of plants and promote their use in breeding programs. The strategy includes 42 actions to address six targets: 1) Enhance the knowledge of the prioritized species to support conservation decisions and promote their use; 2) Establish an efficient network of genetic reserves with active management guidelines; 3) Improve the representativeness of CWR in germplasm banks; 4) Identify useful genetic variation and make it available for breeding programs, considering the access and benefit-sharing; 5) Integrate the strategy into the policies of different sectors across all levels of government; 6) Provide training to professionals working in conservation and farmers so they can manage the genetic reserves themselves, and raise awareness among the public. The strategy adopts two different approaches: one focuses on a specific geographical area and the CWR conserved within its boundaries, while the other concentrates on the CWR of a particular crop. To measure progress, 76 indicators have been defined. Furthermore, an official checklist of priority CWR and wild food plants has been generated. The list contains 521 species that can contribute desirable genetic traits to 141 crops (including food, forage, industrial and ornamental crops) or have the potential to be cultivated for food.

P.0678 First steps in the implementation of the Spanish strategy for conservation and use of crop wild relatives and wild food plants

Elena Torres[1], María Luisa Rubio Teso[2], Carlos Lara-Romero[2], Dolores Cuadra[2], Ada Molina[2], José M. Iriondo[2]

1 Dpto. Biotecnología-Biología Vegetal, Universidad Politécnica de Madrid, Madrid, Spain. 2 Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, Móstoles, Spain.

Given the importance of crop wild relatives and wild food plants (CWR/WFP) for food security, in 2022, the Spanish Ministry of Agriculture approved a national strategy to conserve them and promote their use in breeding programs. In this context, we present the priority actions for the period 2023-2026 and the first results of their implementation. To improve the knowledge of the 521 target species, occurrence data from GBIF and other sources were integrated into a database containing over 1.8 million records. The resulting chorological maps were used to estimate the coverage of the Natura 2000 network and other protected areas for CWR/WFP. The gap analysis results show that most species (421) have between 75% and 100% of their ecogeographical variability represented in protected areas. Additionally, the Natura 2000 network provides semi-active protection for 47 CWR/WFP as they are characteristic species of habitats listed in Annex I of the Habitats Directive. Importantly, only 11 of the 57 legally protected CWR/WFP species have recovery or conservation plans in place. Based on these data and applying complementary algorithms, 40 hotspots will be selected as potential sites for the establishment of genetic reserves (10 of which will be visited to confirm their suitability). A similar analysis will be carried out to assess the ecogeographical representativeness of CWR/WFP in germplasm banks, and to identify priority sites for seed collection. Also, information on the biology, ecology, vulnerability to climate change and traits of interest to plant breeders will be compiled in a database for each species. The database is already designed according to FAIR principles. The remaining actions focus on defining the minimum requirements for a site to be designated as a genetic reserve, developing an official register of genetic reserves, and providing guidelines for farmers and environmental technicians on how to manage and monitor CWR/WFP.

S.078. GRASSROOTS MULTIDISCIPLINARY AND INTEGRATIVE RESEARCH ON THE GLOBAL DIVERSITY OF THE GRASSES (POACEAE)

P.0679 Investigating the genetic diversity in two species of Avena from the cereal family in Iran

Zahra Aghajani[1], Maryam Keshavarzi[1], Samaneh Mosaferi[1]

Department of Plant Ecology and Systematics, Al-Zahra university of Tehran, Iran.

Avena sometimes called the common oat, are annual plants that have been cultivated and consumed as human and animal food sources for thousands of years. There are 27 species of Avena around the world 7 of which are found in Iran. The dispersal of this genus extends throughout Europe, Asia, and northwest Africa. In this study, we examined different populations of *A. fatua* and *A. sterilis* from Iran. These two species show great similarities, based on previous experiments and morphological studies. Therefore, molecular and genetic analysis can be very effective in distinguishing between these two species. In this research, we examined these two species by applying 10 ISSR molecular markers. We administered the CTAB method for DNA extraction and multiple software including DARwin, GenAlex, PAST, POPGene, and STRUCTURE for statistical analysis. AMOVA test showed high genetic diversity within the studied populations, indicating that 22% of the genetic diversity is interspecific and 78% is intraspecific. Mantel test discloses a direct correlation between geographic distance and genetic distance, where genetic distance increases along with geographic distance. Based on the Nm value obtained in this study (Nm: 0.1117), gene flow between species is very low. *A. fatua* and *A. sterilis* showed relatively high genetic similarity and are located near each other. Such studies on these two species were conducted for the first time in Iran.

P.0680 Multidisciplinary reconstruction of the evolution and systematics rearrangement of Heteropogon and Themeda (Andropogoneae)

Watchara Arthan1, Elizabeth A. Kellogg[2], Caroline E. R. Lehmann[3, 4], Jonathan Mitchley[5], Maria S. Vorontsova[6]

1 Department of Pharmaceutical Botany, Faculty of Pharmacy, Mahidol University, Bangkok, Thailand. 2 Donald Danforth Plant Science Center, St. Louis, USA. 3 Tropical Diversity, Royal Botanic Garden Edinburgh, Edinburgh, UK. 4 School of Geo-

sciences, University of Edinburgh, Edinburgh, UK. 5 School of Biological Sciences, University of Reading, Whiteknights, Reading, UK. 6 Accelerated Taxonomy, Royal Botanic Gardens, Kew, Richmond, UK.

Grasses in the genera *Heteropogon* and *Themeda* make a significant contribution to the world's C_4tropical grassy biomes. Phylogenomic analysis reveals non-monophyly of both *Heteropogon* and *Themeda*. *Heteropogon melanocarpus* and *H. ritchiei* form a clade with *Themeda* and the remaining *Heteropogon* species are placed outside this clade. Discordant phylogenetic positions suggest possible hybridization history in *H. contortus*, *H. triticeus*, and *T. triandra*. These phylogenetic relationships reflect evolutionary histories shaped by associations between climatic niches and morphological traits. Pantropical *H. contortus* and *H. fischerianus* populations are grouped in a single clade that encompasses diverse morphotypes characterized by distinct leaf shape, indumentum, and awn length. Such morphological plasticity may facilitate adaptations to low or high precipitation and seasonality regimes. The *Themeda triandra* clade includes two morphologically distinct species *T. quadrivalvis* and *T. unica*, suggesting an ongoing speciation process and diverse morphology in a single species adapting to different climatic regimes. A biome shift from savannas to wetlands is associated with the origin of the Southeast Asian *Themeda* clade which developed greater culm height, leaf size and straight awns absent from savanna counterparts outside this clade. Ecological analysis supports quantitative characters such as culm height, awn type, and awn length as meaningful for species classification. Morphological diversity in inflorescence branching patterns, fertile spikelet arrangement, and indumentum also effectively delimit species. Better understanding of the phylogenetic relationships and the related morphology enables us to update the classification. The circumscription of *Themeda* is broadened to include *H. melanocarpus* and *H. ritchiei*, and *Heteropogon* encompasses the remaining *Heteropogon* species. Numerous homogamous and fertile spikelets delimit *Heteropogon* while these are reduced to 2-4 pairs in *Themeda*. This study highlights multidisciplinary integrative approaches that can be applied to other to use the evolutionary and ecological history to improve classifications.

P.0681 Generic delimitation of Oropetium (Poaceae) based on molecular phylogeny and its biogeography

Alok R. Chorghe[1], S. Surveswaran[2], R. N. Kulloli[3]

1 Regional Museum of Natural History, Gangtok, Sikkim, India. 2 School of Life Science, University of Hyderabad, Hyderabad, Telangana, India. 3 Central Arid Zone Research Institute, Jodhpur, Rajasthan, India.

An interesting study on the phylogeny of resurrection Oropetium grasses using barcoding loci and on the correlation of species distribution models and functional traits in desert to dry and tropical African and Asian biomes.

P.0682 Plagiarism in the Poaceae: the role of lateral gene transfer in grass evolution

Catherine Collins[1], Lara Pereira[1], Luke T. Dunning[1]

1 Ecology and Evolutionary Biology, School of Biosciences, University of Sheffield, Sheffield, UK.

Lateral gene transfer (LGT) has been reported in multiple eukaryotes. This process seems particularly widespread amongst grasses where the transfer of large DNA fragments has been shown to spread functional genes across the family, in wild and crop species alike. However, we know very little about the underlying dynamics. Using multiple reference genomes within the grass *Alloteropsis semialata* we show that the rate of LGT varies among lineages, and that LGTs are more likely to appear as accessory genes in a species pan-genome than those vertically inherited. By comparing expression patterns between the donor and recipient species, it also appears that trans-regulated genes are more likely to be retained post transfer than those that are cis-regulated. Finally, we also propose that 'reproductive contamination' is the underlying mechanism behind these transfers. Ultimately, the sharing of adaptive genetic material within grasses has the potential to accelerate adaptation and drive evolutionary shifts in this globally important group of plants.

P.0683 The DNA barcoding of the genus Festuca L. in Turkey

Jelena Erdal[1], Gencer Yaprak[1,2], Esra Mine Ünal[3,4], Emre Keskin[3, 4]

1 Department of Biological Sciences, Middle East Technical University, Ankara, Turkey. 2 Nature Conservation Centre, Ankara, Turkey. 3 Evolutionary Genetics Laboratory, Ankara University, Ankara, Turkey. 4 AgriGenomics Hub, Animal and Plant Research Innovation Center, Ankara, Turkey.

A DNA barcoding analysis was conducted on the genus *Festuca* L. in Turkey as part of a comprehensive review of the genus in the same region. Following extensive field surveys and sampling, along with detailed morphological, micromorphological, anatomical and ecological analyses, a total of 75 fescue specimens were chosen. These specimens included representatives of known fescue taxa, new records for Turkey, and several specimens from populations that exhibited notable distinctions from recognized fescue species. These distinctions potentially suggest the presence of new taxa. The technique of DNA barcoding has been employed to genetically analyze the distribution of the genus *Festuca* L. in Turkey. rbcL loci present in the chloroplast DNA were amplified from genomic DNA samples extracted from tissue samples of fescue specimens and examined to determine the effectiveness of DNA sequences in identifying species. The phylogeographic relationship was determined by calculating the distance between populations and comparing them with specimens from different countries and populations. The study also examined the effectiveness of DNA barcoding in detecting intra-genetic differences within the species. These differences were then utilized to create evolutionary relationship trees and median joining networks. Our expectations are that the results of this study will help in resolving taxonomic problems and obtaining a contemporary systematic account of the genus *Festuca* L. in Turkey, based on the integrative approaches. Besides, we hope that our data will be a humble contribution to the global genetic sequence databases and future phylogenetic studies regarding both fescues and grasses in general.

P.0684 Novelties in the genus Festuca L. (Poaceae) in Turkey

Jelena Erdal[1], Gencer Yaprak[1,2], Musa Doğan[1]

1 Department of Biological Sciences, Middle East Technical University, Ankara, Turkey. 2 Nature Conservation Centre, Ankara, Turkey.

We present preliminary results of the ongoing revisional study of the genus *Festuca* L. in Turkey. Over the past five years, extensive field surveys have been conducted across the country, with an aim to detect, collect, and examine all known and potentially new fescue taxa. The comprehensive collection of approximately 2500 specimens that reflects the diversity and variability of fescues from various regions of Turkey has been established. Analyses of the assembled material and herbarium collections have been performed using morphological, micromorphological, anatomical, and ecological methods. Phylogenetic analyses are also in progress. In Turkey, we currently recognize the genus *Festuca* L. sensu lato, comprising four subgenera, five sections and 59 taxa (47 species, nine subspecies and three varieties). The preliminary fescue checklist in Turkey includes three new taxa, *Festuca timoniona* J.Erdal, G.Yaprak and M.Doğan, *Festuca woronowii* subsp. *rizensis* J.Erdal, G.Yaprak and M.Doğan, and *Festuca adanensis* var. *alexandretta* J.Erdal, G.Yaprak and M.Doğan and two new records, *Festuca pseudodalmatica* Krajina and *Festuca rupicola* Heuff. The nomenclature statuses of two taxa have been changed as *Festuca pseudorivularis* (Markgr.-Dann. ex H.Scholz) J.Erdal, G.Yaprak and M.Doğan and *Festuca uluana* (Markgr.-Dann.) J. Erdal, G. Yaprak and M. Doğan. The presence of the two species *Festuca sommieri* Litard. and *Festuca ziganensis* Markgr.-Dann. is now considered doubtful, while *Festuca decolorata* Markgr.-Dann. has been rediscovered and neotypified. We anticipate that the number of fescue taxa in Turkey will increase further as integrative approaches yield new findings. Eventually, we aim to provide a contemporary systematic account of *Festuca* L. in Turkey and suggest conservation measures for threatened taxa. Furthermore, we expect that this study will contribute to the understanding of fescues diversity in Turkey and set the foundation for future botanical research and conservation efforts.

P.0685 Conservation status of populations of the endangered F. vasconcensis subsp. actiophyta (M.I. Gut.) Mart.-Sagarra & Devesa (Poaceae)

Eva Martínez-Veiga[1], Iván Rodríguez-Buján[2], Manuel Pimentel Pereira [1], Elvira Sahuquillo Balbuena[1]

1 Universidade da Coruña, Grupo de Investigación de biología evolutiva, Facultade de Ciencias, A Coruña, Spain. 2 Universidade da Coruña, BIOCOST research group, Centro Interdisciplinar de Química e Bioloxía, A Coruña, Spain.

Festuca vasconcesis (Markgr.-Dann) Auquier subsp. *actiophyta* (M.I. Gut.) Mart.-Sagarra & Devesa (Poaceae) grows exclusively on ultrabasic rocky outcrops in the north-west of the Iberian Peninsula. Its limited range, the specificity of its habitat and the pressures and threats to its populations have led to it being declared as vulnerable species. This entails an obligation to regularly monitor the conservation status of its populations. This study presents the results of the most recent census and compares them with previous ones in order to understand the impact of land use changes on this vulnerable taxon. Several problems were identified during the survey: First, being a caespitose plant, it was very difficult to determine what was an individual, so the number of panicles was used to assess the number of specimens. Tussocks were also considered in some populations in order to calibrate an alternative method of counting. Other problems were the definition of the size of the sampling area to be used during fieldwork and the determination of the right survey period. Forty-one 1x1km grids were surveyed during the peak flowering period (June-August 2023), the most appropriate time to detect the presence of the species. The comparison with previous data reveals the impact of using different methodologies in the final results, and it stresses the need to standardise the protocol for working with caespitose endangered species.

P.0686 Festuca sect. Eskia under the scope: phylogeny of fine-leaved Loliinae (Poaceae) with focus on south-eastern European taxa

Ivana Rešetnik[1], Maja Mucko[1], Dmitar Lakušić[2], Sandro Bogdanović[3], Marko Doboš[4], Ivica Ljubičić[3], Nevena Kuzmanović[2], Božo Frajman[5]

1 Faculty of Science, University of Zagreb, Zagreb, Croatia. 2 Institute of Botany and Botanical Garden, Faculty of Biology, University of Belgrade, Belgrade, Serbia. 3 Faculty of Agriculture, University of Zagreb, Zagreb, Croatia. 4 Papuk Nature Park, Velika, Croatia. 5 Department of Botany, University of Innsbruck, Innsbruck, Austria.

Grasslands, encompassing roughly 30% of the Earth's land area, play a pivotal role in biodiversity serving as vital ecosystems for numerous plants and animals. One of the largest globally distributed genera dominating various types of grasslands is *Festuca* (Loliinae, Poaceae). Recent phylogenetic studies revealed two main evolutionary lineages within *Festuca*, corresponding to broad-leaved and fine-leaved species. Within fine-leaved fescues, the earliest diverging groups included species of the Euroasian *F.* sect. *Eskia* and *F.* sect. *Dimorphae*, collectively named the Eskia-Dimorpha Group, comprising 34 species. These species often coexist in sympatry, sharing morphological similarities that pose challenges for taxonomic classification due to frequent interspecific hybridization and polyploidization events. In this study, we inferred phylogenetic relationships using nuclear ITS and plastid *trnT–trnF* regions of 157 taxa, encompassing the systematic diversity of Loliinae, with a specific focus on elucidating interspecific relationships within the Eskia-Dimorpha Group. Additionally, we investigated the incidence of polyploidy and inferred relative genome size variation and its evolutionary dynamics within *F.* sect. *Eskia*. Our findings support the early sequential divergence of Eskia-Dimorpha Group lineages within fine-leaved Loliinae, revealing several well-supported and geographically segregated groups of species from the Alps, the Pyrenees or the Balkan Peninsula. We uncovered instances of phylogenetic incongruence, notably pronounced among Balkan species, suggesting complex evolutionary processes at play. This study revealed for the first time the presence of tetraploid and hexaploid cytotypes within *F*. sect. *Eskia* on the Balkan Peninsula, with tetraploids restricted to the southern Dinaric and adjacent north Scardo–Pindic ranges, and hexaploids found only on Mt Pirin (Bulgaria). Overall, our study underscores the intricate evolutionary history and differentiation of species within the Eskia-Dimorpha Group, emphasizing the need for further research to refine phylogenetic hypotheses and taxonomic circumscriptions, thereby enhancing our understanding of grassland biodiversity and evolution.

P.0687 Are annuality and C4 photosynthesis jointly beneficial or independent strategies for grasses in hot, dry climates?

Laura Schat[1], Siri Fjellheim[2], Aelys M. Humphreys[1]

1 Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden. 2 Department of Plant Sciences, Norwegian University of Life Sciences, Ås, Norway.

An annual life history and C4 photosynthesis are both common strategies in hot, dry climates. Annual plants avoid the hottest, driest periods by staying dormant as seeds, and C4 photosynthesis is most effective in climates with drought and high temperatures. Both of these traits have been linked to (sub)tropical and Mediterranean climates, and C4 photosynthesis has been linked to transitions to open habitats. Around half of all known C4 species are grasses (Poaceae), and C4 species account for 42% of the circa 11,000 grass species. Overall, ca. 17% of Poaceae are annuals but their distribution differs among subfamilies: the largest subfamilies in the PACMAD clade (both C3 and C4) comprise around a third annual species (Micrairoideae, 32%; Panicoideae, 29%; and Chloridoideae, 26%), compared to only 11% in the largest subfamily (Pooideae) in the BOP clade (exclusively C3). This suggests that there are more annuals in C4 than in C3 lineages. Both annuality and C4 photosynthesis have evolved multiple times within the grasses; however, it is unclear whether the two traits evolve independently and represent alternative strategies, or are jointly favoured, in warm, dry climates. The two traits also co-occur in the Amaranthaceae (s.l.). However, there are probably not more C4 than C3 annuals in the amaranths and C3/C4 transitions happen at the same rate in both annual and perennial lineages. An equivalent analysis for the grasses is lacking. Here, we use comparative methods to test for correlated evolution between life history and photosynthesis type using Pagel's method. Should these two traits be correlated, we determine if C4 photosynthesis evolves more frequently in annual lineages, annuality evolves more frequently in C4 lineages, or neither. We use methods to address known type I errors. Our results provide new insights into the evolution of annuality in the context of photosynthetic mode.

P.0688 Morphometric analyses help to elucidate species delimitation in Eriochrysis (Poaceae, Andropogoneae)

Lisandra P. Souza[1], Tamara Pastori[2], Cassiano A. D. Welker[1]

1 Universidade Federal de Uberlândia, Uberlândia, Brazil 2 Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil.

Eriochrysis (Poaceae, Andropogoneae) is a monophyletic genus with about 11 species distributed in tropical and subtropical regions of the Americas, Africa, and India. The genus is characterized mainly by its inflorescences with golden-brown to light-brown trichomes and heterogamous spikelets. The main morphological features used to distinguish its species are the density of trichomes in the inflorescences and the shape and size of the spikelets. Although it is a small genus, *Eriochrysis* has many species delimitation problems, which require studies with multiple approaches. Morphometric analyses including multiple individuals of New World *Eriochrysis* taxa were performed, based on 34 characters (16 qualitative and 18 quantitative). Data were analyzed with principal coordinate analysis (PCoA) and discriminant analysis (DA), using characters that differed statistically significantly between groups by SPSS software version 29. Scatter plots of PCoA analyses performed with qualitative and quantitative characters showed that the multiple individuals of *Eriochrysis cayennensis* (the type of the genus) formed a group distinct from the group formed by individuals of *E. villosa*, indicating a strong morphological differentiation between these two groups of specimens. This suggests that *E. villosa* is a distinct species rather than a synonym of *E. cayennensis*, as proposed by some authors. Likewise, scatter plots of PCoA and DA analyses demonstrated discrimination between individuals of *E. warmingiana* and *E. laxa*, suggesting the recognition of two distinct species, contrary to what is accepted by some authors. These results are in agreement with molecular phylogenies carried out with *Eriochrysis* taxa, which demonstrates the relevance of morphometric analyses to assist in species delimitation in the genus. Morphometric analyses also indicated strong discrimination between a group of specimens from Brazil and individuals of other species of the genus already described, suggesting that these plants may be a new species, which needs to be further investigated.

S.079. HABITATBOUND BRYOPHYTE EVOLUTION

P.0689 Speciation linked to altitudinal gradients: the case of Lewinskya hookeri (Orthotrichaceae, Bryophyta) in southeast Asia

Pablo Aguado-Ramsay[1,2], Francisco Lara[2,3], Ricardo Garilleti[4], Isabel Draper[2,3]

1 Doctoral School (EDUAM), Universidad Autónoma de Madrid, Madrid, Spain. 2 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain. 3 Departamento de Biología, Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain. 4 Departamento de Botánica y Geología, Universidad de Valencia, Valencia, Spain.

Lewinskya F. Lara, Garilleti & Goffinet is one of the most diverse genera of Orthotrichoideae Broth. (Orthotrichaceae Arn.). It includes ca. 80 globally distributed taxa, some of which are potential species complexes. This is the case for *L. hookeri* (Wilson ex Mitt.) F. Lara, Garilleti & Goffinet, a species reported to be widespread in the eastern Himalayas, the Hengduan Mountains and the high plateaus of Tibet (Sino-Himalayan region). It is characterized by conspicuous sporophytic features (long seta, cylindrical capsules, and endostome with 16 wide segments), but it is considered to be a highly variable species in some other aspects, such as calyptra hairiness, seta length or leaf shape. Despite its great variability, only two varieties are so-far recognised: *L. hookeri* var. *hookeri* and *L. hookeri* var. *granulata* (Lewinsky) F. Lara, Garilleti & Goffinet, separated by differences in spore papillosity. Results from recent altitudinal transect surveys in Nepal, India and China suggest much greater complexity, with ca. ten morphotypes identified that succeed each other in altitude. Thus, what is currently known as *Lewinskya hookeri* could represents a complex of pseudo-cryptic species that segregate at altitude due to microenvironmental factors. Previous differentiation of these morphotypes may have been hampered because some of the most conspicuous shared characters have been considered to be of great taxonomic significance. The aim of this work is to unravel the diversity found in these transects using integrative taxonomy. At the same time, it explores the relationship of these morphotypes with the environment, which may have played an essential role in speciation and in the observed changes in morphology.

P.0690 Epiphyllous bryoflora in a forest in the Amazon basin – Colombia.

Marco T. Estepa-Ruiz[1], Laura V. Campos[1]

1 Escuela de Ciencias Básicas y Aplicadas, Maestría en Ciencias - Biología, Universidad de La Salle, Bogotá, Colombia.

Bryophytes form an inconspicuous group of the planet's flora; however, their contribution is fundamental to the balance of ecosystem services, mainly in water cycle. Given this importance and seeking to respond to the composition of mosses and epiphyllous liverworts in a forest in the Colombian Amazon, 16 trees (canopy) and 16 shrubs (understory) were chosen, which were distributed in 4 plots of 50 x 50 m, each of these separated by 500m. Epiphyllous bryophytes were collected on leaves of both the canopy and understory, in small plots of $10cm^2$. From 200 samples collected, 28 species of liverworts and 2 species of mosses were identified, obtaining a total of 30 species distributed in 14 genera and 5 families. The bryoflora was represented in 93.3% by the Marchantiophyta division, presenting the Lejeuneaceae family as the most representative in the study (86.7%). The genera with the highest number of species were *Cololejeunea* (36.7%), *Archilejeunea, Ceratolejeunea, Cyclolejeunea, Drepanolejeunea, Lejeunea* and *Leptolejeunea* (6.7%). In addition, a new record was found for Colombia *Cololejeunea papillosa* and for the Colombian Amazon a total of 18 new records. For the distribution between the epiphyllous bryoflora of the canopy and understory of the 30 species identified 11 species were shared followed by 12 canopy species and 7 understory species; the only 2 species of mosses were identified in the understory. These records provide valuable information to the understanding of the diversity and distribution of epiphyllous bryophytes in the Colombian Amazon.

P.0691 Diversification and biogeography of Asian Meteorium species

Thien-Tam Luong[1], Sanna Huttunen[1], Lars Hedenas[2]

1 Biodiversity Unit, University of Turku, Turku, Finland. 2 Swedish Museum of Natural History, Stockholm, Sweden.

Meteorium Dozy & Molk. is a pantropical moss genus consisting of many epiphytic species with a center of diversity in Asia. Together with *Papillaria* Lorentz., they form a major clade in the Meteoriaceae subfamily Meteorioideae. The confusion between the two genera is more or less resolved (Huttunen *et al.* 2004, Quandt *et al.* 2004), and while *Papillaria* has been treated systematically (de Olivera *et al.* 2020), taxonomy, evolution and phylogenetic relationships within the genus *Meteorium* remain ambiguous although the generic delimitation is clear. Hence, our project aims to provide a fundamental systematic framework including taxonomic solutions, evolutionary and biogeographical knowledge for the genus *Meteorium*. We combine a morphological taxonomical revision with molecular data from four regions (nuclear *ITS1-5.8S-ITS2 & 3A3* regions; plastid *trnL-F* & *rpl16* regions) to reveal and clarify evolutionary history, species diversification and biogeography within the genus. We could resolve the American species altogether in a clade separate from Asian taxa. The analysis also shows that the species diversification has originated from continental Asia (China, Nepal, Bhutan, etc.) then diverged farther south into the archipelagos of Malesia and Australia.

P.0692 Reviviscence determination of the Brazilian endemic moss Polytrichadelphus pseudopolytrichum (Raddi) G. L. Sm. (Polytrichaceae)

Tamara M. Matos[1], Bianca K.A. Paulino[1], Fungyi Chow[1], Denilson F. Peralta[2], Déborah Y.A.C. Santos[1]

1 Biosciences Institute of São Paulo University, São Paulo, Brazil. 2 Environmental Research Institute, São Paulo, Brazil.

Bryophytes are considered pioneer embryophytes to lead with land environment stresses such as desiccation. Approximately 158 moss species are described as revivescents, plants that remain viable for long anabiosis periods, activating the vital processes when water is again available. Polytrichaceae presents species able to survive under extreme desiccation conditions and, when rehydrated, recover themselves in a few seconds (Wood, 2007). Considering the intrinsic characteristic of desiccation tolerance of this family, the main goal of this study was to verify resurrection ability in the Brazilian endemic moss Polytrichadelphus pseudopolytrichum. For that, gametophytes were acclimatized in the greenhouse (30 days), transferred to a growth chamber (15 days), and distributed in three groups: control (15 days), desiccation (15 days), and rehydration followed by collect (t= 0 minutes and 24 hours). Afterward, photosynthetic parameters, total pigment content, relative water, lipid peroxidation, antioxidant enzymatic activities, and cuticular wax profiles were analyzed. During desiccation, P. pseudopolytrichum gametophytes presented preserved photosynthetic parameters (p= 0,300/Fv/Fm, p= 0,100/Y(II), p= 0,400/ETRmax), chlorophyll contents (p= 0,0540/Chla, p= 0,0547/Chlb), and lipid peroxidation rate (p= 0,700). However, carotenoid content (p= 0,0078), antioxidant enzymatic activity (p= 0,0011/CAT, p= 0,0001/SOD, APX, GR), and cuticular waxes (p= 0,0001/content, p= 0,0124/alkanes) were statistically changed under the desiccation state, returning after 24 hours of rehydration to control values (p= 0,300/carotenoids; p= 0,350/CAT, p= 0,0510/SOD, p= 0,050/APX, GR; p= 0,1000/wax content, p= 0,0563/alkanes). Our data suggest

P. pseudopolytrichum is a revivescent moss, activating repair mechanisms such as photoprotection, cell membranes conservation, scavenging free radicals, and avoiding non-stomatic water lost, essentials during the desiccation/resurection in revivescent plants (Marks et al. 2021).

References: Wood, A.J. (2007). The Bryologist. 110, 163–167.); Marks, R.A. et al. (2021). Am. J. Bot. 108, 346–358.

P.0693 Photosynthetic capacity of mosses along a Year of Elevated CO2

João Paulo S Souza[1], José Ángel Morales-Sánchez[1], Kristiina Mark[1], Ülo Niinemets[1,2]

1 Institute of Agricultural and Environmental Sciences, Estonian University of Life Sciences, Tartu, Estonia. 2 Estonian Academy of Sciences, Tallinn, Estonia.

Concentrations of atmospheric carbon dioxide (CO_2) are globally constantly increasing with major impacts on terrestrial vegetation. While the elevated CO_2 effects on vascular plants have been extensively studied, there is only limited information for bryophytes. Yet, globally, bryophytes store large amounts of carbon. To assess how the photosynthetic capacity of mosses behave along a year of elevated CO_2 concentration, we carried out *in vitro* growth chamber experiment with eight common boreal forest floor species with differing ecology and structure collected from different habitats in Estonia. The moss specimens, collected as cushions in early summer, were acclimatized in growing chambers at 400 ppm for seven months until half of the plants were exposed to 1000 ppm (as the treatment) and the other half were kept at 400 ppm (as the control) for another 12 months. During the elevated CO_2 treatment, photosynthesis measurements (net assimilation and chlorophyll fluorescence) were conducted every two months. The exposure to elevated CO_2 had a positive effect on carbon assimilation during the first six months for most species. However, a decrease in assimilation rate occurred during the experiment and in the last months, the long-term elevated CO_2 had a negative effect, showing lower CO2 assimilation (A) values than the control. The maximum quantum yield of photosystem II (ΦPSII) and electron transport chain (ETC) did not exhibit significant changes over time. These results underscore the importance of measuring the effects of long-term exposure to elevated CO_2 in bryophytes, as it seems to impose multifaceted impacts on photosynthesis and, consequently, could have negative implications on bryophyte flora productivity and acclimation potential.

P.0694 Offsite landscapes around mines: A focus on boreal forest understory biodiversity

Xiangbo Yin[1,2,3], Christine Martineau[4], Abdul Samad[4], Nicole J. Fenton[1]

1 Université du Québec en Abitibi-Témiscamingue, Rouyn-Noranda, Canada. 2 National Institute of Scientific Research, Quebec City, Canada. 3 Philipp University of Marburg, Marburg, Germany. 4 Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, Québec City, Canada.

More landscapes will be exposed to mining disturbances with increased mining activities for the green energy transition. The ecological effects associated with mining could extend beyond the edge of the immediate mine location and reach into surrounding (offsite) landscapes because dust, salt, excess nutrients, or other contaminants move from mines into surrounding ecosystems via air, water or human activities (e.g., vehicle movement). However, how mining affects understory biodiversity in offsite landscapes is largely unknown especially in Canada's boreal forest – the world's largest intact forest ecosystem. Here we selected six gold mine sites in Quebec, Canada. To address this gap, we investigated three groups of bryophytes, vascular plants and phyllosphere microbiota in the understory layer within 1-km mosaic landscapes around six mines at different mining stages in the Canada's boreal zone. We found three potential mechanisms of mining affecting surrounding understory biodiversity: 1) Changing or reshaping the community structure directly, e.g., invasive species occurred and bryophyte ground cover was reduced near mines; 2) Integrating with global ecosystem shifts, e.g., the shifting from coniferous forests to deciduous forests could exacerbate mining effects on bryophyte community structure; 3) Affecting associated microbial community composition, e.g., some important functional microbial groups (e.g., Cyanobacteria) that provide nutrients to support biodiversity in boreal forest were affected by mining. Therefore, offsite landscapes around mines should receive more attention on biodiversity in ecological assessment. Beyond the boreal forest, it's crucial to assess the effects in other eco-biomes to understand and mitigate the impact of human activities on global biodiversity.

S.080. HERBARIOMICS, AN INVALUABLE RESOURCE FOR PLANT RESEARCH

P.0695 MAF Herbarium. Collections for botanical research: 19th and 20th centuries

Paloma Cantó[1], David Cossío-Felipe[1], Jorge Romero-Morte[1], José M. Pizarro[1]

1 Department of Pharmacology, Pharmacognosy and Botany, Complutense University of Madrid, Madrid, Spain.

The MAF Herbarium was founded in 1892. The origin was the Herbarium of the Linnean Society of Madrid which was set up in the Faculty of Pharmacy of the Complutense University of Madrid. The number of currently preserved specimens is near 223000, among which historical collections stand out. In 1970 it became a member of the Index Herbariorum, in 1993 it participated in the creation of the Ibero-Macaronésicos Herbarium Association AHIM. In 2003 it joined the GBIF (Global Biodiversity Information Facilities) database. Our general aim is the digitization with images of the nomenclatural types of the MAF Herbarium, in order to facilitate its accessibility to researchers who need it. Previous to this study, we presented, in tribute to Professor Rivas-Martínez, the types of the species described by him. Our current objective is the digitization of the most relevant botanical types from the late 19th century and first half of the 20th century. Firstly, a thorough bibliographic search of the new species described by the aforementioned authors has been carried out, secondly, they have been located in the MAF-general collection, then the images have been obtained with an EPSON Expression scanner. 12000 XL. Finally, distribution maps of the specimens have been made by authors. The results obtained will be uploaded to the MAF Herbarium website, as well as to scientific platforms such as GBIF. Of the total amount of specimens in MAF Herbarium, just over 10000 make up the historical collections of Pourret and the Linnean Society of Madrid. The rest of the historical material (e.g., L. Née, H. Ruiz & J.A. Pavón, J.M. Pérez Lara, B. Lázaro Ibiza, M. Rivas Mateos, P. Font Quer, S. Rivas Goday, J. Borja, J. Cuatrecasas) is integrated into the general herbarium. Currently 30% of the total is digitalized.

P.0696 Oceanic island herbariomics: diversity, evolution and human impact on Trochetiopsis (Malvaceae) from Saint Helena

Annabelle R. de Vries[1,2,3], Mark Carine[2], Robin G. Allaby[1]

1 School of Life Sciences, Gibbet Hill Campus, University of Warwick, United Kingdom. 2 Department of Life Sciences, The Natural History Museum, London, United Kingdom. 3 Tropical Botany, Naturalis Biodiversity Center, Leiden, The Netherlands.

Oceanic islands have been, and continue to be, used for in-situ studies of evolution. They provide striking examples of adaptive radiations, while at the same time, their endemic diversity is globally endangered. This project aimed to better understand how human impact has affected island biodiversity patterns and questions how robust islands are as model system for studying evolution. St. Helena has historical records of human impact and a history of botanical collection spanning the last three centuries. Additionally, it highlights classic examples of evolutionary processes such as adaptive radiation. Here we focused on the plant genus *Trochetiopsis*, endemic to St. Helena, as example study of an island plant lineage, which is currently endangered due to past anthropogenic pressure. *Trochetiopsis* consists of three species, one globally extinct (*T. melanoxylon*), one extinct in the wild (*T. erythroxylon*) and one recently re-discovered (*T. ebenus*). *Trochetiopsis'* herbarium collections spanning 320 years, allow us to look closer at these extinction events. Ancient DNA was obtained from 14 herbarium specimens of the *Trochetiopsis* species using Novaseq. This data was aligned to the *de novo* assembled genome obtained for *Trochetiopsis ebenus*. PCA, Admixture, and Treemix analyses based on genotype likelihood showed that *T. melanoxylon* is more distinct from *T. ebenus* and *T. erythroxylon* than the latter two species are from each other. Watterson's estimator of heterozygosity showed a loss of genetic diversity over time for the genus and for *T. erythroxylon*. Throughout the analyses modern samples showed different patterns compared to the herbarium material, suggesting the modern material is not representative of the historically diverse plant lineage. This indicates the importance of herbaria to fill in the gaps of extinct lineages or lost diversity when studying evolution on oceanic islands that have been heavily impacted by humans.

P.0697 DigiHerb: a pilot project to digitise specimens in a consortium of small European herbaria

Eva Dreyer[1], Rainer W. Bussmann[2], Christina Campbell[1], Lars Chatrou[3], Colin T. Kelleher[1], Darren Reidy[1], Wuu Kuang Soh[1]

1 National Botanic Gardens (OPW), Dublin, Ireland. 2 Staatliches Museum für Naturkunde Karlsruhe, Karlsruhe, Germany. 3 Department of Biology, Ghent University, Ghent, Belgium.

Digitised herbarium collections can be used to address important research questions on biodiversity issues across diverse disciplines, benefiting both science and societal needs. However, the knowledge on specimens is highly skewed towards large herbaria, which have resources to fully catalogue and digitise their collections. Thus, a common challenge is to mobilise biological data from smaller herbaria (less than ~1,000,000 specimens), which are often limited in resources and capacity. The DigiHerb project aims to build innovation capacity in a small consortium of herbaria in North-West Europe (NWE) in the areas of digitisation and biodiversity informatics. Our approach is a pilot joint digitisation project between three herbaria in the Interreg NWE region: Dublin (DBN), Karlsruhe (SMNK) and Ghent (UGhent). The project will utilise a novel high-throughput conveyor-belt digitisation technology to digitise specimens and create a unified digital portal for the digital contents. The main output of the project will be this unified digital portal and data management system to facilitate access to the herbarium collections within the consortium. Small herbaria hold unique collections of great scientific and historical significance that cannot be found anywhere else. This project will address the outlined issues for smaller herbaria by democratising funding and technical capacity, thus making freely accessible these precious biological collections and opening doors to new botanical and historical research.

P.0698 Overcoming liquid nitrogen dependency: development of an affordable modified DNA extraction protocol for dried plant specimens

Renerio P. Gentallan Jr.[1], Kristine Joyce O. Quiñones[1,2], Emmanuel Bonifacio S. Timog[1,3], Juan Rodrigo A. Vera Cruz[2,4], Nadine B. Coronado[5], Michael Cedric B. Bartolome[1], Daryl B. Ceribo[1], Roselle E. Madayag[6], Jessabel B. Magtoltol[6], Teresita H. Borromeo[1]

1 Institute of Crop Science, College of Agriculture and Food Science, University of the Philippines Los Baños, Laguna, Philippines. 2 Department of Science and Technology, Science Education Institute, Taguig, Manila, Philippines. 3 Department of Forest Biological Sciences, College of Forestry and Natural Resources, University of the Philippines Los Baños, Laguna, Philippines. 4 Philippine Rice Research Institute, Maligaya, Science City of Muñoz, Nueva Ecija, Philippines. 5 Institute of Biological Sciences, College of Arts and Sciences, University of the Philippines Los Baños, Laguna, Philippines. 6 Agricultural Systems Institute, College of Agriculture and Food Science, University of the Philippines Los Baños, Laguna, Philippines.

The availability of liquid nitrogen poses a limitation for developing countries interested in conducting herbariomics research. Hence, we present a cost-effective method of CTAB DNA extraction from silica-dried samples and herbarium specimens, eliminating the need for liquid nitrogen. Two protocols were evaluated to determine the effectiveness of grinding dried plant samples without liquid nitrogen in comparison to the standard protocol for tissue homogenization and cell lysis. Protocol 1 involved grinding fresh leaf samples with liquid nitrogen, while Protocol 2 entailed incubating dried plant samples at -20°C for 1 hour before grinding in the absence of liquid nitrogen. Both protocols produced comparable DNA yields suitable for short-read sequencing. Using Illumina sequencing, chloroplast genomes from fresh, silica-dried, and ten-year-old herbarium samples were successfully assembled and annotated. Moreover, the extracted DNA from silica-dried samples using Protocol 2 produced a library size that met the quality requirement for PacBio HiFi sequencing. The quality achieved was adequate for the assembly of 15 complete chloroplast genomes. Thus, the developed liquid-nitrogen-free protocol from dried plant samples can serve as an alternative DNA isolation method for barcoding and genome assembly. It is particularly advantageous for research workflows involving the collection of samples in the field as a long-term source of genetic material, and it offers a practical solution for resource-limited laboratories.

P.0699 Phylogenetic analysis of Deschampsia (Poaceae) in the Southern cone of South America through Angiosperm353 target sequencing

Pablo C. Guerrero[1,2,3], Micaela Conejeros-Palma[1,2,3]

1 Universidad de Concepción, Concepción, Chile. 2 Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos, Concepción, Chile. 3 Instituto de Ecología y Biodiversidad, Concepción, Chile.

The genus *Deschampsia*, characterized as a lineage of grasses common in areas subject to freezing, constitutes a monophyletic group with cosmopolitan distribution. This genus thrives in cold and temperate regions of both hemispheres. It consists of at least 30 species, of which 15 are present in South America, with the southern Andes of Chile and Argentina considered a significant hotspot of diversity for the genus. The main disagreements on the systematic delimitation of *Deschampsia* are related to the high degree of morphological similarity, the overlap of diagnostic characters, and the high phenotypic variation, generating taxonomic complexes within the genus. This work aims to infer the phylogenetic relationships of the species of the genus *Deschampsia*, focusing geographically on the southern cone of South America. This research was conducted using historical herbarium samples from the Herbarium of the University of Concepción (Chile) and the National Herbarium of Paris (France). We sequenced a total of 30 samples corresponding to 17 species. We used the Target Sequencing genomic technique and the "Angiosperm353" probe set, which allow sequencing hundreds of previously identified genes highlighted for their phylogenetic informative value. We performed Bayesian phylogenetic reconstruction to infer the evolutionary relationships between the species. Our results show a well-resolved consensus tree with high posterior values at the nodes. The species present in the Southern Cone of America do not form a monophyletic group. The clade with the highest number of southern cone species includes *D. elegantula, D. setacea, D. patula, D. cordillerarum, D danthonioides,* and *D. pulchra*. However, other species were positioned in different clades. The genomic analysis tool used allowed sequencing old samples, one of them over 100 years old. Additionally, it provided a robust tree highlighting that native species of the southern cone have different evolutionary and biogeographic histories.

P.0700 How to distinguish Himalayan birches?

Norbert Holstein[1], Narender Kumar[2], Hester van Schalkwyk[1], Nian Wang[3]

1 Natural History Museum, London, UK. 2 CSIR - Institute of Himalayan Bioresource Technology, Palampur, India. 3 Shandong Agricultural University, Tai'an, China.

Two species of *Betula* section *Acuminatae* (6 species in total) are currently considered to occur in the Himalaya. *Betula alnoides* and *B. cylindrostachya* are hard to distinguish and are sometimes even considered to be subspecies. They are supposedly differing in flowering time, number of female catkins, diameter of fruiting catkins and mainly leaf characters. However, neither type material nor protologue of *B. cylindrostachya* offer any clue to flowering times, and leaf characters appear to be variable and overlapping with *B. alnoides*. Also, catkins characters are found to overlap. In addition, some *Betula* sect. *Acuminatae* populations in India, considered to be *B. cylindrostachya*, have a shaggy bark. However, types of *B. alnoides* and *B. cylindrostachya* do not contain bark data, and material from type localities have a smooth bark. The recent discovery of the Chinese species *Betula mcallisteri* differing from *B. luminifera* (both also sect. Acuminatae) only in ploidy and bark characters raises additional questions. Here, we use next-generation sequences from material from types to field collections to try to unravel the taxonomic identity of Indian birches.

P.0701 The relations of contemporary hops with wild populations and archaeological hop finds in Finland

Sanna Huttunen[1], Lidija Bitz[2], Mia Lempiäinen Avci[1] Tanja Ratilainen[1, 3]

1 University of Turku, Turku, Finland. 2 Natural Resources Institute, Jokioinen, Finland. 3 Archaeology and Turku Museum Centre, Turku, Finland.

Almost any kind of ancient organic remains found from archaeological excavations are potential source for ancient DNA (aDNA). In this project we have used hop seeds found from archaeological excavation sites in Finland to study the relations of contemporary hops with wild populations and archaeological hop finds in Finland. We did DNA extractions for archaeological hop finds from eight excavation sites in Finland: four in Turku, one from Kokkola, Porvoo, Kotka and Oulu. Hop remains from these localities were obtained from contexts dating back to 1200 – 1800 centuries. Genotypes of archaeological specimens were compared with already existing genetic data on modern cultivars in extensive genetic database and DNA gene bank by the Natural Resources Institute, Finland, and with historical material deriving from natural history museum collections. Historical samples included 347 hop samples collected from wild and cultivated populations from Finland and neighboring areas in Russia. The hops were genotyped using 13 microsatellite markers and, in case of archaeological material, using next-generation sequencing (NGS). Wild origin has already earlier been confirmed in field for part of hop populations, and therefore our analyses has potential to reveal possible domestication events and farmed hops derived from wild populations. Genetic structure among Finnish hop samples and their relationship with hops from neighboring areas may reveal migration routes to and within Finland, origins due to the trade and exchange as well as potential loss of diversity in this species.

P.0702 Herbariomics and the taxonomic status of Alisma wahlenbergii (Alismataceae)

Samuli Lehtonen[1], Zhi-Zhong Li[2]

1 University of Turku, Turku, Finland. 2 Wuhan Botanical Garden, Wuhan, China.

Species delimitation in the aquatic plant genus *Alisma* (Alismataceae) has historically been difficult due to morphological plasticity. In more recent molecular phylogenetic studies, poor sampling and limited genetic variation in the few studied markers have hindered progress. One peculiar taxon with questionable taxonomic status is *Alisma wahlenbergii*. It is considered a narrow endemic in the Baltic sea and nearby lakes in Sweden and Russia, where it grows as a submerged plant in rather shallow water. However, it is often treated as subspecies of *A. gramineum*, an amphibious species widely distributed in the northern hemisphere. Here, we have investigated the systematics of this species group by applying genome skimming sequencing for a set of specimens mostly originating from herbarium collections. We obtained complete plastid genomes, nearly complete mitochondrial genomes, and over 8,000 bp long sequences containing 18S–26S nuclear ribosomal DNA with the external transcribed spacer regions, from up to over 100 years old herbarium specimens. Results of the phylogenetic analyses showed that *Alisma wahlenbergii* is nested within *A. gramineum* and, furthermore, that *A. wahlenbergii* populations from the Gulf of Bothnia and Gulf of Finland did not group together. Hence, we conclude that there is no molecular support for recognising *Alisma wahlenbergii* at any taxonomic rank.

P.0703 Monitoring genetic diversity loss using herbarium samples

Melissa Viveiros Moniz[1], Ana García-Muñoz[1], Andrea Mira-Jover[2], Juan Lorite[1], Mohamed Abdelaziz[1], A. Jesús Muñoz Pajares[1]

1 University of Granada, Granada, Spain. 2 Miguel Hernández University, Elche, Spain.

It is well known that climate change has had far-reaching consequences on all living beings, altering ecosystems, habitats, and biodiversity worldwide. The disappearance of populations and particular alleles leads to the loss of genetic diversity and emphasizes the importance of monitoring genetic diversity to protect overall biodiversity. Monitoring genetic diversity over time also provides information about the extent to which populations or species may be threatened, leading to more effective conservation actions. By analyzing the genetic diversity of herbarium samples, and comparing them to present-day samples, we can help determine if the low genetic diversity observed in current populations is a result of natural variation or a decline in diversity over time. High mountain species are highly vulnerable to climate change, and Sierra Nevada in particular faces a significant risk of increased climatic stress for key species, especially in the summit areas, which house most communities and endemic species. Therefore, we have assessed the intra-individual genetic diversity using herbarium samples from two *Sideritis* species located in Sierra Nevada. *Sideritis hirsuta* has a wide distribution across the Iberian Peninsula while *Sideritis glacilalis* is endemic to high-altitude areas of the South and East of the Iberian Peninsula. We found a significant decrease in genetic diversity solely in *S. glacialis* samples, while *S. hirsuta* has maintained stable throughout the years. This poses a unique threat to *S. glacialis* since, in addition to its limited distribution throughout the Iberian Peninsula, we also detect it at a greater altitudinal range than *S. hirsuta.* These preliminary findings highlight the challenges that isolated communities face when genetic diversity is reduced, even in the short term. We also emphasize the importance of herbaria as genetic material sources from past populations that can be compared to the present, to foresee the Anthropocene's impact on biodiversity.

P.0704 From tradition to innovation: exploring diverse applications of BC herbarium material

Neus Nualart[1], Laura Gavioli[1,2], Alba Martín[1], Javier Martinez[1], Edgard Mestre[1], Iván Pérez-Lorenzo[1,2], David Pérez Prieto[1], Jordi López-Pujol[1,3]

1 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 2 Laboratori de Botànica, Facultat de Farmàcia i Ciències de l'Alimentació, Universitat de Barcelona, Barcelona, Spain. 3 Escuela de Ciencias Ambientales, Universidad Espíritu Santo, Samborondón, Ecuador.

The BC herbarium of the Barcelona Botanical Institute is the second most important botanical collection in number of specimens (800,000) in Spain and represents a source of basic information to understand the plant biodiversity of the western Mediterranean basin. In addition to the general vascular plant collection (continuously growing), it includes 14 historical collections, different cryptogam collections (containing bryophytes, lichens, fungi and algae specimens) and other collections preserved separately due to their nature (xylotheca, tissue bank, etc.) or origin (tropical plants, cultivated plants, etc.). All this material is available to researchers through online portals, in-person visits or email queries and has been widely used in different research fields such as taxonomy, floristics, phylogeny, biogeography, evolution, conservation, ethnobotany, biological invasions and climate change (Pérez-Lorenzo, 2021). Over the last few years, the uses of the BC herbarium material have been expanding to other non-conventional approaches not necessarily related to botanical research. New queries based on various topics such as chemistry, toxicology, history and archaeology, among others, have been addressed, and even some art performances have been produced through collaborations with artists who got inspired by different BC herbarium collections. In this contribution, our objective is (1) to provide an overview of the materials preserved within the BC herbarium and (2) to assess the multifaceted uses of these materials, encompassing both traditional applications and non-conventional innovative ones.

P.0705 Whodunit? Hyb-Seq with Angiosperms353 probe set helps solve 200 year old botanical mystery

Leopoldo Medina Domingo[1], Elena Quesada Chicharro[1], Mónica García-Gallo Pinto[1], Lisa Pokorny[1]

1 Real Jardín Botánico (CSIC), Madrid, Spain.

The historical collections of the Herbarium of Madrid's Real Jardín Botánico (RJB-CSIC) include a large number of specimens belonging to the Botanical Expedition to the Viceroyalty of Peru (1777–1788), headed by botanists Hipólito Ruiz and José Antonio Pavón. This expedition, of great importance for taxonomic and nomenclatural studies of South American plants, resulted in 3K specimens and 2.5K life-sized botanical illustrations, as well as many living plants. These collections also include ~3 Kg of underground plant structures, likely engrossed stems, that rarely present remains of roots or leaves. These materials, known colloquially at RJB as "*chufas*", due to their original identification as genus *Cyperus*, have remained unidentified for well over 200 years. Here, we present a herbariomic approach to molecularly characterize historical collections. DNA was extracted relying on a modified CTAB protocol with extended incubation times to increase yield from suboptimal tissue template. Following extraction, dual indexed genomic libraries were prepared and pooled for hybridization with the Angiosperms353 probe set. The resulting enriched pool was then processed in a short-read high-throughput sequencing platform. Raw reads were quality filtered and HybPiper was used to assemble our 353 nuclear orthologs. We then used phylogenetic placement algorithms to position our mystery collection in a pre-existing family-level angiosperm phylogeny. Then, we repeated this placement exercise in a genus-level phylogeny we generated just for the resulting family from data publicly available in open access repositories. Additionally, we downloaded ITS sequences from NCBI for closely related taxa. The resulting data matrix was then used to both assemble ITS from off-target reads for our historical collections and to more closely pinpoint their identity. Please, come see our poster if you wish to know what we learned.

P.0706 Genetic variability of Heracleum sosnowskyi and related species in context of giant hogweeds invasion

Elena V. Ptytsyna[1,2], Sergey V. Dudov[2], Margarita A. Ezhova[1,5], Sofia R. Prokopchuk[1], Anton A. Gladilin[3], Dmitry V. Geltman[4], Aleksey A. Penin[1], Maria D. Logacheva[5]

1 Kharkevich Institute for Information Transmission Problems of the Russian Academy of Sciences, Moscow, Russia. 2 Department of Ecology and Plant Geography, Lomonosov Moscow State University, Moscow, Russia. 3 Volunteer non-profit organization "StopHogweed", Moscow, Russia. 4 Komarov Botanical Institute of the Russian Academy of Sciences, Saint Petersburg, Russia. 5 Skolkovo Institute of Science and Technology, Moscow, Russia.

Heracleum sosnowskyi and related species (*H. mantegazzianum*, *H. persicum*), collectively called giant hogweeds, are invasive plants that pose threat to human health and biodiversity. The study of their genetic characteristics is important for understanding the phenomenon of invasiveness. Here we analyzed genetic diversity of *H. sosnowskyi* and related species from different territories within Russia and neighboring countries. More than 160 herbaria (LE, MW, YALT) samples ranging in the year of collection from 1836 to 2022 as well as recent volunteer-collected samples were taken for the analysis. They cover all major regions within the primary (native) and secondary (introduced) areas. Using low-coverage whole genome sequencing we analyzed the variability of the plastid genome and nuclear ribosomal operon; for a smaller subset of plants, we performed a deeper sequencing that allowed to infer the variability on single copy genomic regions. The results show that: 1) neither rRNA, nor plastid genome data allow to distinguish between *H. sosnowskyi* and 2 species: *H. mantegazzianum*, considered as separate species invasive in western Europe, and *H. pubescens*, considered as Crimean endemic; 2) the genetic diversity of *H. sosnowskyi* does not show a decrease in the secondary area; this is the result of multiple introductions; 3) patterns associated with the role of first introduction centers (Komarov Botanical Institute and Polar-Alpine Botanical Garden) were visible in the territorial distribution of groups; 4) events of hybridization and/or introgression of plastids could be observed in the evolution of the genus *Heracleum*.

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P.0707 Speaking of Diospyros… What do we know about Diospyros in Colombia?

Jorge E. Ríos-Cervera[1], Magda Escobar-Alba[1]

1 Universidad del Tolima, Colombia Universidad Pedagógica y Tecnológica de Colombia, Colombia.

The Diospyros genus has simple, alternate leaves; blades with abaxial glands, unisexual axillary inflorescences and with a persistent calyx. The differences with the other genus present in the neotropics (Lissocarpa) are its globose fruits, and with a more expanded calyx, in addition to its flowers with shorter petals and a greater number of glands. This genus is cosmopolitan in distribution, consisting of more than 500 species and widely distributed in the tropics and subtropics of the world, 100 species in America (Bakhuizen van den Brink, 1936–1955, White, 1980, White, 1993, White, 1993, Singh, 2005) and 21 for Colombia (Bernal, R., Gradstein, S. R., & Celis, M. (2015). Catálogo de plantas y líquenes de Colombia. Instituto de Ciencias Naturales, Universidad Nacional de Colombia, Bogotá). It is a genus of nutritional interest, its species are important components in forests between 0 and 1300 m. The collections of Diospyros specimens in the country date back to 1800 by botanists such as Schlim L. or Triana J., with a peak in the 80s and 90s deposited in the herbaria COAH, COL, JAUM, UDBC, the 60% are identified at the species level and the remaining one has yet to be reviewed with two species entered that are not reported by the Colombian Plant Catalog. The mountain range that concentrates the greatest wealth is the central one in the department of Antioquia, although the greatest diversity is found in the departments with "Amazon influence" possibly linked to sampling intensity. The above denotes that it is a group of plants of important contribution to the floristic diversity of the country, whose study is briefly explored and the identity of the Colombian specimens requires verification, and curation, allowing to elucidate their patterns of richness and distribution and with understand its ecological and social importance.

P.0708 Digital plant models: a tool for modernizing herbaria

Ricardo Rivera-Martínez[1], Karen V. Trejo-Yudiche[1], Andrea Salas-Sánchez[1], Mariana Salas-Sánchez[1], Rebeca Salas-Sánchez[1], Pablo Fornés-López[1], José M. Karam-Pacheco[1], David Poot-Herrera[1]

1 Prepa Anáhuac Mérida, Yucatán, Mexico.

Since the 17th century, herbaria have served as vital biological collections safeguarding botanical specimens for study and preservation. These collections house complete specimens or their parts through a process known as herborization, involving the dehydration of plants to later mount and store them alongside specific origin data. However, it is important to note that this process alters the plants' natural physical appearance, resulting in the loss of color, texture, dimensions, and even distinctive features. In an effort to compensate for this loss of information, photographs have been included to visually represent the specimens. Despite these efforts, photographs fall short of capturing all the necessary information to comprehensively portray the plant. Recognizing this challenge, we propose the incorporation of three-dimensional digital models to complement herborization and photography. The significant advantage of using this technology lies in the ability to interact with the 3D model, enabling actions such as zooming, rotating, and more, providing a more comprehensive experience in studying the specimen. In this context, we developed digital models of two endemic cacti from the Yucatán Peninsula: *Pilosocereus gaumeri* and *Mammillaria gaumeri*. The choice of these species is rooted in the difficulty of herborizing cacti due to their physical characteristics, such as succulence, globular or cylindrical shapes, and easily breakable or detachable structures like spines or wool. Both digital models were created using 3D design programs such as 3D Max and Blender, and they were uploaded to the cloud via the CoSpaces platform. To enhance accessibility and interactivity, we linked both models to an object called the Merge Cube, serving as a QR code that allows viewing and interaction with the model from any smart device. Our future plans involve creating more models and assembling a more comprehensive catalog.

P.0709 Typification of Malvastrum thurberi (Malvaceae): a stroll through some confusion in 20th- and 21st-century history and nomenclatural practice

Colin M. Robinson[1], Roy E. Gereau[1], Charlotte M. Taylor[1]

1 Science & Conservation, Missouri Botanical Garden, St. Louis, USA.

The typification of *Malvastrum thurberi* A.Gray is finally resolved by the effective designation of a lectotype. The status of its typification and its country of collection have been misinterpreted by authors for seven decades. We use this species to highlight the importance of considering how the *Code* has and has not changed over the years, and use it as an example to show why the *Code* is an effective tool to clarify questions when it is adhered to correctly. Additionally, we highlight the good representation of specimens of North American plants studied by Asa Gray in George Engelmann's herbarium at MO, and note the importance of considering historical events for detailing species distribution. Finally, this case demonstrates why it is always important to check others' work before taking it at face value.

P.0710 Lichen specimens of the Goettingen Herbarium (GOET) revised

Bastian Steudel[1]*, Marc S. Appelhans[2]

*1 Xi'an Jiaotong-Liverpool University, Suzhou, China. 2 Georg-August University Goettingen, Goettingen, Germany. *bastian.steudel@xjtlu.edu.cn.*

During the last two years, we revised the lichen holdings of the Herbarium GOET enabling the index fungorum (www.indexfungorum.org) to determine the current name of the specimens and to identify historically important specimens and original material. In total, about 1P.00 specimens have been revised and ordered according to their current determination. We identified more than 260 specimens representing type or original material. Most of the type material is from the 19th century, distributed by F.C.G. Arnold, G. Wahlenberg, W. Borrer, L.E. Schaerer, and J.C. Schleicher. Additionally, 18th century specimens collected by J.F. Ehrhart, at least one from Upsala, probably collected under the supervision of Linnaeus, where found. The most diverse lichen families were represented most with Parmeliaceae (38 specimens), Lecideaceae (29 specimens), Verrucariaceae (26 specimens), Pertusariaceae (24 specimens), and Lecanoraceae (22 specimens). Due to the new order and the improved storage system in the lichen collection, the specimens are now easier accessible than before. The identification of type or original material will hopefully attract specialists to visit the collection for further studies.

P.0711 A phylogenetic exploration of Hibiscus section Azanzae (Malvaceae) using ancient DNA from herbarium specimens

Fernando A. Vélez-Esperilla[1], Koji Takayama[1]

1 Kyoto University, Kyoto, Japan.

Hibiscus (Malvaceae, Malvoideae), a widely recognized genus among angiosperms, it is, however, a paraphyletic taxon that encompasses various nested genera. Within *Hibiscus*, section Azanzae currently includes species from three genera (*Hibiscus, Talipariti*, and *Papuodendron*). The species in *Talipariti* have been segregated from *Hibiscus*, forming two subgroups: *H. tiliaceus* group and the little-known malesian group. Meanwhile, species remaining in genus *Hibiscus* have been overlooked over half a century, leaving their relationships within *Hibiscus* section *Azanzae* unclear. Although the genus *Papuodendron* exhibits a different morphology compared to the subfamily Malvoideae, it has been related with the *Hibiscus* section *Azanzae* in broad phylogenetic studies. However, many of these species, particularly from Southeast Asia and New Guinea, have never undergone molecular analysis, rendering the classification system outdated. Traditionally reliant on herbarium specimens, the recent development of museomics approaches offers new avenues for study beyond morphology. In this study, we revisit previous classifications based on morphological characters within this section, and present the first comprehensive phylogeny of *Hibiscus* section *Azanza*, incorporating little-known species from Southeast Asia and New Guinea. Using DNA extraction from ancient herbarium material, our results elucidate the complex relationships within this taxonomic group. We revealed that some species previously classified under the genus *Hibiscus* were more closely related to different sections, while others grouped with genera *Papuodendron* and malesian *Talipariti*. This phylogenomic framework not only sheds light on morphological and ecological evolution of section *Azanzae* species, but also provides insights into the phylogeography of this section through Southeast Asia. Our findings underscore the imperative need for a taxonomical reassessment within this section, ensuring that tis classification remains reflective of its evolutionary history.

P.0712 RedHAr (Argentine Herbaria Network): working towards curatorial management focused on herbarium-based research

Alicia López Méndez[1,4], Eliana de Lujan Exner[2,4], Agustina Yañez[3,4]

1 Herbario BAL, Unidad Integrada Balcarce, Facultad de Ciencias Agrarias, Universidad Nacional de Mar del Plata - EEA Balcarce, INTA, Buenos Aires, Argentina. 2 Herbario SF "Arturo E. Ragonese", Facultad de Ciencias Agrarias, Universidad Nacional del Litoral, Esperanza, Santa Fe, Argentina. 3 Herbario BA, Museo Argentino de Ciencias Naturales (MACN-CONICET), Ciudad de Buenos Aires, Argentina. 4 Red de Herbarios de Argentina

Argentine Herbaria Network (RedHAr as in Spanish) was created in 2017 as an initiative of the Argentine Botanical Society with the purpose of bringing together people linked to herbaria to create a community to maintain and enhance collections through sharing experiences. Currently, RedHAr is integrated by 52 herbaria, located in 11 provinces, with a combination of affiliations (both public and private) and going to big herbariums with over 450,000 vouchers, to small herbariums with less than 5,000. Over the last few years, as RedHAr, we put our efforts into organizing workshops for small and emerging herbaria, database management, digitization, conservation, and regulations for the import/export procedures. We have also organized conferences given by specialists in topics related to the activities of herbaria, open to all public. Our main goal in the near future is to make all the argentine herbaria databases (from small to large ones) accessible to our colleagues and to the general public in a simple way, through a sovereign open access repository. We are working to reunite in the same place the internal management of collections and the open access repository. Here we present the results of the first collections held in herbaria survey carried out as a first step in the construction of that repository. More than 1.5 million specimens are held in 32 of the 52 RedHAr herbaria, among which, the predominant ones are vascular plants, stored as dried and pressed specimens, in envelopes or in fixative liquids. Geographic representation of the flora is in most cases regional (neighbor countries), national (Argentina) or local (provinces). The conservation status of the collections and data digitization process was generally self-defined as very good or good, but in most cases such digital data or specimens' images cannot be accessed remotely, reinforcing the need of a national repository.

S.081. IAPT EARLY CAREER INVESTIGATOR SYMPOSIUM: THE EDGE OF THE UNKNOWN IN PLANT, ALGAE, AND FUNGAL SYSTEMATICS

P.0713 Exploring Chlorella for biotechnological applications in biofuels and food supplements

Portia Alanyo[1], Gabriel K. Ameka[1]

1 Department of Plant and Environmental Biology, University of Ghana, Legon, Ghana.

The species of Chlorella are photosynthetic microalga widely known for their biotechnological application and ability to grow in different environmental conditions. The growing population and increasing demand for energy and alternative food sources to meet the growing demand called for the study of chlorella in large biomass to analyse the protein, carbohydrate, and fat composition of chlorella as an alternative source of food and energy. This study aimed to grow on a large biomass and examine the crude composition of chlorella cells, emphasising the protein, carbohydrate, and fat content. From the study, chlorella was found to have a high carbohydrate content (68.475g) and 0.142 g of fat, which could be explored for the production of biodiesel. (2.972g) of protein, which could also be explored for supplements and food. The findings of this study will be a steppingstone to exploring the biotechnological applications of chlorella in Ghana, as there is a rising need for an alternative source of clean energy and food.

P.0714 Disturbance and diversity: lichen species richness decreases with increasing anthropogenic disturbance

Laura Boggess[1], James Lendemer[2]

1 Mars Hill University and City University of New York, New York, USA. 2 New York State Museum, New York, USA.

Anthropogenic disturbance is rapidly increasing through habitat degradation, development, and deforestation. Gaps remain in understanding the effects of this disturbance on diverse and ecologically important organisms such as lichens. In North America, studies have focused on epiphytic macrolichens and catastrophic disturbance, largely ignoring microlichens and less-severe disturbances. Here we examine the effects of anthropogenic disturbance on overall lichen richness, including microlichens, and species richness of eight lichen functional groups (scored based on growth form, type of photosynthesizing partner, reproductive mode, substrate, lobe width, lobe size, chemical protection, and structures for physical protection). The study draws on a comprehensive data set of 872 species, in 208 one-hectare plots throughout the Southern Appalachian Mountains, a global biodiversity hotspot in eastern North America. A habitat disturbance index based on an established forestry metric was used as a proxy for anthropogenic disturbance. The index was quantified using a 10-part score including categories such as percent native tree canopy cover and degree of fragmentation. Linear models were used to compare habitat disturbance scores to overall species richness and to richness of functional groups. Results show that instead of following the Intermediate Disturbance Hypothesis, all groups uniformly follow a negative linear relationship: as disturbance increases, species richness decreases. Effective conservation of lichen richness should prioritize the maintenance of existing older, less-disturbed stands within large, contiguously forested areas.

P.0715 Cultivation of Pleurotus pulmonarius utilizing substrates derived from local agricultural waste

Anukwuorji A. Chidozie[1], Ebije Inikpi[2], Okigbo N. Raphael[3], Ogbuozobe O Gabriel[4], Eze N Hope[5], Ndubuisi C. Joel[6]

1 Department of Botany, Nnamdi Azikiwe University, Awka, Nigeria. 2 Department of Botany, Nnamdi Azikiwe University, Awka, Nigeria. 3 Department of Botany, Nnamdi Azikiwe University, Awka, Nigeria. 4 Department of Botany, Nnamdi Azikiwe University, Awka, Nigeria. 5 Department of Botany, Nnamdi Azikiwe University, Awka, Nigeria. 6 Department of Science Laboratory Technology, Federal College of Agriculture, Ishiagu, Ebonyi State, Nigeria.

The study was carried out to determine the most suitable substrate for the cultivation of *Pleurotus pulmonarius*. Three substrates were used for this study: palm fruit waste, maize cobs and yam peels. The three substrates were packaged in heat resistant polythene bags and pasteurized for four hours at 100 °C. The substrates were inoculated with mycelia under aseptic conditions. The spawn of *Pleurotus pulmonarius* was used to inoculate each bag of substrate. The substrates were incubated in darkness and covered with newspapers to keep carbon dioxide concentration high (15 - 20 %) in the room to promote mycelia running. Small incisions were made on the bags to give a cold shock to initiate fruiting. The result of the study showed that palm fruit waste produced the highest fresh weight of mushrooms (147.67 ± 24.583 g) while maize cobs produced the lowest fresh weight (119.01 ± 23.065 g). Maize cobs produced the highest dry weight of mushrooms (106.67 ± 4.041 g) while palm fruit gave the lowest dry weight (93.67 ± 2.082 g). Furthermore, palm fruit waste gave the highest biological efficiency of 91.60 ± 13.022 % while yam peels gave the lowest biological efficiency of 82.13 ± 35.072 %. The effects of the various substrates were discussed in relation to the dry weight and the biological efficiency of the cultivated mushroom. The impacts of the substrates especially palm kernel waste in the growth and yield of the cultivated mushroom recommends their use as suitable in the cultivation of mushroom.

P.0716 Building a deep learning classifier for > 200 species of freshwater phytoplankton - perspectives for taxonomy and biomonitoring

Ladislav Hodač[1], Susanne Dunker[2,3], Edwin Carreño[4], Lara Kösters[1], Marie Jamroszczyk[5], Maike Lorenz[6], Patrick Mäder[3,4,7], Jana Wäldchen[1,3]

1 Department of Biochemical Integration, Max Planck Institute for Biogeochemistry, Jena, Germany. 2 Department Physiological Diversity, Helmholtz-Centre for Environmental Research – UFZ, Leipzig, Germany. 3 German Centre for Integrative Biodiversity Research – iDiv (Halle-Jena-Leipzig), Leipzig, Germany. 4 Data-intensive Systems and Visualization Group, Technical University Ilmenau, Ilmenau, Germany. 5 Research Center for Experimental Marine Biology and Biotechnology, University of the Basque Country, Bilbao, Spain. 6 Experimental Phycology and SAG Culture Collection of Algae, University of Göttingen, Göttingen, Germany. 7 Faculty of Biological Sciences, Friedrich Schiller University Jena, Jena, Germany.

Identifying microscopic phytoplankton species is essential for monitoring freshwater ecosystems, but building a reliable deep learning classifier to automatically identify microscopic algae remains a challenge. Two major hurdles are the lack of a comprehensive image database (for training and testing) and the difficulty of assessing morphological variation within species. To address these challenges, we are conducting experiments using both monoclonal strains and phytoplankton samples. We are working towards a deep learning classifier that can identify over 200 freshwater phytoplankton species, representing all major algal groups. We are also exploring how deep learning can capture variation within species cultured as monoclonal strains and imaged using light microscopy and high-throughput imaging flow cytometry. We are also investigating the relative merits of both imaging techniques for real-world applications of our deep learning classifier. Focusing on monoclonal strains allows us to compare the effectiveness of genetic barcodes and images for identifying different species. While for some species genetic barcodes may provide more accurate automated identification than images, the opposite is true for other species. Therefore, we are also fusing both genetic barcodes and images for more accurate classification with deep learning models. Our ultimate goal is to develop a robust deep learning classifier that can accurately identify phytoplankton species from images, regardless of their natural environment, laboratory culture conditions, or image acquisition. We believe this will significantly contribute to the advancement of phytoplankton taxonomy and biomonitoring in freshwater ecosystems.

P.0717 Proximate analysis of Chlorella species in synthetic municipal wastewater (SMWW).

Lartey Olivia Naadu[1], Ameka Gabriel Komla[1]

1 Department of Plant and Environmental Biology, University of Ghana, Legon - Accra, Ghana.

In recent years, microalgae, particularly the genus *Chlorella sp.*, have garnered increasing attention for their diverse applications in nutrition, biofuel production, and environmental remediation. This study investigated the growth of *Chlorella sp.* in a synthetic medium waste water (SMWW) under controlled conditions, with a focus on understanding the nutritional composition, pigments, and growth dynamics. The research revealed a significant increase in optical density, indicating active growth, with replicate A exhibiting the highest growth rate. Chlorophyll analysis demonstrated substantial accumulation, suggesting enhanced photosynthetic activity. Notably, there was a decrease in total chlorophyll concentration, indicative of pigment adaptation. Carotenoids increased significantly, potentially as an adaptive response to changing environmental conditions. Proximate analysis of *Chlorella sp.* in SMWW indicated low crude fat content, making it a promising option for low-fat dietary considerations. The high fiber content suggested potential benefits for human and animal nutrition, while the ash content provided insights into the mineral composition. The protein and carbohydrate content positioned *Chlorella sp.* as a valuable source for food and feed applications, with implications for bioethanol production. These findings underscored *Chlorella's* versatility and potential for sustainable solutions in nutrition, bioenergy, and environmental management.

P.0718 Exploring the Evolution of Saprolegniales: were ancestral Oomycetes Plant Parasites?

Paula Ortega López[1,*], Jose Vladimir Sandoval-Sierra[2], Javier Dieguez-Uribeondo[1]

*1 Real Jardín Botánico-CSIC, Madrid, Spain, *portega@rjb.csic.es. 2 Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Bogotá, Colombia.*

Saprolegniales (Oomycetes) are a group of oomycetes that comprises plant and animal parasites and also saprotrophs. Due to their devastating effects on agriculture and wildlife, there have been numerous studies on plant parasitic oomycetes, including Saprolegniales. However, little is known regarding how lifestyles have evolved in this group. To study patterns and rates of the evolution and diversification of the saprotrophic and parasitic lifestyles, we have performed comparative phylogenetic methods (Bayesian inference and Maximum likelihood) on a large nuclear internal transcribed spacer (ITS) ribosomal DNA sequence database generated by our group. The results indicated that in the Saprolegniales there is a strong phylogenetic signal for the trait lifestyle indicating that ancestral oomycetes were parasites, most likely plant parasites while the saprotrophic lifestyle seems to be a derived character. In addition, the acquisition of the saprotrophic lifestyle appears to be first adopted by ancestral Saprolegniales. However, plant parasitism in the Saprolegniales seems to be a recent innovation acquired during events of diversification of the genus Aphanomyces. The mechanisms leading this transition to a parasitic lifestyle are unknown but appear to be different from those that occur in their close relatives, i.e., the Peronosporales.

P.0719 Almyronema epifaneia gen. nov., sp. nov. (Nodosilineaceae) isolated from an Indian mangrove forest

Arup R. Roy[1], Sandeep Chakraborty[2], Joydeep Mukherjee[1]

1 School of Environmental Studies, Jadavpur University, Kolkata, India. 2 Department of Botany, Achhruram Memorial College, Purulia, India.

Three simple thin thread-like filamentous three cyanobacteria were isolated from the intertidal soil of the lower Gangetic plain of the Indian mangrove forest, the Sundarbans. The three cyanobacterial strains formed a new cluster within the phylogenetic tree developed on the 16S rRNA gene sequence which was distinctive from the clade of the reference strain belonging to the *Euryhalinema* genus. Moreover, the sequence similarity of the 16S rRNA gene showed less than 94.4% similarity with the reference strain which confirmed the test strains to form a separate genus. The folded secondary structure of Box-B, D1-D1' and V3 helices of the internal transcribed spacer (ITS) region was unique in comparison to the reference genus as well as other members of the Nodosilineaceae family. P-distance analysis of the ITS region of the test strains showed 22% dissimilarity with the reference genus *Euryhalinema* which exceeded the cut-off (3%), strongly supporting the claim of a novel species. Differential morphological and ultrastructural characteristics such as the presence of various cellular inclusions (prominent large cyanophycean granule, glycogen α granules, lipid β granules and mucilaginous sheath), conical-shaped apical cell as well as cell width were supportive of the designation of novel species. Therefore, based on morphological, ultrastructural, and molecular analysis we proposed that S1, S6 and S10 cyanobacterial strains be affiliated as a new monophyletic genus *Almyronema epifaneia gen. nov., sp. nov.* under the newly established Nodosilineaceae family.

P.0720 Promoting diatom studies throughout the world and facilitating the exchange of information about diatoms.

Young ISDR[1]

1 International Society of Diatom Research.

The idea for "Young diatomists/Young ISDR" was created at the European Geosciences Union general assembly in Vienna in 2015 as a possibility of bringing the energy of early-career researchers and technicians dealing with diatom research into the council of the International Society of Diatom Research (ISDR). The aim was to create a platform for early career scientists and technicians in order to facilitate networking for them. In relation with this, the Young ISDR team core prepare presential and online activities for everyone and also it´s so active creating post in social media. With this poster we want to promote our community and make diatom research and its importance visible.

S.082. IAWA SYMPOSIUM THE CONTRIBUTION OF WOOD IN FOREST: FROM WOOD DYNAMICS TO TRAIT DIVERSITY AND CARBON GAINS

P.0721 Bronze age waterlogged wooden canoe from Sarno plain (Longola – Poggiomarino; Southern Italy): Insights from anatomical character

Angela Balzano[1*], Maks Merela[1], Alessia D'auria[3], Valeria Amoretti[2], Antonino Russo[2], Paola Sabbatucci[2], Stefano Mazzoleni[3,4]

1 Department of Wood Science and Technology, Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia. 2 Parco Archeologico di Pompei, Pompei, Italy. 3 Department of Agricultural Sciences, University of Naples Federico II, Portici, Italy. 4 Centro Museale – Musei delle Scienze Agrarie MUSA, Portici, Italy.

The excavation site of Longola (in the Sarno plain, about 10 km north-east of Pompeii), discovered in 2000, reveals a perifluvial village from the 2nd millennium BC. The Archaeological Park of Pompeii, MUSA Center, and the University of Naples Federico II are leading the valorisation and conservation of a Bronze Age wooden canoe from Longola. The 7 metre-long canoe (originally 13 metres) with a flat bottom, made from a single oak trunk, is considered one of the longest and oldest in the Mediterranean and was used for navigation on the River Sarno. The University of Ljubljana's Department of Wood Science and Technology conducted a complete anatomical characterization on small (1 cm^3), pre-restoration wood samples. Three wood samples were analysed, including SEM, optical microscopy and X-ray spectroscopy. A post-restoration sample with Kauramin® treatment assessed anatomical differences. The wood, which was identified as European white oak (most likely *Quercus pubescens*), showed characteristic features such as porous ring structure, multiseriate trunks and vessel lumens containing tyloses. The cellular degradation was characterised by thinning of the cell walls, granular secondary cell walls and the exclusive preservation of lignin. SEM revealed detailed structures such as pits and degraded cell walls, while X-ray spectroscopy identified significant Fe, S and Ca on the surfaces of the inclusions, indicating the possible onset of fossilisation processes. After Kauramin® treatment, the wood samples showed colour changes (lightening) and increased degradation of the cell wall structure, possibly due to the long period of time that elapsed between the deposition of the artefact and the conservation measures. This emphasises the crucial role of rapid and careful conservation strategies in preserving our cultural heritage.

P.0722 Secondary sexual dimorphism in wood and leaf anatomy of Mediterranean dioecious species may be responsible for gender-specific stress-response

Angela Balzano[1], Chiara Amitrano[2], Maks Merela[1], Riccardo Motti[2], Veronica De Micco[2]

1 Department of Wood Science and Technology, Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia. 2 Department of Agricultural Sciences, University of Naples Federico II, Portici (Napoli), Italy.

Secondary sexual dimorphism has evolved in response to many constraints, including those related to energy requirements. Plants with different morpho-anatomical traits can perceive and respond to stress factors differently. The stress-response in dioecious plants is an even more complex interplay of factors with sex-specific differences that can influence stress tolerance mechanisms. In Mediterranean ecosystems, the challenges to stress tolerance in dioecious species are exacerbated by changes in temperature and precipitation patterns and by the increase in extreme weather events due to climate change. Studying the wood anatomy of male and female plants in dioecious plants can reveal different sex-specific responses to these stress factors, which can reveal different vulnerability in male and female plants. Differences in the size, density, arrangement of vessels and composition of the secondary xylem may indicate sex-specific adaptations to environmental stress. The aim of this study was to investigate whether male and female plants of the Mediterranean shrubs *Pistacia lentiscus* L. and *Rhamnus alaternus* L. exhibit secondary sexual dimorphism in wood and leaf anatomy that would indicate different water use and gas exchange control. Therefore, we analysed the wood and leaf anatomy of male and female individuals of the two species growing in a Mediterranean site in southern Italy. Microscopy and subsequent image analysis allowed the quantification of functional anatomical traits related to the control of water efficiency/safety against embolism and photosynthetic efficiency. Parameters measured included stem vascular size and distribution, reaction wood formation, stomata characteristics, leaf tissue thickness and mesophyll density. The results indicated a sex-specific coordination of anatomical features leading to either efficiency or safety of water flow as well as different control of gas exchange. This understanding is crucial to better protect the diversity and resilience of these plant populations when confronted with the multiple impacts of climate change.

P.0723 Wood identification from the historical heritage of São Bento Monastery in Rio de Janeiro, Brazil

Thais Síston[1], Mauro M. Fragoso[2], Arno F. N. Brandes[3], Caudia F. Barros[1]

1 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Mosteiro de São Bento/Faculdade de São Bento do Rio de Janeiro, Rio de Janeiro, Brazil 3.Universidade Federal Fluminense, Instituto de Biologia, Departamento de Biologia Geral, Niterói, Brazil.

The São Bento Monastery in Rio de Janeiro, established in the 16th century, is renowned for housing numerous wooden artifacts found in both the cloister and the Church of Our Lady of Monserrate, serving various purposes: structures, coverings, furniture, and sacred images. Wood anatomy plays a crucial role in identifying the woods used and discerning preferences associated with specific historical periods or artists. This study aimed to identify wood samples from artifacts of the São Bento Monastery through macroscopic anatomical analysis and comparison with the wood samples of RBw. A total of 144 samples were collected or analyzed on-site, resulting in the identification of 142 samples belonging to 17 genera across nine families. Remarkably, all analyzed samples were sourced from Brazilian native trees, except one identified as *Quercus* sp. At least three pieces were produced overseas in Portugal and Italy, and even they were made using Brazilian woods, showcasing the relevance of the Brazilian wood trade since the 16th century. *Cedrela* sp. emerged as the most frequently used wood. The most common woods for each category were *Dalbergia nigra* (Brazilian rosewood) for furniture, *Cedrela* sp. (cedar) for coverings, and *Cedrela* sp. (cedar) and *Cordia* sp. (freijo) for sacred images. The use of *Cordia* in sacred art is not common in Brazil. The study identified four sculptors frequently cited in the monastery's records: Frei Domingos da Conceição, who worked for the Benedictine monks between 1669-1718 and favored *Dalbergia* nigra; José da Conceição and Simão da Cunha (1734-1774), who preferred *Cordia* sp.; and Inácio Ferreira Pinto (1787-1794), who showed a preference for *Cedrela* sp. In conclusion, this study not only provides valuable insights into the materials and preferences of artists but also contributes to our understanding of the native trees' uses over the centuries and its cultural context of woodworking in Brazil.

P.0724 Differences in fire regime impacts radial growth and recruitment of fire-resistant species

Rafael P. Albuquerque[1], Arno F. N. Brandes[2], Leonardo B. Nascimento[1], Jerônimo B. B. Sansevero[3], Andrea Sánchez-Tapia[1], Louise Klein Madureira[1], Cláudia F. Barros[1]

1 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, , Rio de Janeiro, Brazil. 2 Universidade Federal Fluminense, Instituto de Biologia, Departamento de Biologia Geral, Niterói, Brazil. 3 Universidade Federal Rural do Rio de Janeiro, Departamento de Ciências Ambientais, Instituto de Florestas, Seropédica, Brazil.

Fire-resistant trees play a significant role in the regeneration of fire-prone secondary formations in the Brazilian Atlantic Forest. These trees possess characteristics such as thick bark, high wood density, resprouting ability, and efficient seed dispersal, which enable them to withstand wildfires and establish themselves in unfavorable environments. However, alterations in fire regimes can have an impact on the growth of these trees and interfere in the ecological processes of forest regeneration. In this study, we used tree-ring analysis to compare the radial growth and age structure of a fire-resistant species under different fire regimes. We collected samples from 90 trees of *Moquiniastrum polymorphum* in two areas: one that experienced a single fire event and another that was subjected to wildfires in four different years. Trees subjected to multiples fires exhibited reduced radial growth compared to those in areas with a single fire event. It was observed a higher number of young individuals in the single burn area compared to the multiple burn area, highlighting negative effects of multiple burning in trees recruitment. The recruitment of new trees did not present clear pattern, suggesting that the propagules are able to germinate in the pastures. Despite functional traits that allows *M. polymorphum* trees to overcome wildfires, multiple burning reduce trees growth and jeopardize forest regeneration. Therefore, it is crucial to continue advocating for wildfire prevention measures within protected areas to enhance the effectiveness of passive restoration in the Atlantic Forest.

P.0725 Vascular cambium anatomy: a starting point for studies of the seasonality of radial growth and wood production

Thaís J. Vasconcellos[1], Monique S. Costa[2], Cátia H. Callado[1]

1 Instituto de Aplicação Fernando Rodrigues da Silveira, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Laboratório de Anatomia Vegetal, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, Brazil.

The speed of plant responses to the environment can vary significantly. Some of these responses can be recorded in the plant's body, and tree species, due to their longevity, have been the most indicated for understanding how forests have developed and how they will respond to future environmental changes. This is because tree species have cambial cells that, directly or indirectly influenced by the environment, integrate various signals into the produced structure. Thus, vascular cambium activity is crucial for the quantity and quality of wood produced, and understanding it is essential for elucidating aspects of anatomy and the periodicity of growth rings. However, unlike the anatomical study of wood, where there are adjusted processing protocols and manuals with parameters that must be analyzed and quantified, anatomical studies of vascular cambium often restrict to evaluating the number of cells in the cambial zone. Difficulties in collecting and processing samples are also on scientific agendas. Some of these difficulties are attributed to the heterogeneous resistance of tissues in the sampling zone. The cambium consists of layers of cells with small radial dimensions and no intercellular spaces. Because they are constantly dividing and differentiating, cambial cells are fragile, and their handling in the field and laboratory is challenging. The analysis of histological sections also deserves scientific standardization, regarding which anatomical aspects should be considered and which parameters show the greatest response to environmental fluctuations. This study aims to be a starting point for cambium analyses to be replicable and comparable. Here, we compile the main analysis protocols from collection to fixation and histological sectioning of the cambium. Additionally, we highlight the main measurable characteristics of this tissue that may provide clues to the records that can be retrieved in the xylem.

P.0726 Characterisation of the wood of Cordia L. species that occur in contrasting environments

Andrieli L. da Silva[1], Aline R. de Almeida[1], André L. Carvalho[1], Carmen R. Marcati[1]

1 São Paulo State University (UNESP), Botucatu, Brazil, andrieli.lima14@gmail.com

The genus *Cordia* L. has around 350 species distributed from humid to dry forests. In dry regions, the species have morphological and physiological attributes that suggest adjustments to cope with recurrent periods of drought, such as the presence of narrower xylem vessels. Drought events have become more frequent and are associated with the mortality of large populations of trees. Thus, the anatomical characteristics of the secondary xylem of plants that occur in different locations may contain information about the trees' adaptations to the climate. In this study, we characterized the wood anatomy of *Cordia* species in environments with different water availability. We used samples of *Cordia* wood collected in the Caatinga, a Seasonally Dry Tropical Forest in Brazil. *C. oncocalyx* (Allemão) Baill., native to the northeast of Brazil, occurs in the "Depressão Sertaneja", where the average rainfall is 817.7 mm/year (rains occur in 3 months of the year), and the average temperature varies between 26 °C and 28 °C. Meanwhile, *C. bicolor* A. DC. occurs in humid forests, but in the Caatinga it is found in milder environments, such as "altitude swamps". In this place the average rainfall is 1.483,5 mm/year (rains occur in 5 months of the year), and the average temperature varies between 24°C and 26°C. Both species have semi-porous rings, but the transition from wider to narrower vessels in *C. oncocalyx* is abrupt. This species, which occurs in semi-arid areas, has characteristics associated with drought resistance, such as narrow vessels and connective parenchyma between the vessels. *C. bicolor*, on the other hand, which occurs in humid environments, has wider and more widely spaced vessels, as well as a wide radius and procumbent cells, which help to translocate solutes between the xylem and phloem. Studies like this contribute to understanding the anatomical adaptations of the xylem to drought events.

P.0727 Foss-AI, an exploratory project using deep learning to extract paleobiological and paleoenvironmental data from fossil woods

Anne-Laure Decombeix[1]

1 CNRS-UMR AMAP, Montpellier, France.

Fossil wood is one of the most common types of plant fossils and often preserves fine features of the tissue (e.g., growth-ring boundaries) and of the individual cells themselves (wall thickness, ornamentation, etc.). Fossil wood provides information on the systematic affinities of extinct plants but also on their physiology and on the environmental conditions in which they grew. However, their study is time consuming and relies on a small number of experts worldwide, meaning that the paleobiological and paleoenvironmental information recorded in fossil woods remains largely unexploited. The exploratory project Foss-AI aims to automate the extraction of relevant qualitative (e.g., cell types) and quantitative (e.g., cell size) data from fossil wood sections using deep learning, the part of artificial intelligence that replicates the way humans gain certain types of knowledge. Recent studies have already demonstrated the feasibility of this approach on photos of histological thin-sections of extant plants, but fossil woods pose a few additional challenges due to their variable preservation and to the way they are prepared. In the first stage of the project, we are concentrating on the analysis of transverse sections of Devonian, Carboniferous, and Permian woods from key localities. High-resolution images of slides acquired with a digital microscope are labelled by human experts and used to train the AI. Results of the AI based analysis of new images will then ben compared to analysis by the human experts to assess the validity of the results on different types of fossil wood material. The long-term goal of this project is to develop tools that can help and promote the work of fossil wood experts by facilitating large-scale analyses, with significant implications for our understanding of past plant communities and their dynamics.

P.0728 Unveiling the wood anatomy of the overlooked agarwood Aetoxylon sympetalum (Thymelaeaceae)

Sarah D. Wilson[1], Peter Gasson[1], Teresa Terrazas[2]

1 Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, United Kingdom. 2 Department of Botany, Institute of Biology, UNAM, Mexico City, Mexico.

Agarwood is one of the most valuable non-timber forest products due to its gratifying aroma. This has led to overexploitation of agarwood produced by species from Thymelaeaceae such as *Aquilaria* spp., *Gyrinops* spp., *Gonystylus* spp. and a mostly unnoticed species, *Aetoxylon sympetalum*. Although a candidate, *A. sympetalum*has not been included in CITES, in contrast with other agarwood. This could be due to the difficulty in identifying this species owing to a lack of information regarding its wood anatomy. The aim of this study is to elucidate the wood anatomy of *A. sympetalum* and there by determine the features that distinguish this species from other agarwood species. Three wood samples of *A. sympetalum* were examined and sectioned. The resulting slides were then compared with the reference sample in the slide collection of the Jodrell Laboratory in the Royal Botanic Gardens, Kew. More samples were prepared for observation under scanning electron microscopy. The anatomical features were described according to the standard IAWA terminology. *A. sympetalum* is a diffuse-porous wood, with alternate and minute intervessel pits, vestured pits, very thick-walled fibres; mostly uniseriate rays and prismatic crystals within ray cells. The absence of diffusely arranged islands of phloem differentiates *A. sympetalum* from *Aquilaria* spp. and *Gyrinops* spp. The only noticeable difference with *Gonystylus* spp. is the thickness of the fibres which results in very high-density wood. The wood anatomy described agrees with Mandang & Wiyono (2002) but varies greatly from Tian *et al.* (2021) which is arguably a misidentification. This study is a reference point for identifying *A. sympetalum* which is paramount to its potential conservation and thus encourages its inclusion within CITES.

S.083. INTEGRATING CONSERVATION BIOLOGY AND SOCIETY ENGAGEMENT TO ENHANCE PROTECTION OF AT RISK FLORA

P.0729 Biodiversity of aeroterrestrial algae on selected ancient megalithic complexes in Bulgaria (South-Eastern Europe)

Miroslav I. Androv[1], Kristian R. Ivanov[1], Blagoy A. Uzunov[1], Georg Gärtner[2], Maya P. Stoyneva-Gärtner[1]

1 Department of Botany, Faculty of Biology, University of Sofia 'St. Kliment Ohridski', Sofia, Bulgaria. 2 Institut für Botanik der Universität Innsbruck, Innsbruck, Austria.

The peculiar ecological group of the aeroterrestrial algae comprises heterogeneous species inhabiting various substrates (rocks, tree barks, soil, etc.), which differ in chemical composition, humidity, temperature and illumination. This unusual group of algae contributes to the formation and enrichment of the soil by playing a part in the process of rock weathering and erosion. Although their key role in such crucial for the development and well-being of mankind events is acknowledged, aeroterrestrial algae are oftentimes overlooked and remain unexplored or poorly studied due to the need of cultivation for their correct identification. Considered a "white spot" for the biodiversity of Bulgaria and the Balkan Peninsula as a whole, the general data on this peculiar ecological algal group remain scarce and incomplete. The presented studies serve as a natural continuation of previous research done on the topic and are aimed at achieving a better knowledge on the biodiversity of algae that colonize and thrive in such diverse and often times inhospitable for other plant life habitats. Samples were taken during the summer of 2022 and 2023 from 16 ancient megalithic complexes located in Haskovo province (Bulgaria), considered to be the richest in such monuments. These man-made structures are completely exposed to the various environmental factors all year round, allowing the formation of various "pocketed" microhabitats, which might be housing unique and undescribed species. The collected material was cultivated in the laboratory environment under artificial conditions, until visible growth was present. So far, 31 species were identified: Cyanoprokaryota (8), Chlorophyta (15), Streptophyta (5) and Ochrophyta (4). The isolated species were deposited as monocultures in the Living algal collection of Sofia University (ACUS).

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P.0730 A biotope in a museum: positive feedback between conservation and scientific outreach

Lisa Angelini*[1], Helen C. Wiesinger[1], Chiara Steffanini[1], Jessica Zanotti[1], Alessandro Cavagna[1]

1 MUSE - Museum of Science, Trento, Italy.

Trento is a small city and capital of the Autonomous Province of the same name, located southeast of the Alps. The new science museum was built in 2013 and the biotope in 2022. The main wetland habitats of the Alpine valley floors in the region have been recreated here. It covers 2,000 square meters and includes a 2m high body of water (at its deepest point). The biotope represents a small oasis of biodiversity in the city center and is ecologically connected to other nearby wetlands. It is home to 76 typical wetland botanical species, half of the marsh species recorded in the Province. In all, there are more than 4,000 specimens. Of these as many as 53 accessions come from native genetic material, often from declining sites. The importance of the project, from a conservation point of view, lies in its status as a reservoir of biodiversity for aquatic ecosystems. In fact, 31 species are listed on the local red list, of which 26 are in the first three degrees of threat (VU, EN, CR) and 2 are regionally extinct. The communicative objective, on the other hand, is to bring society closer to an understanding of the importance of residual ecosystems such as wetlands, which were once considered useless and often cleared to make way for agriculture in particular. Of great interest is the complementarity of research activities, which also include the monitoring of invertebrate fauna, with educational activities and the social component. The activation of one element has so far led to the increase of others in a positive feedback system. The biotope was created in collaboration with the Employment Support and Environmental Enhancement Service of the Autonomous Province of Trento and can be freely visited every day.

P.0731 Biodiversity conservation assessment to protect two micro-endemic oaks from western Mexico: Quercus cualensis and Q. tuitensis

Maribel Arenas-Navarro[1,2], Jhenifer Reyes-Galvez[2], Javier Piña-Torres[3], Andrés Torres-Miranda[2]

1 Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México, Mexico. 2 Escuela Nacional de Estudios Superiores Unidad Morelia, Universidad Nacional Autónoma de México, Michoacán, Mexico. 3 Red de Biología Evolutiva, Instituto de Ecología, Xalapa, Mexico.

Oaks are recognized as a key species and play vital ecological roles across several ecosystems. In Mexico, oaks mainly inhabit temperate forests, although they can also be found in scrublands, dry forests, and humid tropical mountain forests. In western ranges from Mexico (Jalisco), at least 30 oak species have been recorded, considered a high richness and endemism center for red oaks (*Lobatae* section). *Quercus cualensis* and *Q. tuitensis* are two micro-endemic species in this region. The 2020 IUCN evaluation classified *Q. cualensis* as endangered and Q. tuitensis as vulnerable. However, neither species is protected under Mexico's standard norms, leaving them vulnerable to threats like deforestation, land use change, and climate change. The main objective of this study was to carry out a risk assessment method through the robust analysis of its current distribution (ecological niche modeling) and their projection to different climate change scenarios (optimistic and pessimistic), along with intrinsic and anthropogenic threats. This analysis will facilitate its inclusion in the Mexican standard norms. As a result, the risk method analysis determined that both species are in danger of extinction due to the reduced habitat and recent anthropogenic pressures such as the reactivation of an old gold mine and the illegal extraction of pine wood in the forests. These two species have very small distribution areas (between 125 - 154 km2), and with the climate change models, they reduced their environmental suitability by 100 % in pessimistic scenarios, even though these species inhabit different environments but with very narrow tolerance ranges. As a first step into conservation actions, we established educational strategies in the local schools with kids and adults about the importance of endemic species in the region, the importance of preserving species with local knowledge, and a legal framework to achieve their long-term protection.

P.0732 Evaluation and monitoring of populations of Huperzia selago in the Ayllón mountain range, Spain

Cristina Benavente-Mena[1], Sara García-Matesanz[1], Joaquín Castelo-Schremmer[2], Enrique Valencia-Gómez[1], José Mª Postigo-Mijarra[1], Felipe Martínez-García[3].

1 Complutense University of Madrid, Madrid, Spain. 2 Segovia, Spain. 3 Polytechnic University of Madrid, Madrid, Spain.

Huperzia selago (L.) Bernh is a boreoalpine lycophyte whose southern distribution limit in the Iberian Peninsula is found in the Central Range. Its presence in these mountain ranges is very scarce, with only two relictual populations in the study area, the Sierra de Ayllón. It is protected under various regional conservation figures, although it lacks national protection status. For instance, it is classified as a taxon of preferential attention in Castilla y León, rare in the Basque Country and vulnerable in Castilla-La Mancha. The objective of this study has been to assess the viability and conservation status of *Huperzia selago* populations in a specific area; the northern slope of the Sierra de Ayllón (Segovia, Castilla y León), which is the easternmost range of the Iberian Central Mountain Range. To achieve this, monitoring of some of these populations was conducted through the establishment of permanent monitoring plots, individual marking, and tracking throughout a vegetative period. Variables were measured to assess their development from a vegetative, phenological, and reproductive perspective, employing the chorological and demographic methodology outlined in the AFA project (Atlas of Threatened vascular Flora of Spain). In order to evaluate the viability of current populations, spore germination essays were conducted on collected spores, and the results were compared with previous data to understand the chorological and demographic trends of these populations, indicating differences among different plots based on their conservation status. The presence and conservation status of these populations of *Huperzia selago* suggest that protective measures need to be implemented in the study area as soon as possible, given that current land uses may be detrimental to the species.

P.0733 Monumental trees: a research project of the Monumental Trees Working Group of Italian Botanical Society

Giuseppe Brundu[1], Ignazio Camarda[1], Michele Lonati[1], Bernabè Moya[1], Antonio Morabito[1], Gianluca Piovesan[1], Giovanna Pezzi[1], Francesco Tarantino[1]

1 Italian Botanical Society, Working Group on Monumental Trees.

Primary and old-growth forests compared to semi-natural forest formations account for a very small part of the surface area in Europe. Currently, their scientific importance is also recognized due to their rarity in relation to the dynamics of natural vegetation. At the same time, their role may be affected by global change drivers such as the introduction of exotic species and climate change. It is assumed that the process will become more and more pronounced in the coming decades. An important role, linked to climate warming, will be played by thermophilic sclerophylls of the Mediterranean maquis. The spread of new diseases and exotic xylophagous insects is an increasingly pronounced problem, and it can affect more large trees. The unique structural characteristics associated with old forests and monumental trees support the existence of a whole series of exclusive habitats and microhabitats for many highly specialized species, which have no place in the younger phases of the forest. The scarcity of this type of natural forest ecosystems means that forest biodiversity related to senescent phases is highly threatened. This is also the source of the nationwide census carried out by the Ministry of Forestry and the protection measures to preserve old forests and monumental trees heritage, including its considerable scientific, feed, ornamental and cultural interest, including their role and importance in natural and urban environments.

P.0734 Digitalization and methodological innovation in protected flora monitoring in Spain

Carmela Capistrós Bitrián[1], Jorge Miguel Isabel Rufo[1], Luz Mauro Gutiérrez[1], Marta Viu Cuerda[2] , Noelia Vallejo Pedregal[2]

1 Department of Natural Environment, TRAGSATEC, Madrid, Spain. 2 Directorate-General of Biodiversity, Forests, and Desertification, Ministry for Ecological Transition and the Demographic Challenge, Madrid, Spain.

The United Nations Convention on Biological Diversity (1992), community regulations (Directive 92/43/EEC), and national legislation (Law 42/2007 and Royal Decree 139/2011) emphasize the importance of implementing monitoring and assessment policies for the biodiversity conservation status. Emerging technologies provide an opportunity to promote digitization and innovation in the data collection and processing for this purpose. The Ministry for Ecological Transition and the Demographic Challenge of Spain (MITECO) launched an innovative project in 2022 to improve the knowledge of protected flora at national level. Digitization is the key element driving the entire process, from data collection in the field to obtaining results. The methodology for real-time data collection relies on mapping and preset forms in the ArcGIS Field Maps application as the central tool to optimize the field workflow. These data will be compiled in the Integrated Information System of the Directorate-General of Biodiversity, Forests, and Desertification of MITECO, enabling visualization, analysis, and automatic download of results that will allow compliance with Spain's legal obligations and coordinated conservation actions to be proposed. The implementation of this technology for the monitoring of flora species presents strengths and challenges. Although it requires periodic maintenance and overcoming the digital divide, the app effectively replaces paper processes and enhances the convenience, traceability, and efficiency of data collection and processing. The complete digitization of the national-level protected flora monitoring programme is a milestone in biodiversity management and establishes a new replicable paradigm for future projects.

P.0735 Conservation approaches in species-rich Anatolian steppe ecosystem in Ankara, Turkey

Hayri Duman[1], Murat Doğan[2,3], Özge Atlı[4], Ferhat Celep[5]

1 Gazi University, Faculty of Science, Department of Biology, Ankara, Turkey. 2 Bülent Ecevit University, Department of Biology, Zonguldak, Turkey. 3 Ekoiz Environment, Çankaya, Ankara, Turkey. 4 Kazan Soda Electric, Yenikent, Sincan, Ankara, Turkey. 5 Kırıkkale University, Faculty of Engineering and Natural Sciences, Department of Biology, Yahşihan, Kırıkkale, Turkey.

Ex-situ conservation can provide a safety net for species that are at high risk of extinction in the wild, while in-situ conservation can help maintain the ecological processes and biodiversity of natural ecosystems. There are around 13,000 plant taxa in Turkey, of which around 4,000 taxa are endemic. However, despite its rich plant biodiversity, Turkey's plant species are under threat mainly from natural habitat destructions (i.e. deforestation, agricultural and mining activities, industrialization etc.), constructions (urbanization, dam and road constructions), overgrazing and climate change. Due to the rapidly growing population and surface area of Ankara city center, many plant species which are distributed the immediate surroundings of the Ankara city center are under high extinction risk, particularly local endemic species. Therefore, we aimed to establish a plant protection area with both ex-situ and in-situ conservation approaches in Kazan Soda license area in Kahramankazan county of Ankara-Turkey. 185 plant taxa belonging to 43 families, 29 of which are local or regional endemic, were taken under protection in this newly established plant conservation area. We also tried to raise public awareness about biodiversity and conservation for local people and students. In this way, we want to contribute to the continuity of some endangered taxa in their natural habitats.

P.0736 Use and conservation of wild agaves that are used to produce mezcal. The case of Agave potatorum and Agave marmorata

Juan A. Cruz-Rodríguez[1], Areli Buenabad[1], Raymundo Hernández[1], Atenógenes Licona[1]

1 Universidad Autónoma Chapingo, Texcoco, México.

Mezcal is a drink that is produced in Mexico from different species of the genus *Agave* (Asparagaceae). It has a high demand in the national and international market and although there are domesticated species, much of the species used are wild. Given that there are no strategies that ensure the persistence of their populations, this work proposes management options to harmonize their use and conservation. For this reason, a study was carried out on the conditions under which individuals of *Agave marmorata* and *Agave potatorum* develop. These are wild species from which high-quality mezcal is obtained. The study was carried out in xeric shrubland areas of the Tehuacán-Cuicatlán Biosphere Reserve, in central Mexico. The results show that individuals of both species depend on nurse plants for their establishment. However, *A. marmorata* prefers sites with deep soils and the presence of trees and shrubs, while A. potatorum grows on shallow soils where low-growing shrubs dominate. Although *A. marmorata* reproduces vegetatively, both species maintain their populations through seed production. Unfortunately, its inflorescences are cut to feed goats, which limits this process. To use and conserve these species, it is proposed: a) Guarantee the dispersal of seeds in the shrubland; b) Collect a small portion of seed to produce a plants in a nursery; c) To plant individuals within the shrubland according to the conditions that are favorable for each species; d) Do not establish monocultures; e) Incorporate agaves into the agroforestry component of agricultural areas, favoring their association with nurse plants. People will continue to consume mezcal if the conservation of agaves and the ecosystems in which they develop is guaranteed.

P.0737 A small agricultural land surrounded by urban development in eastern coastal Sri Lanka is a biodiversity refuge

Thanigasalam Shahirajh[1], Neela de Zoysa[2]

1 Mannankulam (Pvt) Ltd, Colombo, Sri Lanka. 2 Sudbury, USA.

Agricultural lands are undervalued as potential refuges for biodiversity. In a pioneering effort, the managers of Mannankulam Estate, a private agricultural landholding in Akkaraipattu, on the east coast of Sri Lanka, documented the flora and the habitats of the 12.5 ha property. The area is surrounded by urban sprawl, and is a remnant of extensive coconut plantations and rice fields for over a century, converted in the last two decades to residential and commercial use. The site consists of 32% coconut plantation, 32% plantation edge with natural regeneration, 27% rice fields and 9% lagoon edge with natural vegetation. The farm has been certified as organic and regenerative agriculture has been practiced since 2009. The in-depth 3-year (2021 – 2023) survey recorded 227 plant species belonging to 179 genera and 63 families. The proportion of native flora is high (78.4%), and includes one endemic shrub *Jeffreycia zeylanica.* Seventeen species recorded at the site are designated as Threatened on the National Red List, amounting to 9.6% of the native flora. This included 2 Critically Endangered (CR), 3 Endangered (EN), 6 Vulnerable (VU), 6 Near Threatened (NT). The Endangered woody climber *Argyreia elliptica* and epiphytic orchid *Vanda tessellata* are found in significant populations. The high floristic diversity was supported by regenerative cultivation practices, varied habitats with 40% semi-natural and natural areas, living fences, 900 coconut trees, and large old trees. The trophic complexity and niche availability increased due to fruiting trees, herbaceous and woody flowering species and rice fields which attracted a variety of frugivorous and granivorous birds, insect and avian pollinators, butterflies and caterpillars. This study exemplifies the potential of small privately owned agricultural areas to contribute to the research and to serve as vitally important biodiversity refuges in the larger hostile landscape.

P.0738 Conserving a critically endangered microendemic tree of the family Zygophyllaceae: Guaiacum unijugum

Victor Garcia Balderas[1], Kate Good[1], Daniel Wblesther Perez[2], Silvia Alvarez Clare[1]

1 The Morton Arboretum, Lisle, USA. 2 Centro de Investigaciones Biológicas del Noroeste S.C., La Paz, México.

Guaiacum unijugum is a critically endangered, micro-endemic shrub occurring in the southeastern coast of Baja California Sur, Mexico. Since 1995, only 29 living individuals have been documented, and the last known survey took place in 2007, when a genetic study was conducted across the genus. Before our study, the population's status was unknown, even though threats continue to expand in the region, and there are currently no living *ex situ* collections for this species. The goals of present study were to 1) document the status of the native population of *G. unijugum*, 2) quantify the propagation success under three experimental treatments, and 3) establish living *ex situ* conservation sites that will serve as an insurance policy against extinction. We conducted a plant survey in the area of occurrence to geolocate, measure, assess the reproductive status, and collect germplasm. We documented a total of 53 individuals and successfully collected over 2000 seeds. In order to quantify the propagation success, we tested three treatments: storage for 30 days, exposure to 200 ppm gibberellic acid (GA) as a germination enhancer, and leaching with water to reduce the effects of abscisic acid in germination inhibition. The seeds exposed to GA had the highest germination rate both when stored (73%) and planted fresh (74%). The leaching treatment decreased germination rate, resulting in 47% for stored seeds and 24% for fresh seeds. Results from this study are summarized in a propagation protocol published in English and Spanish, which provides recommendations for the reproduction of this species. We have also shared seeds with three botanic gardens in Mexico, which will result in the first living *ex situ* collections for this rare and threatened shrub. Next steps include working with local communities to promote *in situ* conservation and sustainable management practices.

P.0739 Evaluation and monitoring of populations of Swertia perennis in the Ayllón mountain range, Spain

Sara García-Matesanz[1], Cristina Benavente-Mena[1], Joaquín Castelo-Schremmer[2], Juan P. Martín-Clemente[3], Carlos Ruiz-López[3], José Mª Postigo-Mijarra[1], Felipe Martínez-García[3]

1 Complutense University of Madrid, Madrid, Spain. 2 Segovia, Spain. 3 Polytechnic University of Madrid, Madrid, Spain.

Swertia perennis L. (Gentianaceae) is a borealpine species whose most southerly populations in the Iberian Peninsula are found in the Central and Iberian mountain ranges. It is very scarce in these mountains, with relictual populations in the Ayllón range (province of Segovia, Autonomous Community of Castilla y León) and in the Albarracín range (province of Teruel, Autonomous Community of Aragón). In Spain, this species is protected under different regional protection categories: in Castilla y León, as a taxon of Preferential Attention and in the Foral Community of Navarra as Endangered. The aim of this study is to assess the viability and conservation status of its populations located on the northern slopes of the Ayllón range, the easternmost of the Central System. For this purpose, some of these populations have been monitored by installing permanent monitoring plots, marking individuals and monitoring them throughout the growing season. Variables that provide information on their evolution from a vegetative, phenological and reproductive point of view have been measured, applying chorological and demographic work methodology proposed in the project Atlas of Endangered Vascular Flora of Spain. In order to assess the viability of current populations, seed germination trials have been carried out, the results of which have been compared with previous data to determine the chorological and demographic trend of these populations. In addition, a preliminary study has been carried out to determine the phylogenetic relationships of this population nucleus with the rest of the known and characterised European populations, which are located from the Pyrenees to the north of Europe.

P.0740 Social perception of ecological systems: the view of technicians and managers in Spain

Ester Hernández-Correas[1], Alicia M. Navarro[2], Adrián E. Alcántara[1]

1 Biodiversity and Conservation Area, Rey Juan Carlos University, Madrid, Spain. 2 Department of Plant Ecology, Desertification Research Center (CIDE-CSIC), Valencia, Spain.

Drylands (precipitation/evapotranspiration < 0.65 mm/mm) hold significant ecological importance globally due to their high biodiversity, which is a crucial component for ecosystem functionality and ecosystem services that provide to human societies. Despite their ecological significance, drylands are generally undervalued compared to other ecosystems. Recognizing that endorsement and social support are vital for effective nature conservation, it becomes imperative to comprehend and define the scope of this collective psychological bias. Environmental managers and technicians have a direct impact in ecosystem conservation, so they constitute a priority group for evaluating whether they exhibit this bias and identifying the factors that may modulate it. For this purpose, we conducted an online semi-structured survey among environmental professionals in Spain. It consisted of three sections: general questions, landscape perception and management case studies. In the perception part, each landscape was always asked per se, without ever looking for a comparison. Here, we present a descriptive analysis of the data and the main patterns found in landscape perception among professionals engaged in natural environment management in Spain, based in both demographic and environmental variables.

Reference: Devesa, J.A. & Martínez-Sagarra, G. 2023. Plantas vasculares endémicas de Andalucía. Villa del Río, Córdoba: MG Marketing. https://doi.org/10.20350/digitalCSIC/15691

P.0741 Current state of the algal collection of the Sofia University "St. Kliment Ohridski"- ACUS

Kristian R. Ivanov[1], Blagoy A. Uzunov[1], Georg Gärtner[2], Miroslav I. Androv[1], Maya P. Stoyneva-Gärtner[1]

1 Department of Botany, Faculty of Biology, University of Sofia 'St. Kliment Ohridski', Sofia, Bulgaria 2 Institut für Botanik der Universität Innsbruck, Innsbruck, Austria.

Living algal collections are an important tool for biodiversity studies and serve as an important genetic archive for species conservation. In addition, they provide quick and easy access to algal strains that can be used both for research purposes, for bioremediation of contaminated habitats, for biotechnological purposes, etc. This necessitates the maintenance and future development of the algal collections, which includes their continuous enrichment with new strains and equipment updates. The Living algal collection of SU "St. Kliment Ohridski" was established in 2006 and in 2010 it was registered in the WDCM (Word Data Centre for Microorganisms) under number 965, with the acronym ACUS (Algal Collection of the University of Sofia) (Uzunov et al. 2011). The collection is also a member of the WFCC (World Federation for Culture Collection) and the GCM (Global Catalogue of Microorganisms). To date, the algal strains in the collection are nearly 300 including representatives from the blue-green, green and yellow-brown evolutionary lines. The number of strains is constantly increasing with each subsequent year being fulfilled by local and foreign materials. Currently, the photo-documentation by electron microscopic images (SEM, TEM) is going-on, and the collection was equipped with new growing chambers, inverted fluorescence microscope with micromanipulator and horizontal tubular photobioreactor.

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P.0742 Is peyote Lophophora diffusa (Cactaceae) a species destined for extinction?

Cecilia Leonor Jiménez-Sierra[1], Omar Díaz-Segura[1], María Loraine Matias-Palafox[2], Erika Arroyo-Pérez[1]

1 Universidad Autónoma Metropolitana-Iztapalapa, Ciudad de Mexico, México. 2 CONABIO, Ciudad de Mexico, México.

Lophophora diffusa (Croizatl) Bravo (peyote or peyote queretano) is a Cactaceae used by natives and collectors for its chemical and ornamental properties. However, its population dynamics are unknown. Data were obtained by following a population of Querétaro (Mexico) for nine years, and for this data we constructed four annual matrices, one five-year matrix and a mean matrix. Individuals were categorized by size as: seedlings, juveniles and adults (1-4). The finite population growth rates (λ) were calculated with transition matrices. The relative importance of size categories and demographic processes: stasis (S), growth (G), regressions (R) and fecundity (F) were determined using sensitivity and elasticity matrices. Prospective and projection analyses of population size are presented. The annual lambda (λ) varied from (0.8 - 0.98), and only for one year this value was significantly < 1. The relative importance of demographic processes was Stasis > Growth > Regression > Fecundity. In relation to the relative importance of individual by sizes, adult 2 (A2) had the highest influence on the λ value. Projections indicate that the population could disappear in < 50 years. To conserve the peyote queretano, it is necessary protecting its habitat, and reconsidering the legal restrictions to facilitate the cultivation of this species.

P.0743 Analysis of the degree of compliance with protected species legislation in Spain

Felipe Martínez García[1], Álvaro Suero Barrado[1]

1 Polytechnic University of Madrid, Madrid, Spain.

Spain has an important biodiversity which, as in other countries, is suffering from the impact of human activities. To conserve the natural heritage, Spain has a set of legislation at both national and regional (autonomous) level. These laws contain, among other things, catalogues of protected species wich have been established at national level (National Legislation) and at regional level (Legislation of the Autonomous Communities). In all of them, taxa are classified in categories according to their degree of threat. The Laws also establish that these administrations, within the scope of their respective competencies, must approve management plans for these species. Therefore, by comparing the number of management plans approved and those that should have been approved, we can assess the degree of compliance with the legislation on protected species. This comparison shows that: 1.- Overall (national plus autonomous administrations): only 24% of the plans that should have been made have been approved. 2.- At national level: the Ministry for Ecological Transition has only approved 3.7% of the plans for the species under its jurisdiction. 3.- At regional level: the 17 Autonomous Communities that make up the Spanish state do not comply with the legislation either: 3.1. The vast majority have only drawn up a maximum of 30% of the plans to which they are obliged by national legislation. Some administrations stand out negatively, such as the Community of Madrid, which has not drawn up any plans at all. 3.2.- The vast majority do not comply with their own legislation. Only one of them (La Rioja) has fully complied with its duty to approve all the management plans for the endangered species in its own regional catalogue. In conclusion, therefore, we can state that the degree of compliance with the legislation by the administrations is very low and varied.

P.0744 Important areas of flora: methodological proposal and tool for the conservation of the Sierra de Guadarrama National Park (Spain)

Felipe Martínez García[1], José Luis Izquierdo Moreno[2]

1 Polytechnic University of Madrid. Madrid, Spain. 2 Research, Monitoring and Evaluation Center, Sierra de Guadarrama National Park. Madrid, Spain.

The Sierra de Guadarrama National Park and its Peripheral Protection Zone (SGNP-PPZ) (Iberian Central System, provinces of Madrid and Segovia), harbors a rich vascular flora (about 2000 native species) subjected to strong anthropic pressures. The aim of this work has been to establish an objective methodology for the identification and mapping of priority areas for the conservation of flora, as a basic tool for the management of the National Park. Some 500 taxa of conservation interest have been analyzed. From these have been selected 189 that meet the following two conditions: being scarce: found in less than 100 UTM squares of the SGNP-PPZ; being of chorological interest: taxa endemic to the Iberian Peninsula or be a relict population. Each of these has been evaluated using 4 criteria: General area of distribution; Abundance within the SGNP-PPZ; Habitat in which it is found; Degree of threat according to the 2008 RedList. For each criterion a scale of 10, 7, 4 or 1 point has been established to indicate the degree of threat to the survival of the species. All the populations (totaling 2474) were georeferenced in 1x1 km grids and valued. Subsequently, the maps were cross-referenced, adding the score obtained in each grid, which made it possible to identify and map the priority territories for conservation. A total of 521 grids have been identified with some population, 47% of those of the SGNP-PPZ. The valuation range was 8 points the grids with the lowest scores and 602 points for the grids with the highest number of populations of interest. All the 2,474 populations of the selected species were georeferenced in 1x1 km grids and valued with the proposed scale. Maps were cross-referenced, adding the score obtained in each grid, which made it possible to identify and map the priority territories for conservation.

P.0745 Development of new extinction threat assessment based on locality counts: A case study of 3,180 vascular plants in Kanagawa, Japan

Chihiro Myotoishi[1], Wataru Ohnishi[2], Tetsukazu Yahara[3], Akiko Satake[4]

1 Department of System Life Sciences, Kyushu University, Fukuoka, Japan. 2 Kanagawa Prefectural Museum of Natural History, Kanagawa, Japan. 3 Kyushu Open University, Fukuoka, Japan. 4 Faculty of Science, Kyushu University, Fukuoka, Japan.

Due to ongoing urban development, vascular plants inhabiting Kanagawa Prefecture, adjacent to the megacity of Tokyo, are expected to have undergone continuous decline in their localities. To quantify this decline, we utilized a database constructed through presence-absence surveys conducted during three survey periods, Phase 1(1979-1989), Phase 2(1996-2000), and Phase 3(2013-2017), for 3,180 vascular plant species across 111 localities in Kanagawa. This database enables us to monitor transitions from presence (1) to absence (0) or from absence (0) to presence (1) at each locality between phases. Subsequently, we calculated per-year increase and decrease rates for species i, *bi*and *di*, between phases. Consequently, we obtained four rates for each species, *bi,12*, *bi, 23*, *di,12*, and *di,23*, where subscripts 12 and 23 indicate the transition from phase 1 to 2 and phase 2 to 3. We then calculated the medians of four rates, *Mb,12*, *Mb,23*, *Md,12*, and *Md,23*. As a result, *Mb,12*, *Mb,23*, *Md,12*, and *Md,23* were P.040 (95%*CI*[P.003, P.170]), P.068(95%*CI*[P.005, P.333]), P.284(95%*CI*[P.117, P.636]), and P.143(95%*CI* [P.036, P.497]), respectively. Notably, *Mb,12* increased to *Mb,23*, whereas *Md,12* decreased to *Md,23*, suggesting an acceleration in new locality generation and a deceleration in existing locality loss. However, medians of net changes, *bi,12- di,12* and *bi, 23- di,23,*were -P.237(95%*CI* [-P.613, P.002]) and -P.077(95%*CI*[-P.484, P.280]). This result indicates the locality loss exceeds the locality generation in Kanagawa. Notably, both *bi,12- di,12* and *bi, 23- di,23* are negative for 1,057 species, suggesting the potential extinction of these species in future. This calculation introduces a new indicator to quantify the extinction threat in vascular plants.

P.0746 Generating species threat abatement and restoration metri for Brazil's national red list of plants: lessons learned and prospects

Eduardo P. Fernandez[1,2,3], Lara M. Monteiro[4,5], Eduardo T. Amorim[2,3], Gláucia F. Crispim[2,3], Lucas S.B. Jordão[2,3], Marinez F. de Siqueira[1,2,3], Monira Bicalho[2,3], Pablo H.A. Melo[2,3], Vicente Calfo[2,3], Renata de T. Capelão[4], Nina Pougy[4], Bernardo B.N. Strassburg[4], Louise Mair[6]

1 Rio de Janeiro Botanic Garden Research Institute, Rio de Janeiro, Brazil. 2 Brazilian National Centre for Plant Conservation - CNCFlora, Rio de Janeiro Botanic Garden Research Institute, Rio de Janeiro, Brazil. 3 IUCN Species Survival Commission, Brazil Plant Stand Alone Red List Authority, Rio de Janeiro, Brazil. 4 Instituto Internacional para Sustentabilidade, Rio de Ja-

neiro, Brazil. 5 University of Vermont, Vermont, USA. 6 University of Newcastle, Newcastle, UK.

To effectively track the progress of the Convention on Biological Diversity (CBD)'s 2030 Global Biodiversity Framework (GBF), the scientific community has been working on creating a set of policy-relevant indicators. The Species Threat Abatement and Restoration (STAR) metric was developed to quantify the potential contribution of threat abatement and habitat restoration actions at a particular site to the reduction in species global extinction risk. Brazil, renowned for its vast biodiversity and as a signatory member of the CBD, has been testing the application of such metrics to monitor conservation action impacts. We discuss the outcomes of the application of the threat abatement component of STAR to the Brazilian plants national red list, alongside a debate of its caveats and potential applications. We included in downstream analyses 2,791 endemic species assessed as near threatened or threatened between 2010-2020 by Brazil's flora Red List Authority, CNCFlora/JBRJ. We found that tackling threats from agriculture could reduce extinction risk for 29% of evaluated species, while mitigating threats from urban expansion and fires could reduce risk by 21% and 10%, respectively –especially at the Cerrado and Mata Atlantica Hotspots and in parts of the Amazon. The full application of STAR nationally, including advancing with its restoration component, will involve increasing assessments of endemic species to reduce selection and geographic data biases, effective translation of targets from global to national level and further engagement of distinct societal sectors to consistently track the regional impact of threat reduction on global conservation goals.

P.0747 Conservation and recovery of threatened cacti from a global hotspot: the role of Rio de Janeiro Botanic Garden and partners

Eduardo Fernandez[1,2,3], Marcio Verdi[1,2,3], Eduardo Amorim[2,3], Fernanda Wimmer[2,3], Gláucia Crispim[2,3], Lucas Jordão[2,3], Luara Tourinho[3], Tainá Rocha[3], Deyse Reis[3], Mario Gomes[2,3], Marinez Siqueira[1], Camila Nardy Delgado[2,3], Monira Bicalho[2,3], Gustavo Martinelli[2,3]

1 Rio de Janeiro Botanic Garden Research Institute, Rio de Janeiro, Brazil. 2 Brazilian National Centre for Plant Conservation, Rio de Janeiro Botanic Garden Research Institute, Rio de Janeiro, Brazil. 3 IUCN Species Survival Commission, Brazil Plant Stand Alone Red List Authority, Rio de Janeiro, Brazil.

The IUCN Green Status of Species (GSS) enables the evaluation of the recovery potential of threatened species and helps to refine needed/ongoing conservation actions. Rio de Janeiro Botanic Garden (JBRJ) play a key role in furthering research in plant diversity and conservation in Brazil and relies in its national and international plant conservation authority, the Brazilian National Centre for Plant Conservation (CNCFlora), to detect at-risk species and to develop and implement Conservation Actions Plans (CAPs). The current challenge of JBRJ/CNCFlora is to monitor progress of these integrated frameworks in order recover species' populations and to attest actions' efficiency. Here, we explore the role JBRJ/CNCFlora played in promoting the conservation of 10 cacti species of the *Cerrado* Hotspot and applied the GSS protocol to evaluate the recovery potential and the validity of in-place conservation actions. Species were selected based on their conservation status, inclusion in conservation mechanisms and because they are the focus of tailored and participatory conservation projects. These are *Uebelmannia buiningii*, *Discocactus horstii*, *Discocactus pseudoinsignis* (Critically Endangered - CR), *Arrojadoa eriocaulis*, *Brasilicereus markgrafii*, *Micranthocereus auriazureus*, *Micranthocereus violaciflorus*, *Pilosocereus fulvilanatus*, *Uebelmannia pectinifera* (Endangered - EN) and *Cipocereus minensis* (Vulnerable - VU). Our results showed that all target cacti are rare, with narrow distribution and/or with unknown population tendencies, suggesting elevated Conservation Dependence and Recovery Potential because they are particularly sensitive to environmental changes. These results indicate that it is highly likely that without these actions these species' situation would be twice worse as today. It is urgent reinforcing conservation actions related to the 10 cacti, as if other conservation strategies are not taken urgently and effectively, it is possible that in 10 years many subpopulations will be extirpated. Further studies should help to catalyze conservation actions that will drive sustained conservation for these iconic species of the Brazilian flora.

P.0748 Enhancing biodiversity conservation in Madagascar: MNP-Biodiv database for improved data management and knowledge exchange

Lantotiana Randriamanana[1], Bernard Riera[2], Lalatiana Randriamiharisoa[3] Timothée Le Pechon[4,5], Sylvain G. Razafimandimbison[6], Florian Jabbour[1].

1 Institut de Systématique, Évolution, Biodiversité, Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France. 2 Muséum National d'Histoire Naturelle, mécanismes adaptifs et Évolution, Paris, France. 3 Madagascar National Parks, Ambatobe Antananarivo, Madagascar. 4 Meise Botanic Garden, Meise, Belgium. 5 Fédération Wallonie-Bruxelles, Service Général de l'Enseignement Supérieur et de la Recherche Scientifique, Brussels, Belgium. 6 Department of Botany, Swedish Museum of Natural History, Stockholm, Sweden.

Madagascar, renowned for its rich biodiversity, hosts 123 protected areas (PAs), with 43 under the management of Madagascar National Parks (MNP). Since its establishment in 1991, MNP has meticulously curated a vital biodiversity database for these PAs. Despite the wealth of data, the absence of a dedicated Database Management System (DBMS) has hindered seamless data consultation and exchange with external entities. This research project addresses this critical gap by introducing the "MNP-Biodiv" database, with a specific focus on the botanical component, termed "MNP-Flora." The primary objective is to enhance access to biodiversity information and knowledge tools through the implementation of a robust DBMS. This technological intervention aims to facilitate efficient data retrieval, analysis, and sharing, ultimately fostering collaboration with other institutions dedicated to biodiversity research and conservation. The study centers on the development and optimization of the MNP-Flora database, considering factors such as data accuracy, user-friendly interfaces, and compatibility with existing biodiversity databases. By establishing a dedicated DBMS, the research seeks to streamline the process of managing and disseminating crucial flora-related information, thereby contributing to informed decision-making in biodiversity conservation efforts. The implications of this research extend beyond the immediate benefits to MNP, encompassing broader implications for biodiversity research and conservation initiatives in Madagascar. The proposed database management system serves as a foundational step towards creating a comprehensive and interoperable platform, fostering collaborative efforts and advancing our understanding of Madagascar's unique and fragile ecosystems. The study also outlines the subsequent development of "MNP-Fauna," the second component of the MNP-Biodiv database, ensuring a comprehensive and integrated platform for biodiversity management in Madagascar.This research aligns with global efforts to leverage technology for conservation and underscores the pivotal role of database management systems in enhancing biodiversity research, management, and conservation practices.

P.0749 Preserving the Menabe ecosystem: A community-driven approach to baobab habitat restoration

Onja Hariveloniaina Morilline Razanamaro[1], Nirintsoa Raharinomena[2], Stephano Andriamiadana[2], Tahiana Andriaharimalala[3], Seheno Andriantsaralaza[2]

1 Parc Botanique et Zoologique de Tsimbazaza Rue Fernand Kassanga, Tsimbazaza, Madagascar. 2 Mention Biologie et Ecologie Végétales, Faculté des Sciences, Université d'Antananarivo, Antananarivo, Madagascar. 3 Centre National de recherches sur l'Environnement, Fiadanana, Antananarivo, Madagascar.

Understanding and predicting the consequences of species extinction is crucial for conservation efforts worldwide. The Menabe region of Madagascar faces alarming deforestation rates, losing 4,000 hectares in 2014 within the Menabe Antimena protected area, one of the region's largest. This highlights the urgent need for solutions based on ecological restoration principles to address both economic and conservation challenges. Our study investigates the success of baobab habitat restoration efforts in the Andranomena Special Reserve and the Mangoky Ihotry Protected Areas Complex within the Andranopasy rural commune. Through close collaboration and empowerment of local communities, reforestation activities, nursery programs, and monitoring have been implemented for the two sites. After two years in the nursery, the seedling survival rate reaches an impressive 70%. The implemented awareness strategy and active involvement of local communities near the restoration sites have proven effective in safeguarding the area from fire, livestock encroachment, and woodcutting. This strong sense of ownership and stewardship fostered through community engagement ensures the long-term protection of the restored baobab habitats, setting a remarkable example for conservation efforts across Madagascar.

P.0750 Threatening factors of Iranian bulbous plants

Khadijeh Riahi Rad[1], Sajad Alipour [2]

1 Department of Horticultural Science, Faculty of Agriculture, Tarbiat Modares University, Tehran, Iran. 2 Department of Horticultural Science, School of Agriculture, Shiraz University, Shiraz, Iran.

Iran, with its unique climatic and topographic conditions, is home to about 8200 species of vascular plants. Approximately 400 of the 8200 species are classified as Bulbous plants. Iran is home to a diverse range of bulbous plants, many of which are threatened by various factors. This paper provides an overview of the threatening factors facing Iranian bulbous plants, including habitat loss, overgrazing, illegal bulb and flower harvesting, flower smuggling and supply to the market, climate change, urbanization, road construction, mining activities, drought and pests and diseases. The impact of these factors on the conservation status of these plants is discussed, along with potential conservation measures to mitigate these threats. The paper also highlights the importance of addressing these threatening factors to ensure the survival of Iranian bulbous plants and the preservation of their ecological and cultural significance.

P.0751 New records and new localities of rare and threatened algal species in Bulgaria

Blagoy A. Uzunov[1], Maya P. Stoyneva-Gärtner[1], Georg Gärtner[2], Miroslav I. Androv[1], Kristian R. Ivanov[1]

1 Department of Botany, Faculty of Biology, University of Sofia ‘St. Kliment Ohridski’Sofia, Bulgaria. 2 Institut für Botanik der Universität Innsbruck, Innsbruck, Austria.

The poster presents selected unpublished data on new findings in regard to the biodiversity and conservation of Bulgarian algae. They concern both the first records of some prokaryotic and eukaryotic species and the new localities of algae considered rare or threatened in the country. All data have been obtained during the sampling campains conducted during the last twenty years in different regions of Bulgaria from both aquatic and aeroterrestrial habitats. The habitats include standing and running waters, such as large and small reservoirs, natural lakes and streams, but also some thermal waterbodies and rock formations. The selection of algae for this presentation was based on their taxonomic position combined with the rare global distribution, findings in protected areas or significant reservoirs, or on their extremophilic way of life. Some examples of newly recorded for the country potentially harmful toxin-producing species or their localities are also provided. For example, poster presents the first records of the cyanoprokaryotes *Merismopedia ferrophila, Asterocapsa* sp., the chrysophycean *Dinobryon annulatum* as well as data on new localities of the cyanoprokaryote *Nostoc zetterstedtii*, the red alga *Hildenbrandia rivularis*, the green algae *Macrochloris multinucleata* and *Paradoxia multiseta*.

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P.0752 Community work and orchid flowers listing in the south region of Oaxaca, México

Alejandra Villafuerte-Salazar[1], Emmanuel Méndez-García[1], Héctor Elid Orduña-Eslava[1], Oswaldo R. Castro Martínez[1]

1 Department of Biology, Universidad Autónoma Chapingo, Texcoco, Mexico.

In Mexico, the family Orchidaceae is noteworthy with 1,263 species. Its greatest diversity is reported in the Mexican southeast; unfortunately, that region presents one of the highest levels of marginalization in the country. For this reason, we decided to carry out a community work in the south region of Oaxaca, Mexico to do a diagnostic about the general panorama, the biodiversity and the orchids applications to propose conservation alternatives and a sustainable management. The project was carried out from June to December 2022 and 2023, monthly visits were scheduled in which the local people were interviewed about orchid's knowledge. Environmental education workshops and field trips to document and photograph the species richness *in situ* were also organized. As a result, 14 visits were made in which we included 6 environmental education workshops, the field trips and the assessment of the Mexican orchids. We characterized 4 types of vegetation, Mesophile Mountain Forest, pine Forest, pine-oak Forest, tropical deciduous forest and we documented 33 species, from which 10 are in risk of extinction (i.e., *Laelia dawsonii, Artorima erubescens, Prosthechea karwinskii, Cypripedium molle, Rhynchostele cervantesii,* etc.). With the information collected, we elaborate two manuals for intern use in the community. Progress was made in the construction of a shade house to preserve specimens of rescued orchids for their protection and maintenance by the communal authorities. In the ethnobotanic part of the project, we documented the use of *Laelia dawsonii* in the celebrations of the deceased saints as part of the biocultural wealth of the region. For 2024 we planned the consolidation of the Environmental Management Unit as a strategy for the exploitation and conservation of community species.

P.0753 Seed banks: conserving the threatened flora of Spain

Silvia Villegas-Navarro[1], Yolanda Ruiz[2], Carlos De Mier[3]

1 Real Jardín Botánico, CSIC, Madrid. Spain.

The seed bank together with the laboratory unit at the Real Jardín Botánico, CSIC (in the future RJB, CSIC) are developing a project to raise awareness in society about the need for the work carried out in the field of *ex situ* conservation at the RJB, CSIC. The project brings scientists, technicians, teachers and students from five secondary schools in Madrid, Spain working in *ex situ* conservation together to share knowledge and expertise. It is structured in five actions: (1) to develop a photography exhibition with images of seeds capturing different techniques such as macrophotography and scanning electronic microscope and combining information on *ex situ* conservation of threatened species in Spain, (2) to create a morphological seeds digital atlas and a (3) identification guide available on the RJB, CSIC website and printed, (4) to set an educational programme for secondary school students to help them learn about the floristic diversity of Spain and the risk of threats to wild plants; their vulnerability and the threats to their populations and habitats, as well as the need and importance of developing conservation strategies through scientific knowledge. Plants and their seeds will be used as teaching resources and will promote inquiry-based learning to develop critical thinking. And finally (5) to develop library resources and dissemination of the project. The different actions will make it possible to show differences and numerous facets of seeds unknown to society and most of the time not visible to the human eye, such as the beauty, rarity and variety of forms and ornamentations of a vital organ for the life of plants.

P.0754 China's conservation on Plant Species with Extremely Small Populations (PSESP)

Yang Jing1

1 Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China.

China is one of the most biodiversity-rich nations worldwide, with the third largest inventory of vascular plant species (ca. 35,000). The country is recognized as one of the world's biodiversity hotspots and a conservation priority region globally. Despite unprecedented efforts aimed at conserving endangered species, the loss of biodiversity in China is a serious problem. Plant Species with Extremely Small Populations, PSESP, is a conservation concept developed in China from 2005, aimed at rescuing most threatened plant species of China. Species qualify as PSESP if they are less than 5000 mature individuals in total and fewer than 500 individuals in each isolated population. In 2012, the China government began the Implementation Plan of Rescuing and Conserving China's PSESP (2011–2015), which specified 120 PSESP and assigned their conservation priorities. Located at the Himalaya region and having half of the plant species in China, Yunnan Province, has taken a major lead in rescuing and conserving PSESP. From 2009 to 2017, Yunnan Province invested 21.58 million RMB (ca. 3 million USD) in special funds for the rescue and conservation of PSESP and implemented 92 conservation projects. Several species are part of successful conservation programs including Acer yangbiense, Cyclobalanopsis sichourensis, Craigia yunnanensis, Manglietia ventii, Manglietiastrum sinicum, and Paphiopedilum armeniacum. In 2022, new government plans for conserving PSESP in China and Yunnan Province were issued, including 100 national and 101 provincial species in the lists respectively. In 2023, the first International Training Course on Conservation and Utilization Techniques of PSESP was held in Kunming City, Yunnan Province, where techniques, case analysis, practical experience and according theories or researches of China's PSESP conservation system were introduced. Hopefully, with the experience gathered in the last decade, the China's conservation practice of PSESP could achieve more results and dedicate its success to global biodiversity conservations.

S.084. INTEGRATING ECOLOGY INTO MACRO AND MICROEVOLUTIONARY STUDIES PROBLEMS AND OPPORTUNITIES IN CURRENT AND PAST DATA SOURCES

P.0755 Adaptive potential of the Leaf Economics Spectrum in the Brassicaceae

Luis Chausson Garate[1], José Miguel Valderrama[1], Urte Schlüter[1], Andreas P.M. Weber[1]

1 Institute of Plant Biochemistry, Heinrich Heine University, Düsseldorf, Germany.

Carbon concentrating mechanisms (CCM) refer to the diverse mechanisms plants have evolved to maximize the efficiency of CO_2 assimilation in photosynthesis, avoiding or compensating the photorespiratory loses derived from the oxygenase activity of RuBisCO. C4 photosynthesis is the utmost example of carbon fixation efficiency. Plants displaying intermediate carbon compensation points (CCP) between C4 and C3 species (10-40 ppm) have been described, termed as C3-C4 intermediates. These plants achieve carbon concentration via the photorespiratory glycine shuttle, a CCM that requires fewer and less complex modifications than C4 photosynthesis. Convergent evolution of the photorespiratory glycine shuttle indicates a substantial improvement of carbon economy under certain environmental conditions. Trade-offs between resource allocation to growth, reproduction and survival are key in determining plant ecological strategies and evolution. The Leaf Economics Spectrum (LES) is a set of six leaf traits that provides a quantitative basis for evaluation of interspecific differences across ecosystems based on leaf trait trade-offs. Variation in several LES subtraits between C3 and C3-C4 intermediate species has already been reported in the Brassicaceae, linked to differences in physiology and genome structure. Interspecific variance in the LES across environmental conditions can facilitate the identification of correlations between photosynthesis type and fitness in the Brassicaceae. The family of the Brassicaceae, where C3-C4 intermediates do not encounter C4 relatives, defines an excellent framework for addressing this question. Overall, a combination of morphological features, together with molecular and physiological data, will be employed to elucidate the interspecific differences in the LES across various environmental conditions in a panel of species of the Brassicaceae.

P.0756 Drivers of variation in the ecological strategy of a Mediterranean early flowering geophyte across a coast-inland gradient

Gabriel Cainelli[1], Paola De Giorgi[1], Gianni Bedini[1,2], Daniela Ciccarelli[1,2]

1 University of Pisa, Pisa, Italy 2 Centro interdipartimentale per lo studio degli effetti del cambiamento climatico (CIRSEC), Pisa, Italy

Crocus etruscus Parl., an early-flowering geophyte endemic to central Italy, may serve as a pivotal focus for conservation efforts amidst the ongoing challenges posed by climate change. This study aims to elucidate the ecological adaptations of *C. etruscus* by investigating its leaf functional traits and employing the Competitor-Stress tolerant-Ruderal (CSR) systems. Through this research, we seek to decipher the relationships between *C. etruscus* and its environment. We selected 12 locations spanning a coast-inland gradient within the distribution range of *C. etruscus*. At each site, vegetation surveys were conducted, encompassing soil sampling and the collection of leaves from both *C. etruscus* and the dominant species in the local communities. We measured key functional traits, including Leaf Area, Leaf Dry Matter Content, and Specific Leaf Area. Furthermore, we calculated the CSR strategy of *C. etruscus* and the Community Weighted Mean CSR strategy of the surrounding communities. Additionally, relationships among soil variables (R matrix), species abundance (L matrix), and traits (Q matrix), were studied using RLQ analysis to discern the impact of soil properties on the CSR strategy of the surrounding plant communities. *Crocus etruscus* showed a SC/CSR strategy, while the surrounding communities exhibited higher variability, mainly on the S-R axis. Our investigation underscores the robust influences of soil nutritional properties on the functional traits of both *C. etruscus* and the surrounding plant communities. Specifically, we observed a shift towards more conservative strategies in nutrient-poor soils and a prevalence of more acquisitive strategies in nutrient-rich soils. This study pioneers the application of a functional framework to analyze an early-flowering geophyte within the context of Mediterranean forest communities, providing a crucial baseline for assessing the potential impacts of climate change on this species and for guiding future conservation efforts.

P.0757 Evaluating the performance of hindcasts in ecological models combining phytogeographic and palaeobotanical data

Simone De Santis[1,2], Carlos Vila-Viçosa[3,4], João Gonçalves[3,5], Salvador Arenas-Castro[6], João Honrado[1,3], Francesco Spada[7], Donatella Magri[2]

1 Department of Biology, Faculty of Sciences, University of Porto, Porto, Portugal. 2 Department of Environmental Biology, Sapienza University of Rome, Rome, Italy. simone.desantis@uniroma1.it. 3 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal. 4 Museu de História Natural e da Ciência da Universidade do Porto – Herbário PO, Universidade do Porto, Porto, Portugal. 5 proMetheus—Research Unit in Materials, Energy, and Environment for Sustainability, Instituto Politécnico de Viana do Castelo, Viana do Castelo, Portugal. 6 Department of Botany, Ecology, and Plant Physiology, Faculty of Sciences, University of Córdoba, Córdoba, Spain. 7 Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden.

Species Distribution Models (SDMs) are often used to predict present and past geographic ranges, although they are rarely validated with paleodata. By combining current occurrence data, fossil records, and SDMs, we investigated the postglacial dynamics of *Arbutus* and the bioclimatic constraints that shaped its demographic history as an important representative of the Mediterranean broadleaved evergreen element. We applied an ensemble-modelling approach (BIOMOD2) to obtain present and past predicted distributions for the whole genus *Arbutus* in the Mediterranean regions, along the Atlantic coast of Europe, and in Macaronesia. SDMs were based on double-checked occurrence records from literature and bioclimatic variables that were retrieved from the CHELSA and PaleoClim databases. Spearman correlation allowed us to select three subsets of variables with moderate/low correlation ($|r|<0.7$) for model development. Past distribution maps for the last 30 ka at 1000-year intervals were obtained from >1000 chronologically controlled pollen and macrofossil records. First, we trained the current model with modern occurrences to provide hindcasts for each Paleoclim period (LGM, HS, BA, YD, EH, MH, and LH), which were further validated through metrics retrieved by a 2x2 confusion matrix (modelled presences/absences vs. observed presences/absences). Secondly, we trained models for each PaleoClim period using past occurrences and then validated them through the 2x2 confusion matrix. Results show excellent performance for the BIOMOD2 models (TSS>0.9) and the balanced accuracy of the confusion matrix, which does not show a linear correlation between the hindcast performances and the distance in time. This result indicates that the combination of fossil records and modelling techniques is an effective tool to depict the Quaternary demographic history of tree taxa, to explain the modern biogeography of the Mediterranean evergreen ecosystems, to anticipate potential range shifts in relation to ongoing climate change, and to raise hypotheses to inform phylogeographic research.

P.0758 Study of the ecological condition of the vegetation present in the Cantoblanco campus prior to the reintroduction of grazing

Celia González López[1], César A. López Santiago[1], Francisco M. Azcárate[1,2]

1 Department of Ecology, Universidad Autónoma de Madrid, Madrid, Spain. 2 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain.

The mosaic structure of Mediterranean dehesa systems is greatly dependent on the presence of herbivores. Abandonment of traditional pastoralist practices, such as transhumance, results in a decrease in ecosystem diversity, altering its multifunctionality and causing a loss of its resilience to changes. In the frame of this social and ecological context, we propose the reintroduction of these low-intensity practices in the Cantoblanco campus of the Autonomous University of Madrid as a tool for ecological restoration. This work centres on the characterization of the plant communities found before the arrival of herds and its comparison with natural grasslands with a history of traditional grazing practices. We obtained results that concur with what was expected based on previous knowledge. The campus plant community was scarcely diverse and the more abundant species present showed a clear dominance above the rest. This makes for an ecosystem with a marked homogenous structure. Comparison with grazed grasslands showed significant differences with the abandoned system. Not only did grazing enhance species richness and functional diversity, but it also improved evenness between plant families' occurrence rates. Reintroduction of herbivory under a correct management that ensures an intermediate grazing intensity has the objective of restoring lost ecological processes that regulate the ecosystem to ensure future functionality in a context of global change. Moreover, the maintenance of traditional pastoralist practices has a broader goal of bestowing these activities with a higher value as providers of cultural and regulation ecosystem services.

P.0759 Are we ready for macrogenetics? A meta-analysis of genetic databases for macrogenetic analyses in Europe

Marvin Klümpen[1], Laura Rose[1], Piyal Karunarathne[1]

1 Institute of Population Genetics, Heinrich-Heine University, Duesseldorf, Germany.

The rapid increase in publicly accessible genetic data in recent years has spurred the emergence of macrogenetics, focusing on large-scale genetic analyses to understand evolutionary questions, including the impact of environmental factors and life-history on genetic variation. Such large-scale analyses not only enhance our broader understanding of population genetics but also offer insights for biodiversity monitoring and conservation strategies. Despite abundant genetic data, large-scale analyses remain rare. Within this context, we conducted a comprehensive meta-analysis of Europe's vascular plants using the NCBI nucleotide database. The primary objective of this study was to evaluate the potential of public genetic data for large-scale biogeographical analyses. For a total of 9,763 native plant species occurring in Europe, we systematically examined 23.5 million sequences, focusing on georeference indexing and the presence of barcoding genes, crucial for spatial genetic diversity studies. Our initial results show that over 13% of the data is either georeferenced or traceable to their location. The percentage of native species with at least 10 sequence hits ranges between 40-80% in most countries, gradually decreasing with the number of hits. We identified the most common gene markers used in studies and the georeferenced data for these markers are available for ca. 30% of the species within Europe, making it possible to conduct large-scale genetic diversity analyses.

P.0760 Regeneration niche of Abies religiosa (Kunth) Schltdl & Cham. in a high mountain forest of Mexico

Lauro López-Mata[1], Gabriel Arroyo-Cosultchi[1]

1 Colegio de Postgraduados, Texcoco Estado de México, Mexico.

The regeneration niche is a concept closely related to ecological processes of seed germination and the establishment and recruitment of seedlings. The seedling stage is a demographic bottleneck, where high risks of death and high mortality rates occur, causing significant impacts on the natural regeneration processes of forests. Based on a survival and mortality risk analysis of a cohort of seedlings, we investigated which variables are most important for their survival, under two conditions of canopy openness, and their light environment and soil properties. We placed 17 1-m^2 plots in which all seedlings of *A. religiosa* from the 2019 cohort were marked, numbered and followed for a year. Seedlings were measured for height, embryonic leaves, nodes, visible damage, and survival at 3-week intervals. We evaluated the light environment with hemispheric canopy photographs taken from each plot, and based on these, we stratified the canopy into two categories: partially closed and open canopy. The soil properties per plot were analyzed from composite samples taken from the corners of the plots. Soil humidity and temperature were evaluated with data loggers placed 10-15 cm from the soil surface. Analyzes were performed using the SAS LIFETEST and LIFEREG procedures. Survival curves differed between canopy categories (Log-Rank: $X^2 = 8.35$, df = 1, P < P.5). Survival was higher under open canopy (0.29 ± P.1) than under partially closed canopy (0.20 ± P.1). The most important variables, with positive effects on seedling survival, were associated with seedling height and number of nodes, proportion of direct incident light, soil bulk density, average soil temperature and soil humidity. Such a set of variables clearly defined the regeneration niche of *A. religiosa*.

P.0761 Current distribution and future range shift projections of six common soil moss species in Europe.

Manuel Molina-Bustamante[1], Rosa M. Chefaoui[2], Cristina Ronquillo[3], Jennifer Morales-Barbero[1], Nagore G. Medina[1], Joaquín Hortal[3]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Instituto de Investigación en Cambio Global, Universidad Rey Juan Carlos, Móstoles, Spain. 3 Museo Nacional de Ciencias Naturales - CSIC, Madrid, Spain.

We assess the climatic determinants influencing the current geographic distribution of six moss species in Europe, and use this information to project their potential distributions under future climatic scenarios, emphasizing the impact of geographic habitat suitability shifting in this region. Our focus on bryophytes allows accounting for their unique dispersal mechanisms, particularly the role of spores in overcoming geographic obstacles. The six species include *Ptychostomum capillare*, *Hypnum cupressiforme* and *Syntrichia ruralis* widespread across temperate areas; *Dicranum scoparium*, from cool temperate areas in Northern Hemisphere; and *Homalothecium aureum* and *Tortella squarrosa* which are restricted to temperate and warm temperate areas of Europe and North America, associated to the Mediterranean climate. We apply Species Distribution Models (SDMs) to estimate and project habitat suitability in present conditions and under different climate change scenarios. Then, we assess the likelihood of future suitable areas being colonized by each species in the future by calculating the minimum distance to a future cell with a habitat suitability value equal or greater than the current one, thus accounting for the proximity of potential source cells for colonizing future suitable areas. Further, we measure the distance of known populations (i.e. occurrence records) to future suitable cells. We found that all species show cells with adequate habitat suitability (>0.5) that are closer than 1 km from future cells with higher or equal habitat suitability than present. However, the analyses based on known populations show that *T. squarrosa* and *H. aureum* populations are located far from future cells with high habitat suitability 0.8. This analysis indicates that Mediterranean species such as *T. squarrosa* and *H. aureum* are at increased risk due to climate change, as their current populations are situated significantly further from areas projected to have high habitat suitability in the future.

P.0762 Population genetics, thermotolerance and acclimation: an integrative approach to study diversification of tropical plants

Sara S. Pedraza Narváez1

1 Department of Ecology and Evolutionary Biology, University of California, Los Angeles, USA.

Understanding the mechanisms of species diversification in the tropics is a fundamental goal in ecology and evolutionary biology. Tropical mountains have gained special attention due to their vast number of species and the varying conditions along elevation gradients, making them valuable for studying the influence of abiotic factors on species evolution. Janzen's seasonality hypothesis provides crucial insights into the mechanisms of speciation in tropical montane species and the role of temperature in the diversification process. This hypothesis states that the stability of climate in the tropics results in narrower elevation ranges in tropical mountains, limiting the migration of species across elevation due to marked physiological adaptations in organisms. The limited dispersal and specific thermal adaptations in montane tropical organisms can drive speciation in isolated populations via parapatric or allopatric speciation. My research project aims to integrate phylogenomics, ecology, and physiology to evaluate these two mechanisms of speciation and rigorously test the connection of Janzen's seasonality hypothesis with speciation. Using a comparative phylogeographic approach on several co-distributed, unrelated tree species, I will link phylogeographic patterns with organismal performance to examine signals of isolation along elevation and across geography. Specifically, I will quantify gene flow, genetic divergence, and thermotolerance (T50) of plant populations from eight species across elevation gradients to assess the prevalence of isolation along elevation (i.e., parapatry) *vs.* isolation across mountain ranges (i.e., allopatry). In addition, harnessing the power of a transplant experiment in the Colombian Andes, I will assess the thermal plasticity of these montane species at both physiological and genetic levels by analyzing transcriptomes, gene expression, and thermotolerance (T50) of plants transplanted at different elevations. This integrative approach will shed light on the mechanistic role of thermal performance in plant speciation and will contribute to understanding the evolution of tropical flora in the Anthropocene.

P.0763 Areas of endemism of Angiosperms in the U.S.A.

Anna Saghatelyan[1], Tania Escalante[2], Gerardo Rodríguez-Tapia[3]

1 Biology Department, McMurry University, Abilene, USA. 2 Grupo de Biogeografía de la Conservación, Universidad Nacional Autónoma de México, Mexico City, Mexico. 3 Instituto de Ecología, Universidad Nacional Autónoma de México, Mexico City, Mexico.

The use of large databases and quantitative methods might help resolve some disagreements in the delineations of North American floristic provinces. We aimed to find spatial patterns of a set of plants in the U.S.A. by conducting endemicity analysis (EA). We compiled a dataset with 775 species belonging to 321 genera and 93 families of seed plants from the U.S.A. floras. We chose unrelated taxa in order to reveal patterns that might not be apparent from single taxon analyses. Half of the species came from Asteraceae, Fabaceae, Hydrophyllaceae, Apocynaceae, Ranunculaceae, Melanthiaceae, Boraginaceae, Rosaceae, Ericaceae, Nyctaginaceae, Cactaceae, Grossulariaceae, Cornaceae, and Gentianaceae. Digitized herbarium specimen data were downloaded from iDigBio and cleaned. With the final dataset, which included 223,929 specimen point records, we performed six endemicity analyses with different parameters using the NDM/VNDM program. Obtained consensus areas (CAs) were converted into shapefiles (.shp), mapped with QGIS, and used to identify areas of endemism (AoEs) by selecting each AoE under the grid size that yielded the highest number of high-scoring endemic species. We identified 31 AoEs and 12 nested AoEs. The study area splits into three floristic centers, the Northwestern and Eastern, both supporting the Boreal subkingdom, and the Madrean, supporting the Madrean subkingdom of the Holarctic Kingdom of Takhtajan. All analyses recovered AoEs with the highest scores in the Madrean region (endemicity score 90; 164 endemic species) with particularly high numbers of narrow endemics in dryer areas. The Madrean region showed two significant centers of accumulation of nested or partially overlapping AoEs: the Southwestern and Southcentral CAs. Most significant in endemism AoEs, the Sonora–Mojave arid center, Chihuahuan Desert, California Floristic province, Gulf Coastal Plain, and southern Appalachians, harbor basally branching taxa of several genera, subfamilies, and even families, based on the observations of some species, which allowed identification of the AoEs.

S.085. INTEGRATING FLORISTIC, BIOGEOGRAPHIC AND ETHNOBOTANICAL STUDIES FOR CONSERVATION

P.0764 Dilemmas and challenges in the knowledge of the genus Cinchona in Peru

Joaquina Alban-Castillo[1,2], Isabeu Cruz-Ríos[1], Eder Chiquillo[1,2], Mery Suni[2], Giovana Vadillo[2], Julio Torres[1], Lizeth Huamán[1], Elizabeth Cochachin[1]

1 Natural History Museum. UNMSM. Lima, Peru. 2 Faculty of Biological Sciences, UNMSM, Lima, Peru.

The quinas and pseudoquinas (*Cinchona* L., *Ladenbergia* Klotzsch and related species) belong to monophyletic genera included in the Cinchoneae tribe, Rubiaceae. Their origin is myocenic and the diversification of recent lineages is concordant with the final stages of the elevation of the Andes. Currently, the genus *Cinchona* in Peru comprises 18 species that are scarcely collected and restricted to the eastern montane forests, 30% of which are endemic. Recent collections in the tropical Andes have allowed the recognition of new species, both in *Cinchona* and *Ladenbergia*, demonstrating that there are still many gaps in knowledge in the delimitation of their species, which need to be understood before establishing adequate conservation and reforestation plans. This study proposed to determine the diversity of quinas (Cinchona L.) species in Peru, their current and potential use value, and in particular those species that are endemic or categorized at some level of vulnerability. Determining the uses and forms of use by local populations has defined the degree of utility that these species represent for said populations. Likewise, it has contributed to know how intrinsic and extrinsic factors affect the propagation of quinine, providing answers for the correct form of seed storage and seedling establishment. Three new species of quinas were described for science: *Cinchona sholletsii* sp nova, *Cinchona aticochensis* sp nova and *Cinchona reynelii* sp nova. The distribution of four species is extended for the Peruvian territory: three of them registered only for Ecuador (*Cinchona officinalis* L., *Cinchona capuli* L. Andersson, and *Cinchona mutisii* Lamb.) and one species registered so far in Venezuela, Colombia and Ecuador (*Cinchona lancifolia* Mutis.). A total of 20 species of the genus *Cinchona* were recorded for Peru, establishing the differences and similarities among them.

P.0765 Documenting the floristic diversity of the ancient Minoan city of Faistos, Crete

Eleftheria Antaloudaki1, Emmanouil Avramakis[1]

1 Natural History Museum of Crete – University of Crete, Crete, Greece. eri@nhmc.uoc.gr

The Minoan city of Faistos in Crete was the second most important city of the Minoan civilization dated back from 2.000 BC to the 1st century BC. Archaeological sites often preserve, indirectly, the biodiversity of an area as human activities are restricted by their legal protection status. The research project entitled "Biodiversity and Archaeological Sites - Documenting the Flora and Fauna in Archaeological Sites" was implemented for twenty archaeological areas across Greece and it was funded by the Natural Environment and Climate Change Agency (NECCA). The first stage of the project has already finished and the present contribution is a preliminary inventory of the floristic research of Faistos archaeological site, located at Messara Valley, south-central Crete. The area shows a quite remarkable variety of species and a floristic catalog has been created by field observations and search of the relevant literature. In Faistos archaeological site, ca. 100 taxa (species and subspecies) belonging to more than 70 genera and 45 families have been recorded so far. Apart from the wild flora documented in the site, many alien species have been recorded, as they were planted as ornamental and the overall alien flora constitutes ca. 15% of the total recorded flora. The field investigation will continue in spring 2024, aiming to record as far as possible the complete flora of the area.

P.0766 Assessment of the potential of plant resources for human nutrition in the Ethiopian highlands through the past millennia until the

Casas-Gallego, Manuel[1, 2], Bruch, Angela A.[3], Neumann, Katharina[1], Bodin, Stéphanie[1], Demissew, Sebsebe[4], Schmidt, Marco[5], Hahn, Karen[4]

1 Department of Palaeoanthropology, Senckenberg Research Institute, Frankfurt am Main, Germany. 2 Department of Geodynamics, Stratigraphy and Paleontology, Complutense University of Madrid, Spain. 3 ROCEEH Research Centre "The role of culture in early expansions of humans" of Heidelberg Academy of Sciences at Senckenberg Research Institute, Frankfurt am Main, Germany. 4 Department of Plant Biology and Biodiversity Management, College of Natural and Computational Sciences, National Herbarium, Addis Ababa University, Addis Ababa, Ethiopia. 5 Palmengarten der Stadt Frankfurt am Main, Germany. 6 Institute of Ecology, Evolution and Diversity, Goethe University Frankfurt am Main, Germany.

Ethiopia is a hotspot of biodiversity and home to more than 6,500 vascular plant species. It comprises numerous endemic species and harbours the largest area of Afromontane forests in Africa. Ethiopia is also a location of great archaeological significance and, therefore, it has the potential to shed light on the use of plant species as food resources by prehistoric humans. In this study, we assess the potential availability and distribution of plant food resources for humans in the vegetation units of the Ethiopian highlands for the past 22,000 years. To do so, we compiled comprehensive lists of species that occur in each vegetation unit. An extensive database currently under development (*PlantBITES*) gathers ethnobotanical information of these species, mainly on edibility and other uses of plants that occur in natural environments. Based on such records it is possible to analyze and quantify the potential availability of plant resources for humans in a given vegetation unit. The identification of wild edible plants with high utilization potential is also useful to current nature conservation and sustainable plant use, as vegetation units with higher utilization potential of wild plants are more easily classed as worthy of protection. Our data show that dry and moist Afromontane forests have a similar but much higher exploitation potential of food resources than the vegetation types of higher altitudes. In a further step, we plan to use ecological niche modelling to simulate the probability of occurrence of species with high potential to be used as staple food under the effect of changing climatic conditions of the past 22,000 years. This will allow us to estimate which species were more likely to occur in the area where archaeological sites are located and which ones were more likely to have played a key role as food resource for humans.

P.0767 Spanish hña-hñu ethnobotanical microherbarium from El Olivo, Ixmiquilpan, Hidalgo, Mexico

Sonia Rojas[1], Carlos Castillejos[1], Reynalda Roldán[1], Carolina Rojas[1]

1 Universidad Nacional Autónoma de México, Ciudad de México, México.

Mexico is home to great plant and traditional diversity, in terms of the use of plants; and ethnobotany is responsible for recording that interaction. In Mexico, xerophilous scrub is favored by this activity, as it covers approximately 40% of the territory, but Hidalgo stands out for its flora, and it also shows a great variety of ethnobotanical uses. In Ixmiquilpan, specifically in El Olivo, Hña-Hñu is spoken, a variant of Otomi, which is one of the 68 indigenous languages of Mexico. Here the population actively and traditionally uses its flora and in its language, but despite this, there are no records that allow this knowledge to be preserved, since it is transmitted orally and much of it is lost. Therefore, a bilingual floristic-ethnobotanical study of the xerophytic flora of El Olivo was carried out, which was recorded in a microherbarium to preserve its local use. Interviews were carried out in Spanish and Hña-Hñu with residents where common names, uses, plant organs used, photographs, among others, were obtained. A microherbarium was built with 31 species grouped into 19 families and 29 genera, it contains information on the species in Spanish and Hña-Hñu and is accompanied by the pressed specimen and organized in a handmade book. The microherbarium, containing the pressed specimen, taxonomic, morphological, ethnobotanical information and an image of the specimen, allows for a quick consultation without the need to have experience in the area, and also helps to preserve the use and management of the species in the locality in the regional language and to the development and consultation of future works.

P.0768 Traditional edible plants from home garden and ecosystems provide food for Riacho do Mel Quilombola Community, Brazilian Northeast

Rodrigo Mortari[1], Consuelo L.N. Andrade[1], Nildon C.S. Pitombo[1], Abel A. Conceição[1]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Bahia, Brazil.

The knowledge of traditional edible plants benefits the subsistence of the people to meet an adequate nutrition, especially in local rural communities, as quilombolas communities in Northeast of Brazil. Thus, our objective was to survey the edible plants used as traditional food in Riacho do Mel Quilombola Community (Chapada Diamantina, Bahia State, Northeast Brazil) to evaluate the plant parts used and to identify the environment where these plants can be obtained. We interviewed 21 informants from Riacho do Mel Quilombola Community who cited 83 species (495 citations) which were grouped into eight plant parts categories (root, stem, cladode, leave, flower, fruit, seed, and oil) found in four environments (home garden, *carrasco* [forest], *gerais* [savanna], and caatinga). Fruit was the main plant part used (75%), followed by leave (18%) and cladode (4%). Fruit and cladode were the unique parts used that can be get in the four environments, while root, stem and leave parts were exclusive from home garden, which was the environment with the most diversified plant parts used (six). The most frequent food acquisition environment was the savanna (40% [256/640]), followed by home garden (29% [183/640]), forest (26% [166/640]), and caatinga (5% [32/640]). So, the ability to get food from different species and parts of plants, in three ecosystems and in the home gardens, enable feed supply, showing the importance of biodiversity and the traditional plant knowledge in the Riacho do Mel Quilombola Community. Our study highlights the savannas, home gardens, and forests as environments to get traditional food, the savannas and forests offering a high variety of fruits, while the home gardens are easier and provide more diversified plant parts and the totality of leave supply, the second plant part most cited by informants.

P.0769 An updated inventory of the cultivated plants of Cuba

Miguel Esquivel1, Karl Hammer[2]

1 National Center for Laboratory Animal Production, CENPALAB, Havana, Cuba. 2 The Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany.

As a result of the exploration, collection and systematic study of plant genetic resources in Cuba from the 80s of last century, an unexpected diversity was discovered, that arose from the combination of varied ecological conditions throughout the Cuban archipelago, as well as the influence of diverse cultural groups that have made up the Cuban ethnos along centuries. An Inventory of Cultivated Plants in Cuba (ICPC) was compiled in 1992, that includes 1,045 taxa, from 531 genera and 117 families, associated to 727 synonyms and 1,671 folk names. In the last three decades, numerous actions have been carried out related to the spheres of agricultural production, the environment, health and popular religions, among others, which have involved the intensive use of new and diverse plant species. This information has allowed us to update the ICPC with 167 new taxa, belonging to 65 families and 131 genera, which adds 18 new families and 72 new genera, as well as 62 new synonyms and 268 new folk names. The current figure of the ICPC amounts to 1,212 taxa, belonging to 603 genera and 135 families, which has 789 associated synonyms and 1,939 common names. Many of the new species included are not only new reports of cultivated plants in Cuba, since 89 of the new 167 reported taxa (53 %), are not included in the Mansfeld's World Database of Agricultural and Horticultural Crops. Very interesting is the presence on 15 endemic taxa from Cuba, that reflex the very wide used made of natural plants resources. These results have made it possible to recommend that Central America and the Caribbean be considered as a new extended region of cultivated plant diversity.

P.0770 Vanilla genetic resources from Cuba

Miguel Esquivel[1], Thaisbel Esquivel[1], Edgar López Herrerea[2]

1 National Center for Laboratory Animal Production, Havana, Cuba. 2 Autonomous University Chapingo, Texcoco, México. elopezh@chapingo.mx

The *Vanilla* genus is represented in Cuba by a total of 11 species, of which nine grow in the wild, and two (*V. planifolia* and *V. pompona*) are mainly cultivated in collections. The first reports of *Vanilla* in Cuba were made by Alexander von Humboldt, who during his first trip to Cuba in 1800, found it growing in the surroundings of Havana, but did not publish it until after visiting Mexico years later. Ramon de la Sagra y Periz, Director of the Botanical Garden of Havana, promoted its cultivation without success. Juan Tomas Roig y Mesa, at the Agronomic Experimental Station of Santiago de Las Vegas, studies its cultivation in detail already in the second half of the 20th century, without it becoming a crop of economic importance. In conjunction with the Autonomous University Chapingo and Veracruzana University, among other Mexican entities, and the support of the Spanish companies Eyaika Salnés and Fabrez, a project for the collection, maintenance and evaluation of *Vanilla* genetic resources in Cuba is being developed, with a view to its potential use in the gastronomic, biotechnology and cosmetics industries. To date, we are working with five *Vanilla* species (*V. dilloniana, V. phaeantha, V. planifolia, V. poitaei, and V. pompona*), which are maintained and multiplied *in vitro* and *in vivo*. Other Cuban institutions such as the National Botanical Garden and the Soroa Orchid Garden, among others, participate in the project, with whom a Germplasm Bank of the species present in Cuba is organized. Preliminary results are presented.

P.0771 Eleven millennia of landscape and peatland vegetation dynamics in the Xistral Mountains (NW Spain)

Álvaro Hernando Bartolomé[1]*, Álvaro Moreno Martín[1], Saúl Manzano Rodríguez[2], Antonio Martínez Cortizas[3], Lourdes López-Merino[1]

*1 Universidad Complutense de Madrid, Madrid, Spain. 2 Universidad de León, León, Spain. 3 Universidade de Santiago de Compostela, Santiago de Compostela, Spain.*alvahe06@ucm.es.*

The Xistral Mountains host a significant cover and diversity of peatlands that act as active carbon sinks in southwestern Europe. However, these peatlands are receding due to anthropogenic pressures. Consequently, understanding peatland dynamics and responses to environmental disturbances is key for effective management. Palaeoenvironmental research in these peatlands have focused on ombrotrophic mires (bogs), revealing climate- and human-induced vegetation changes during the Holocene. However, minerotrophic mires (fens) in the region remain understudied, despite their sensitivity to local environmental changes, often linked to slope processes. Our study presents the results of a palynological study of a fen, supported by geochemical and charcoal records, along with radiocarbon dating. Results indicate that the landscape was dominated by a grassland at the onset of the Holocene, transitioning to deciduous *Quercus* forests around 10.4-9.0 cal. kyr BP, coeval to the establishment of the fen. Wildfires were recurrent during this period. From 9.0 cal. kyr BP, *Betula* and *Corylus* joined the tree assemblages, and *Sphagnum* became a crucial peatland species. At 4.7 cal. kyr BP, both the forest and the *Sphagnum*-dominated peatland stability were disturbed as attested by increased values of *Calluna vulgaris*, Ericaceae, and Cyperaceae. This change is coeval with an episode of rapid sedimentation of coarse sands, indicating an abrupt change in slope dynamics, followed by an increase in the fire regime that lasted until 3.2 cal. yr BP. Despite the partial recovery of *Sphagnum* after this fire episode, increased fire recurrence at 2.5-1 cal. kyr BP led to a subsequent decrease. While the last millennium is not reconstructed as a pyrogenic phase, *Sphagnum* recovery is not detected, possibly linked to indicators of recurrent soil erosion impacting the fen. Further analysis is needed to understand the role of fire disturbance and soil erosion on *Sphagnum*-dominated fens to prevent their damage.

P.0772 Medicinal and food potential of endemic species from the Natural Municipal Park of Niterói (PARNIT) - Rio de Janeiro, Brazil

Andre Hoffmann[1], Adriana Q. Lobão[1], Odara H. Boscolo[1], Selma R. de Paiva[1]

1 Departamento de Biologia Geral, Universidade Federal Fluminense, Rio de Janeiro, Brazil.

Plants represent a valuable source of substances beneficial to human health, and their importance as food and therapeutic resources is noteworthy. The Brazilian flora, the richest in the world, has been drastically reduced, mainly due to human actions. With increasing global environmental impacts, a significant portion of biodiversity is being lost before it is even known to science. Protected areas, especially those located in the Brazilian Atlantic Forest, face obstacles stemming from both the lack of knowledge about the species that make up these plant communities and the scarcity of biological and ethnobotanical data that indicate potential medicinal and food uses of this flora. In this sense, the present study aimed to develop a floristic inventory for the Niterói Municipal Natural Park (PARNIT) - Rio de Janeiro, Brazil, focused on evaluating the medicinal and food potential of native species from the Atlantic Forest. The inventory was conducted through surveys in herbaria and field collections carried out in the Park. Identified species were categorized in terms of their potential for medicinal and food uses, habitus, cultivation data, and conservation status, with the aim of calculating the Medicinal and Food Potential Value (MFPV) associated with them. Prior to the study, 131 species were known for the entire area of PARNIT. After the survey, there are 427 species recorded for the area, with 221 being endemic to Brazil. A total of 97 families of vascular plants were found, with Fabaceae (40) as the largest in terms of diversity, while Myrtaceae (31) scores higher when only endemic species are considered. Preliminary assessments of species' MFPV evidentiate the local flora's potential to integrate Living Pharmacies and provide new, sustainable options for small farmers, positively impacting life quality for the population and the quality of ecosystem services provided.

P.0773 Paeonia in Kosovo: A comprehensive study on distribution, habitats and threats

Elez Krasniqi[1], Naim Berisha[1], Fadil Millaku[1]

1 Faculty of Mathematics and Natural Sciences, University of Prishtina, Prishtina, Kosovo.

As part of our ongoing research into the flora and vegetation of Kosovo (2000-2023), we have undertaken numerous research expeditions. Based on our research, within the floristic diversity of Kosovo, the genus Paeonia L. is distinguished by the presence of three species: Paeonia officinalis L, Paeonia mascula (L.) Mill. and Paeonia peregrina Mill. According to the information available to us, these species are distributed in the vertical profile from the hilly mountainous region to the mountainous-subalpine region. They grow on different substrates, more frequently on limestone and silicate, less frequently on serpentine substrates. The plant species P. peregrina and P. mascula were found in several locations in Kosovo, in the hilly mountainous region, mainly in deciduous forests and less frequently in grasslands. The species P. officinalis was found in Kosovo (in several places in the Pashtriku Mt.) in the mountainous-subalpine region, mainly in deciduous forests and subalpine pastures. All three plant species are under the negative influence of the anthropogenic factor due to their ornamental merits. The above-mentioned species of the genus Paeonia have been evaluated according to the IUCN criteria in the Red Book of the Vascular Flora of the Republic of Kosovo.

P.0774 Habitat and ecology of Agave genus (Asparagaceae: Agavoideae) in Bahoruco Mountains, Dominican Republic

Berleni V. Lebrón Liriano[1,2], Edmundo García Moya[1], Mireya Burgos Hernández[1], Jorge Nieto Sotelo[3]

1 Postgrado de Botánica, Colegio de Postgraduados, Estado de México, México. 2 Herbario Dr. Henri Alain Liogier, Universidad Nacional Pedro Henríquez Ureña, Santo Domingo, México. 3 Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, México.

The species of the *Agave* genus, endemic to the American continent, are ecologically important due to its soil retention capacity, its adaptation to xerophytic conditions, its association with some animals like mammals and birds, its association with other plants, and the uses humans have been giving them, principally. The objectives of this study are to characterize the habitat and determine the ecological variables influencing the growth of *Agave* species in the Bahoruco Mountains, a biodiversity hotspot in the Caribbean region located on the Hispaniola Island. For this, we considered the variables of soil, topography, temperature, relative humidity, wet bulb globe temperature, barometric pressure, dominant vegetation, anthropogenic impacts seen in the area, forest status, elevation, vegetation cover percentage and luminance of localities where

Agave species were found. We performed principal component, factor, and correlation analysis for all ecological variables. Our results showed microclimate variations between the localities in Bahoruco Mountains, such as temperature, topography and elevation, that may be influencing the species distribution in the protected area, although the similarity between vegetation is highly dominated by *Pinus occidentalis*. The principal soil components were explained by potassium, nitrogen and phosphorus content. Also, we found a high correlation between some soil components such as potassium/copper, potassium/manganese, and nitrogen/zinc. More studies are still needed to identify a distribution pattern of *Agave* species along the Bahoruco Mountains that will allow us to understand its relationship with continental species.

P.0775 Ethnobotany in the Churute-Guayas mangroves ecological reserve, as a contribution to the conservation of phytodiversity

Sirli Leython Chacón1, Antonio Caicedo[2]

1 Facultad de Ciencias Agropecuarias, Herbario Misael Acosta Solís (AMAS), Universidad Técnica de Ambato, Ecuador. 2 Profesional de ejercicio libre de profesión, Ecuador.

The Churute Mangrove Ecological Reserve (REMCH) was the first mangrove protected area on the Ecuadorian coast (1979), and with the largest area nationally at 49,389 hectares. It is an ecosystem sensitive to anthropogenic intervention. However, despite its importance for conservation, little ethnobotanical research has been carried out on the communities settled there. Therefore, this study focused on documenting the forms of use of ethnobotanically important species and thereby establishing a list of categories and interactions that will allow conservation strategies to be established for the most vulnerable species. Participatory research techniques, key informant surveys and interviews, participant observations and ethnobotanical collections were applied. The data were analysed with statistical tests of abundance and diversity, and a species similarity index will be considered according to their uses. A total of 147 plant species mentioned by informants were recorded, corresponding to 63 botanical families, with Leguminosae being the most diverse with 13 species. The useful species with the highest *Aristolochia odoratissima*, *Pseudobombax millei*, *Annona muricata*, *Bacharis genistelloides*, *Handroanthus chrysanthus* and *Trialis cumingiana*. The most important uses were medicinal, food and ornamental, mainly using leaves (34%), stems (27%), fruits (23%) and flowers (7%), prepared in various forms such as infusion, food, beverages, cooking and condiments. Cultivated vegetation type accounts for the highest number of species of ethnobotanical use in the reserve, followed by scrub and dry forest. The uses of phytodiversity were documented for the families in the reserve, whose form of conservation and management depend on the family context, mainly influenced and supported by their traditional knowledge.

Note: This abstract was translated using IA.

P.0776 How best to survey modern vegetation to backcast palaeoecological ecosystem functioning? An example from NW Spain

Saúl Manzano Rodríguez[1]*, Álvaro Moreno Martín[2], Álvaro Hernando Bartolomé[2], Rosina Magaña Ugarte[2], Rosario G. Gavilán[2], Martyn P. Waller[3], Kerry A. Brown[3], Antonio Martínez Cortizas[4], Lourdes López-Merino[2]

*1 Universidad de León, León, Spain. 2 Universidad Complutense de Madrid, Madrid, Spain. 3 Kingston University London, Kingston upon Thames, UK. 4 CRETUS, EcoPast, Universidade de Santiago de Compostela, Santiago de Compostela, Spain. *saul.manzano@unileon.es.*

Peatlands are priority protection habitats within European legislation, characterised and typified under various European directives, such as Natura 2000, based on their unique flora. The flora serves as an indicator, reflecting time-transgressive pedogenic processes that led to peat accumulation, shaping these distinctive ecosystems. Consequently, vegetation surveys stand as one of the first steps in recognising them as conservation targets. Despite their significance, surveying peatlands poses challenges, primarily due to environmental factors operating at different spatial scales, that result in complex vegetation mosaics. Variables such as the location within the drainage network, microtopography, and the composition of vegetation itself influence the intricacy of plant microhabitats, complicating the endeavour to recover a representative survey of a specific peat-forming environment. Moreover, the waterlogged nature of peatlands adds complexity to the task, making them difficult to survey at times. Therefore, a detailed survey becomes imperative for accurate estimates of plant richness and abundance. Here, we present findings derived from a seasonal (spring and autumn) modified point quadrat survey methodology applied to the floristically unique peatlands of the Xistral Mountains (Lugo, NW Spain), dominated by the local endemic *Carex durieui*. Despite being a labour-intensive approach, this method has previously demonstrated its efficacy in reconstructing ecological properties over palaeoecological timescales. We calculate biodiversity metrics, identify patterns within the studied region, and further discuss the results within the framework of previous studies on *Erico mackaianae-Sphagnion papillose* peatlands, performed using other, less labour-intensive, vegetation survey methodologies.

Acknowledgments: This research is part of a broader initiative (PALAEOFUN project, Ref.: PID2020-115580RB-I00) focused on reconstructing the long-term ecological functioning of peatlands through a modern-calibration approach using plant functional traits. The aim is to contribute valuable insights into the intricate functioning of peatlands over time, fostering a deeper understanding of these vital ecosystems.

P.0777 Provisional inventory of the vascular flora of the Alto Turia Biosphere Reserve (E Spain)

Berta Miralles[1], Javier Fabado[1], Anna Nebot[1], Jesús Riera[1], Jaime Güemes[1]

1 Jardí Botànic de la Universitat de València, Valencia, Spain.

A provisional list of the vascular flora taxa present in the Alto Turia Biosphere Reserve is the first step to provide a tool in order to facilitate the management of plant biodiversity in the subject area. We started from the data obtained from the Biodiversity Data Bank of the Valencian Community, which contains bibliographic and plant occurrence information. In parallel, we explored the herbaria with the largest number of collections in the area, highlighting the Herbarium of the University of Valencia (VAL). A critical revision of all the herbarium specimens and an update of the nomenclature is carried out, as well as the last time a specimen was observed or collected. This resulted in a preliminary list of the flora of the reserve, composed of 1200 taxa of vascular flora. Each taxon has been assigned its category of protection and its degree of rarity or uniqueness in the territory, according to the number of populations found in the reserve as well as its origin *i.e.* if it is a native or alien taxon and in the latter case its invasive potential. We have also noted those taxa considered crop wild relatives (CWR) present in the reserve. All this allows us to draw up lists of taxa in order of priority, review their threat category or prevent the possible spread of invasive alien species. In addition, an analysis of areas with hardly any floristic data has been carried out in order to prospect in the future and complete the chorological information of the vascular flora of the reserve.

P.0778 Drivers of understory vegetation composition after novel silvicultural treatments in Canadian boreal forests

Marion Noualhaguet[1], Enrique Hernández-Rodríguez[1], Miguel Montoro Girona[1,2]

1 Universidad du Quebec en Abitibi-Temiscamingue, Rouyn-Noranda, Canada. 2 Universidad de Huelva, Huelva, Spain.

Ecosystem-based management uses a wide diversity of harvesting practices to maintain forest ecosystem integrity by reducing differences between natural and managed forests. The success of this approach requires comprehensive assessments of forest community regeneration dynamics after harvesting. Understory vegetation plays a critical role in forest regeneration due to its major implications in biotic and abiotic interactions and is directly impacted by harvest. To guarantee the maintenance of biodiversity, a clear and long-term understanding of understory vegetation evolution post-harvest is crucial. We examined the impacts of novel harvesting patterns, in terms of intensity and spatial configuration of stem removal, over 18 years post-harvest, on understory vegetation diversity and composition in young and old stands of the Eastern Canadian boreal forests. Path analyses were used to assess the indirect impact of harvesting via soil substrate, light condition, live and dead wood covering a period of one year before and 18 years after harvesting. The understory vegetation was divided into the three layers: bryophytes, herbaceous and shrubs. Our analyses revealed that the effects of harvesting patterns on understory diversity were positive or negative depending on the layer, diversity scale (richness, common and dominant species), time after harvest, and stand age. The path analysis revealed that soil substrate was a driver of understory community changes across the 18 years post-harvest. However, herbaceous and shrub communities' changes were mostly explained by the preceding understory composition, especially by bryophytes. These results highlight the complex biotic and abiotic interactions among understory species, underscoring the importance of considering both environmental factors and pre-existing understory composition when guiding sustainable forest management strategies aimed at balancing economic interests with ecological conservation.

P.0779 Herbarium-based analysis of the flora of the Aysén region, Chile: a state of the art.

Carla Novoa Sepulveda[1,2], Gloria Rojas Villegas[2], Alicia Marticorena Garri[3]

1 Bavarian State Collection for Botany, Bavarian Natural History Collections, Munich, Germany. 2 Museo Nacional de Historia Natural, Santiago, Chile. 3 Universidad de Concepción, Concepción, Chile.

The Aysén region in Chile is home to a variety of habitats, such as the Patagonian Steppe and the Magellanic subpolar forests. Despite its unique ecosystem in Latin America, the region remains largely unexplored in terms of its flora. Our objective is to address this gap by conducting a floristic analysis of the Aysén region, and we present the findings from the initial phase of our project. This consisted of an analysis of the geographical distribution of the available herbarium vouchers. Our aims were twofold: i) to pinpoint areas requiring further sampling, in order to increase the floristic and vegetational representation across the entire Aysén region; and ii) to study species distribution in extreme regions. Our analysis draws upon over 7,000 vouchers collected between 1834 and 2022, stored in the following institutions: the SGO herbarium at the National Museum of Natural History in Santiago de Chile, and the CONC herbarium at the Department of Botany of the University of Concepción, Chile. Together, these collections provide the most comprehensive dataset on floristic distribution in the Aysén region available to date. Our findings reveal that a few percent of the region is present in collections, underscoring the need for additional fieldwork. We also provide a list of locations where further investigation is warranted.

P.0780 New records and conservation status of two endemic species of Croton from Brazil

Joesili C. P. Oliveira[1,2], Karen Y. S. Contento[1,2], Yuri Rossine[2,3], Sarah M. Athiê-Souza[1,4]

1 Universidade Federal Rural de Pernambuco, Recife, Brazil. 2 Universidade Federal de Pernambuco, Recife, PE, Brazil.

Croton L. is the second largest genus of Euphorbiaceae Juss., with over 1,200 described species. Brazil is one of the centers of endemism of the genus *Croton*, with approximately 300 species distributed in all of its states and phytogeographic domains, with 230 being endemic to the country. Considering the diversity of the genus and the need for taxonomic and distribution studies of endemic species in Brazil, this work aimed to present two new records of endemic *Croton* species, along with estimating their conservation status. During expeditions in Brazilian states, visits to Brazilian herbaria, and surveying online databases (SpeciesLink and Reflora), new records of two endemic *Croton* species were identified. The conservation status of the two species was estimated using the GeoCAT platform (cell width 2 km). *Croton imbricatus* L. R. Lima & Pirani, was previously considered endemic to the state of Bahia; however, in the present study, it was recorded in the state of Minas Gerais, in rocky field vegetation, while *C. burchellii* Müll. Arg. had occurrences confirmed only in the states of Tocantins, Maranhão, Piauí, and Goiás until now, and in this study, it was recorded in the state of Bahia in cerrado vegetation. Both species are categorized as Least Concern (LC) concerning extent of occurrence and Endangered (EN) when considering area of occupancy. The results presented highlight the importance and necessity of studies with greater sampling for the genus *Croton*, providing primary data for a better understanding of geographic distribution and conservation of endemic species.

P.0781 Changes of the herb community in a high Andean forest, after 23 years

Catalina Quintana[1], Renato Valencia[1]

1 Pontificia Universidad Católica del Ecuador, Quito, Ecuador.

We examined two full censuses of herbs in 1996 and 2019 in a one-hectare forest plot at 3300 m elevation on the Pasochoa Volcano, Ecuador. We found 50 species (20 families) and 56 species (23 families) of vascular plants in the two censuses, respectively. Orchidaceae in both censuses was the most species rich family. Herbs in 2019, increased >100% (from 31119 to 66257) in individuals, even though they cover a similar area in both censuses (8,50% vs. 8.54%). The Cyperaceae, *Uncinia hamata* had the highest Importance Value Index (IVI) for both censuses. Obligately terrestrial herbs increased in 13% by 2019, fallen climbers and epiphytes, which had rooted in the ground decreased by 13% in 2019. We tested the influence of light intensity (LI) and topographic habitats inside the plot; for both censuses 12% of the species were exclusively found in places with high LI, whereas the rest of species grew under medium to low LI. Between topographic microhabitats (ridge, slopes, erosion gully) the floristic composition was relatively uniform. Just a few, rare species (densities <50 individuals/ha), grew exclusively in the erosion gully and on the slopes. Climate change can influence the colonization and reproduction of new species inside the forest. The forest remnant is a refuge of unique herb species, where 71% of the herb species are presumably rare or not easily found in their geographical distribution range.

P.0782 20 years of the Andalusian Network of Botanic Gardens

Cristina San José[1], Sonia Tobar[2], Work team of the Andalusian Network of Botanic Gardens[1]

1 Agencia de Medio Ambiente y Agua de Andalucía, Junta de Andalucía, Spain. 2 Consejería de Sostenibilidad, Medio Ambiente y Economía Azul, Junta de Andalucía, Spain.

The Andalusian Network of Botanic Gardens in Natural Areas, started in 2001, is firmly committed to support the development and efficient application of the World Conservation Strategy for Nature and the Convention on Biological Diversity. These gardens and protected areas contain a good representation of the flora and of endangered plant species of Andalusia (South Spain). As centres for conservation, recovery and reintroduction of wild species, the Network includes 10 botanical and 1 mycological gardens, which take part in the conservation strategy of the Regional Ministry for the Environment and coordinates actions with other regional, national and international organizations and institutions. Andalusia's prime location, between the Atlantic Ocean and the Mediterranean Sea, as well as between two different continents, allows for a huge range of ecosystems and environments, with a great variety of climates and terrains, where a rich botanical and mycological heritage has developed. The region has around 4.500 different species of higher plants and around 2.700 species of fungi. Many of these species are endemic to Andalusia and some of them are endangered due to several factors. The botanic and mycological gardens contribute to the conservation of this natural heritage. They are organised according to ecological criteria, to improve awareness, to promote conservation and to exhibit plants and fungi which make up the Mediterranean Forest of Andalusia. Each of the different gardens in the network is dedicated to local flora and vegetation, paying special attention to rare and endangered flora, in coordination with all the other gardens. The Mycological Garden is a regional showcase of fungi in Andalusia. The total Network of Botanic Gardens contains at present a collection of 2.300 different Andalusian species. This work shows the evolution of the Andalusian Network of Botanic Gardens over more than 20 years.

P.0784 Updated Red Lists of Bulgarian algae

Maya P. Stoyneva-Gärtner[1], Blagoy Uzunov[1], Georg Gärtner[2], Miroslav I. Androv[1], Kristian R. Ivanov[1]

1 Department of Botany, Faculty of Biology, University of Sofia 'St. Kliment Ohridski', Sofia, Bulgaria. 2 Institut für Botanik der Universität Innsbruck, Innsbruck, Austria.

Despite lacking a legislative power, Red Lists are valuable tools for designating the threatened status of species, which face the risk of extinction and are commonly used to raise the public awareness for their conservation. In Bulgaria, regarding the prokaryotic and eukaryotic algae, two Red Lists have been published. First of them was oriented towards macroalgae and was based on standard IUCN criteria comprising 88 taxa (Temniskova et al. 2008), The second one was focused on microalgae and used a novel, original method for an objective evaluation of their threatened status and contained 756 taxa (Stoyneva-Gärtner et al. 2016 a, b). Both published Red Lists embraced 15% of the total algal diversity of the country with more than 5,500 encountered species (Stoyneva 2014). Currently, both Red Lists have been re-evaluated according to the critical reading of the new findings on Bulgarian algae (except diatoms) collected or published during the last 20 and 10 years, respectively. The results from this re-evaluation and suggested updates are provided in the present poster. It has to be noted that small changes in the formulas reflecting the threatened status concern only 15 microalgae and 3 macroalgae, which can be accepted as a prove for the reliability and objectiveness of the previously proposed method and threatened species. In the same time, finding of more than 60 new for the country microalgae from both aquatic and aeroterrestrial habitats, many of which rare, led to the discussion of their conservation status. As a result, the updated Red List was enriched by 36 microalgae from the following phyla: Cyanoprokaryota, Chlorophyta, Streptophyta, Ochrophyta, Euglenophyta and Pyrrhophyta.

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P.0785 Floristic differences between growth habits in montane forests of Colombia

Diego Suescún Carvajal[1], Heidy C. Caro Ayala[1], Susana Arango Carvajal[2], Boris S. Villanueva Tamayo[3], Fernando Álzate Guarín[2]

1Universidad industrial de Santander, sede Málaga. Instituto de Proyección Regional y Educación a Distancia, Málaga, Colombia. 2 Universidad de Antioquia. Medellín, Colombia. 3 Jardín Botánico de Bogotá. Bogotá, Colombia.

Most flora studies developed in natural forests tend to focus on woody plants with a defined minimum diameter (2.5 cm), so other important components such as lianas, terrestrial grasses, shrubs and juvenile individuals of tree species are excluded from sampling and, therefore, from floristic analyze. In this research, we present the contribution of different growth habits in the total terrestrial species richness in three oak forests dominated by *Quercus humboldtii* and located in the northwest of the Eastern Cordillera de Colombia. The RAP methodology was implemented, recording all individuals with DAP <2.5 cm, for an area of 0.1 ha for each forest. A total of 769 individuals were recorded distributed in 38 families of angiosperms with 133 species, for Pteridophytes 37 species distributed in 10 families. Trees represented between 13 and 27% of the total richness, while non-tree species represented between 74 and 87% of the total richness, which shows their importance in the composition, structure and diversity of the oak forests studied. The results obtained here are similar to those presented by other authors and support the proposal of including individuals with diameters different from those established in traditional methodologies in order to more accurately estimate the total species richness. The diversity found is directly related to the sampled diameters, allowing us to know all the life forms present in a forest, which is an indispensable instrument for decision-making in generating policies for the conservation and sustainable management of Andean forests.

S.086. INTEGRATIVE TAXONOMY OF MEDITERRANEAN PLANTS

P.0786 Unveiling the genetic tapestry: Exploring SNPs in the Cyclamen genus.

Khalid Aldhuwaib[1], Alastair Culham[1]

1 School of Biological Sciences, University of Reading, Reading, United Kingdom.

Cyclamen is a genus of 23 perennial flowering plants belonging to the Primulaceae family valued both horticulturally and evolutionarily. *Cyclamen* species are found throughout Europe and the Mediterranean Basin, from the Caucasus to Iran, with one species found in Somalia. However, despite its significance, understanding the underlying genetic diversity and phylogenetic relationships among Cyclamen species remains a challenge. Here, we investigate plastid single nucleotide polymorphisms (SNPs) using paired-end sequencing data in order to unravel the complex evolutionary relationships and variation among Cyclamen species. These SNPs were subjected to strict filtering criteria to ensure robustness and reliability in subsequent analyses and to remove low quality and false positive calls. Our findings could provide pivotal insights for future studies and conservation efforts, as well as a deeper understanding of the evolutionary history forming this genus. Phylogenetic methods and network analyses based on plastid SNPs would enable assessment of genetic structuring and species delimitation concordant with earlier morphological and molecular classifications.

P.0787 First preliminary phylogeny of Frankenia L. (Frankeniaceae) in Africa and Eurasia, based on plastid and nuclear molecular datasets

Mª Ángeles Alonso[1], Jordi Abad[1], Mario Martínez Azorín[1], José Luis Villar García[1], Manuel B. Crespo[1]

1 Department of Environmental Sciences and Natural Resources, University of Alicante, Alicante, Spain.

Frankeniaceae Desv., nom. cons., is a family of mostly halophytic plants, which was usually accepted to include two to five genera. However, partial molecular phylogenies recovered members of those genera embedded in a single clade among species of *Frankenia*, and therefore the latter is currently accepted to be the only genus in the family. It includes ca 70-80 species broadly distributed through arid and semiarid areas worldwide, and most taxa belonging here occur on saline environments (rich in chloride and sulphate compounds), and hence they show salt glands on stems, leaves and calyxes. Scarce phylogenetic data are currently available on *Frankenia*, the present being perhaps the first preliminary approach to the phylogeny of the family and the genus in Europe, eastern Asia, and Africa (incl. Macaronesia). Molecular analyses of nuclear ribosomal (ITS1-5.8S-ITS2 region) and plastid (*matK* and *trnL-F* regions) DNA sequence data yield preliminary phylogenies with several lineages that fit well with biogeography. Most South African taxa form a compact clade that is connected to North African-Iberian taxa of the genus, excepting the outstanding edaphic specialist *F. fruticosa* that forms an independent lineage. The Macaronesian taxa form a compact clade that relates to some Atlantic taxa of northwestern Africa, all those being sister to a group including members broadly distributed in northern Africa plus the Mediterranean group of *F. laevis* s.l. Further, samples of the cosmopolitan annual *F. pulverulenta* (multiple accessions from a wide geographical area) are nested in a clade sister to Mediterranean representatives of the genus. Beside the ongoing phylogenetic work on Frankeniaceae, taxonomic research has revealed several neglected or new species that have been recently described by the authors, this being a promising way to a better understanding of both the phylogenetic relationships and taxonomic arrangement of this genus in the studied territories.

P.0788 Crete Island still surprises: Ornithogalum christinii, a new species to science has been discovered from an offshore islet

Zacharias Kypriotakis[1], Dimitrios Tzanoudakis[2], Eleftheria Antaloudaki[3]*

*1 School of Agricultural Sciences, Hellenic Mediterranean University, Crete, Greece. 2 Department of Biology, University of Patras, Patras, Greece. 3 Natural History Museum of Crete – University of Crete, Crete, Greece. *eri@nhmc.uoc.gr*

Ornithogalum christinii (Hyacinthaceae) sp. nov., collected from the offshore islet of Agria Gramvousa at the Northwestern Crete, is described and illustrated as a local endemic species, new to science. It is related to the species *Ornithogalum montanum*, *O. atticum* and *O. pumilum*, however, it can be distinguished from those by having wrinkled and corrugated leaf surface, thickened fruiting pedicels at base, flexuose rachis of infruitescence and winged capsules. The relationships between the new species and the aforementioned are discussed and information regarding its ecology, conservation status and karyotype is also given.

P.0789 Is there a phylogeny behind this diversity? A molecular assessment of Romulea in the Mediterranean

Alex Baumel[1], Frédéric Médail[1], Anouar Toumi[1], Cécile Chemin[1], Manon Candas[1], Virgile Noble[2], Henri Michaud[2], Katia Diadema[2], Germain Waroquier[2], Annie Aboucaya[3], Alain Delage[4], Lisandru Leandri[4], Mathieu Chambouleyron[5], Jean-François Léger[5,6], Stephen Mifsud[7], Andrea Lallai[8], Gianluca Iiriti[8], Gianniantonio Domina[9], Gabriele Casazza[10], Baptiste Pierre[11], Juan Viruel[12]

1 Aix Marseille University, Marseille, France. 2 Conservatoire Botanique National Méditerranéen, Hyères, France. 3 Parc National de Port-Cros, Hyères, France. 4 Conservatoire Botanique National de Corse, Corte, France. 5 RENECO North Africa, Rabat, Morocco. 6 RENECO International Wildlife Consultants, Abu Dhabi, United Arab Emirates. 7 EcoGozo Directorate, Victoria, Malta. 8 University of Cagliari, Italy. 9 University of Palermo, Italy. 10 University of Genova, Italy. 11 Montpellier University, Montpellier, France. 12 Royal Botanic Gardens, Kew, United Kingdom.

Molecular systematics and species delimitation are highly dependent on phylogenetics. However, incomplete lineage sorting, hybridization, polyploidy, and taxon identification difficulties can combine to make phylogenetics uncertain. We used the Hyb-Seq methods using the Angiosperms353 bait kit to elucidate the relationships between *Romulea* taxa in the Mediterranean. In the first year of the project, 282 accessions from 19 taxa, including narrow endemics and widespread species, were sequenced. Initial results, based on *in silico* sequence extraction, revealed significant phylogenetic conflicts due to the high level of individual heterozygosity probably caused by homo or polyploid hybridization. A second approach, based on variant calling and genotyping with mixed ploidy levels, revealed a pattern of differentiation with several robust genetic groups, some of which matched with the taxa. This work, currently in progress, will be complemented with phylogenetic reconstructions using plastid genomes, genome size estimates, and biometry. This first molecular assessment of the Mediterranean *Romulea* taxa provides a much improved systematic of these small, discreet but charismatic geophytes.

P.0790 Review of benthic microalgae (Bacillariophyceae) investigations along the Adriatic Sea coasts

Ana Car[1]*, Aydin Kaleli[2], Iris Dupčić Radić[1], Dubravka Hafner[3]

*1 Institute for Marine and Coastal Research, University of Dubrovnik, Dubrovnik, Croatia. 2 Department of Marine and Freshwater Resources Management, Faculty of Aquatic Sciences, Istanbul University, Istanbul, Turkey. 3 Bartulovići 4, HR-20357 Blace, Croatia. *ana.car@unidu.hr*

The microphytobenthic community plays a central ecological role within the aquatic ecosystem by regulating nutrients and oxygen flow at the water-substrate interface and contributing significantly to primary production. The benthic microalgae are generally dominated by diatoms (Bacillariophyceae) which colonises the surface sediment layer (2-3 mm thick), characterized by strong chemical-physical gradients. Distinct groups among diatoms are based on sediment typology and include Epipelon (diatoms that live on the sediment), Epipsammon (sand-grain-adhering diatoms) and Epiphyton (diatoms residing on other photosynthetic organisms). In recent years, the discovery of numerous species in coastal marine waters through the application of light microscopy (LM) and scanning electron microscopy (SEM) has improved our understanding of diatom communities in different coastal environments. This review aims to consolidate and update knowledge on Mediterranean benthic diatoms with contribution from the Adriatic Sea, synthesizing findings from studies conducted over the past 33 years. This study systematically analyzes literature data, presents distribution patterns, and compiles a checklist of more than 800 diatom species belonging to 162 genera in the Adriatic. Focused on the reviewed literature, our study highlights gaps in knowledge, emphasizing areas requiring further investigation. Our literature review uncovered a scarcity of studies in the southern Adriatic coastal waters before 2008, with a lack of continuous observations over extended periods. The evolving systematics of diatoms have led to numerous synonyms and taxonomic transfers, underscoring the need for continual updates. The checklist, incorporating the latest data, will serve as a valuable reference for researchers. However, maintaining and expanding this resource over time is crucial for tracking changes in microphytobenthic taxa and deepening our understanding of coastal ecosystem ecology. Despite over three decades of research, a comprehensive understanding of the composition and spatial distribution of benthic diatoms in the Mediterranean, sub-basin of the Adriatic Sea remains elusive.

P.0791 Understanding the distribution and morphological differentiation of native species of alder (Alnus Mill.) in the Iberian Peninsula

Macarena Cuerdo[1], José Ignacio Márquez-Corro[2], Francisco Lara[1,3], Ricardo Garilleti[4], Ilia J. Leitch[2], Eduardo Cires[5,6], David G. del Olmo[1], Alba Romero[7], Carmen Andrés[7], Eduardo Ballesteros[8], Álvaro Prado[9], Juan A. Calleja[1,3]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Kew Royal Botanic Gardens, Richmond, United Kingdom. 3 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain. 4 Universidad de Valencia, Valencia, Spain. 5 Instituto de Recursos Naturales y Ordenación del Territorio, Mieres, Spain. 6 Universidad de Oviedo, Oviedo, Spain. 7 Madrid, Spain. 8 Alcalá de Henares, Spain. 9 Paracuellos del Jarama, Spain.

The riparian environments of the Iberian Peninsula host a remarkable richness of plant communities, typically characterised by the predominance of a single species. In the case of alder groves, while in Western Europe are dominated by *Alnus glutinosa* (L.) Gaertn., in the Iberian Peninsula, the species recently described *A. lusitanica* Vít, Douda & Mandák, appears to be more common. Based on scattered sampling, *A. lusitanica* might be the prevalent alder in the western and southern regions of the Iberian Peninsula, whereas *A. glutinosa* has been recorded in scattered locations in the Pyrenees (Vít et al, 2017) and in the Cantabrian Range (Sanna et al. 2023). Vít et al. (2017) have also noted some morphological differences, although both species seem to be reliably distinguishable only by their ploidy levels: *A. lusitanica* is tetraploid and *A. glutinosa* is diploid. The previous studies consider only part of the Iberian range of the alder forests. Therefore, we aim to improve the knowledge on: 1) the detailed distribution of both species in the Iberian Peninsula; 2) the morphological differentiation of *A. glutinosa* and *A. lusitanica*; and 3) the detection of putative hybrids (triploids), as has been demonstrated for other *Alnus* species (Šmíd et al., 2022). For these purposes, alder fresh and herbaria samples have been obtained from the entire *Alnus*'s range in the Iberian Peninsula plus additional sites from other European regions. Ploidy levels of samples have been analysed by flow cytometry. Likewise, a morphometric study has been carried out considering 26 variables and ratios. Preliminary results indicate a west - east geographic distribution of *A. lusitanica* and *A. glutinosa* respectively.

References: Sanna, M., et al. (2023). Naturalia Cantabricae, 11(3), 41-52; Šmíd, J., et al. (2022). Eur J Forest Res141, 641–648; Vít, P., et al. (2017). TAXON, 66(3), 567-583.

P.0792 Sarcocornia pruinosa and Sarcocornia fruticosa: taxonomical, ecological, and morphological features of two misunderstood species

Vicenta de la Fuente[1], Claude Lemmel[2], Esteban Ramírez[1], Irene Sánchez-Gavilán[1], Daniel Sánchez-Mata[3], Nuria Rodríguez[4], Ricardo Amils[5]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Atlas-sahara.org, Boudnib Morocco. 3 Universidad Complutense de Madrid, Madrid, Spain. 4 Centro de Astrobiología (INTA-CSIC), Madrid, Spain. 5 Centro de Biología Molecular Severo Ochoa, Madrid, Spain.

Our study evaluates the taxonomical, ecological, and morphological disparities between *Sarcocornia pruinosa* and *Sarcocornia fruticosa*, two species within the genus *Sarcocornia*. Confusion between these species has been prevalent in the scientific literature covering the Mediterranean and Atlantic territories of Western Europe and North Africa. Notably, *Sarcocornia fruticosa* has been incorrectly referenced in scientific literature for the southwestern Iberian territories, including Spain and Portugal. However, a comprehensive analysis of taxonomical, molecular phylogeny and morphological characteristics has established that *Sarcocornia pruinosa* is the correct species for these areas. We provide a key including micromorphological characters for *Sarcocornia* species frequently misidentified. Furthermore, our study updates the geographic range of these species covering northern Africa, eastern Mediterranean territories, and the coastal zones of Western Sahara.

P.0793 Biological legacy, challenges, opportunities, and future perspective for plant diversity in Caucasia: The ase of Maleae tribe (Rosaceae)

Ali A. Dönmez[1], Vahid Farzaliyev[2], Vugar Karimov[3], Zübeyde Uğurlu Aydın[1], Shehla Gümüş[4], Arzu Huseynova[4], Validae Alizade[4]

1 Department of Biology, Faculty of Science, Hacettepe University, Ankara, Turkey. 2 Forest Development Service under the Ministry of Ecology and Natural Resources of Azerbaijan, Baku, Azerbaijan. 3 Ministry of Ecology and Natural Resources of Azerbaijan, Baku, Azerbaijan. 4 Institute of Botany, Academy of Sciences of Azerbaijan, Baku, Azerbaijan. 4 Institute of Botany, Academy of Sciences of Azerbaijan, Baku, Azerbaijan.

The Caucasus is globally recognized as one of the most important regions in terms of species diversity. Extensive habitat diversity, hosting various types of climates, and being a meeting point of various floral and faunal provinces are contributing to the glamorous biodiversity of the region. Azerbaijan is the largest part of the Caucasus with an 86,600km² area. Beyond its geographical expanse, the country stands out as a cradle of the Caucasian biodiversity since its extraordinarily diverse habitats range from semi-desert areas around the Caspian Sea to humid subtropical forests in Hirkan National Park. One of the most noteworthy endeavors in the Caucasus has been the exploration of its flora within the framework of the Flora of the U.S.S.R. term, resulting in significant revisions culminating in the volumes of the flora. The local botanists and the plant hunters from abroad have continued to discoveries in the region. Presently, ongoing conservation studies, local floristic research, taxonomic revisions, and other studies, especially at the national level have contributed to a deeper understanding of the floristic diversity of the region. Considering tremendous developments in digitizing historical scientific documents and increased accessibility to scientific materials, such as type specimens and other original materials, identification, and typification of the taxa have become more manageable than ever. Furthermore, advancements in scientific instruments, particularly molecular techniques for plant taxonomy, enable a more objective delineation of taxa compared to traditional taxonomic evaluations. Through extensive field surveys in Azerbaijan and the evaluation of collected specimens, a total of 39 species from seven genera belonging to the *Maleae* tribe (Rosaceae) have been identified, with potential new taxa and new records for the country. Alongside the taxonomic study, observations on the flora and the potential threats to this extraordinary biodiversity area have been discussed.

P.0794 Relationship between benthic microalgae and environmental variables in seawater lakes (Mljet island, South Adriatic, Croatia)

Iris Dupčić Radić[1], Ana Car[1], Dubravka Hafner[2]

1 Institute for Marine and Coastal Research, University of Dubrovnik, Dubrovnik, Croatia. 2 Bartulovići 4, HR-20357 Blace, Croatia.

The community structure of epilithic microscopic algae (= diatoms; class Bacillariophyceae, kingdom Chromista) on an immersed artificial substrate under the influence of different physico-chemical properties was studied in the marine lakes Malo Jezero and Veliko Jezero (Small Lake and Great Lake) in Mljet National Park (South Adriatic, Croatia) monthly from April to October 2019. Biofilm development was studied on two types of surfaces: Plexiglas and glass. During the study, glass and Plexiglas slides of the same size 75 mm x 25 mm x 1 mm were attached to Plexiglas plates of size 50 cm x 30 cm and placed at two depths in seawater lakes: at the bottom (4 m deep in the Great Lake and 2 m deep in the Small Lake) and 0.5 m below the water surface at both stations. Once a month, microscopic slides and Plexiglas plates were removed from the substrate at both depths and stations and the taxonomic composition of the benthic diatoms was analysed in the laboratory of the Institute for Marine and Coastal Research. In order to determine the relationship between the diatom communities and the environmental variables, temperature and salinity were measured monthly during the field trips using a CTD probe (Seabird Seacat 19plus) and seawater samples were taken for the analysis of physico-chemical parameters (nitrates, nitrites, ammonia, phosphates, silicates, oxygen saturation, chlorophyll concentration) in the laboratory. In the analysed samples, 157 taxa (species and lower taxonomic categories) of diatoms within 51 genera were identified. The largest number of taxa was found in the following genera: Mastogloia (29 taxa), Diploneis (12), Nitzschia (11), Navicula (9), and Amphora and Licmophora (7 taxa each). The physico-chemical parameters varied significantly between months and stations and had a major influence on the diatom communities in the periphytic community.

P.0795 From bulbs to blooms: a preliminary morphological and anatomical revelations of Crocus chrysanthus Herb. in Türkiye

Rachel Mollman[1], Almıla Çiftçi[2,3], Bilge S. Kaleli[1], Ceyda Yazici[1], Levent Şık[4], Osman Erol[2]

1 Istanbul University, Institute of Science, Istanbul, Türkiye. 2 Istanbul University, Istanbul, Türkiye. 3 Leibniz Institute of Plant Genetics and Crop Research, Gatersleben, Germany. 4 Manisa Celal Bayar University, Manisa, Türkiye.

The *Crocus chrysanthus* Herb. species complex is a systematically contentious group of 13 taxa containing ornamental plants distributed in the Balkans and Türkiye. This complex contains many species exhibiting great variation and distinguished by minor features. The fact that these species boundaries were defined by characters, especially anther color, tepal shape and stigma length compared to the anther, which show great variation even within a single population, is among the factors resulting in taxonomic problems, although this broad variation also contributes to its value in the gardening trade as a source of countless hybrids and cultivars. Within the scope of an ongoing project (TÜBITAK 222Z016) the relationships between different populations from across their distribution range throughout Türkiye have been collected and examined both morphologically and anatomically. The initial results showed that floral characters are variable within populations as well as between populations. Leaf anatomy, which was considered useful in crocus systematics, also found to be questionable for this group. The upcoming phases of this project will add molecular and cytological investigations to these initial results with the aim of resolving the relationships between taxa and eliminating the taxonomic confusion among the species of the *C. chrysanthus* species complex.

P.0796 Taxonomy, phylogeny, and diversity of the genus Phlox (Polemoniaceae)

Carolyn J. Ferguson[1], Mark H. Mayfield[1]

1 Herbarium and Division of Biology, Kansas State University, Manhattan, USA.

Phlox is the largest genus of the family Polemoniaceae, with over 60 species distributed mostly in North America. The genus exhibits intriguing morphological and ecological diversity, and polyploidy is widespread (including cytotypic variation in some species). These factors have confounded taxonomy, but a present framework enables further development of the genus as a system for evolutionary study. Here we present an overview of diversity in the genus, with context in terms of phylogenetic data and the *Flora of North America* treatment. We discuss several examples of cryptic (or at least, previously underappreciated) diversity, relating to polyploidy, undescribed taxa, disjunct distributions, and rare species. Finally, we outline some priorities for ongoing study in this group.

P.0797 Leiothrix (Eriocaulaceae) since the Flora do Brasil 2020: micro- and macro-evolutionary history

Ana M. Giulietti-Harley[1], Patrícia L. Ribeiro[1][2], Daniele M. Silva[1], Lamarck Rocha[3], Maria J. G. de Andrade[4]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Universidade Federal do Recôncavo da Bahia, Cruz das Almas, Brazil. 3 Instituto Nacional do Semiárido, Campina Grande, Brazil 4 Universidade do Estado da Bahia, Paulo Afonso, Brazil.

The genus *Leiothrix* includes 38 species in South America, with the greatest diversity occurring in the Campo Rupestre of the Espinhaço mountain range (ER) of Brazil. Most species are micro-endemics and considered in danger of extinction due to habitat loss. The Flora do Brazil laid out our knowledge of the taxonomy of the genera and suggested various lines of future study. Today, studies on species delimitation, phylogenetics, biogeography and cytogenetics are revealing both new taxa and the evolutionary history of the group. The phylogeny (37 taxa of *Leiothrix* and eight other genera) was inferred using nuclear (*ITS* and *ETS*) and plastidial (*trnL-trnF*, *psbA-trnH* and *rpl32-trnL*) markers. The dating of *Leiothrix* used secondary data inferred from Eriocaulaceae. *Leiothrix* is monophyletic, sister group to *Syngonanthus* and is characterized by striate seeds and a gynoecium with a column where the nectariferous and stigmatic branches diverge at different heights. The *Leiothrix* lineage originated ca. 45 Mya. and probably occurred in the mountains of northern of South America, becoming widely distributed until the early Oligocene, when it geographically divided into two lineages. One in the ER of Minas Gerais, diverging first at the start of the Miocene, but retaining its distribution principally in this area, with microendemic species. The other lineage started to diverge during the Mid-Myocene, but reached a wider distribution, with species occurring in the area of the ER of Bahia, but also, in the "tepuis" and the coastal "restingas". In this lineage, the delimitation of *L. angustifolia* reveals four evolutionary units, elucidating the biogeography of widely distributed taxa within the genus. Chromosome counts suggests that polyploidy and especially disploidy act as important evolutionary mechanism in the genus. Thus, environmental requirements, disjunction, populational structuring, dispersal capacity and microevolutionary mechanisms are probably at the basis of microendemic diversity of Leiothrix.

P.0798 Cytotaxonomic investigation of two critical endemic species Allium trichocnemis Gay and A. seirotrichum Ducell. & Maire in Algeria

Thinhinan Khedim[1]

1 Departement of Biology and Physiology of Organismes, BPO Laboratory. University of Sciences and Technology Houari Boumediene, Algiers, Algeria.

In the Mediterranean region, several species complex and critical groups belong to the *Allium* section *Brevispatha* Valsecchi. Species previously referred to this section are undoubtedly among the most cryptic and taxonomically difficult to circumscribe. In this study two rare species of *Allium*, endemic to Northern Algeria, namely *A. trichocnemis* and *A. seirotrichum* are examined by morphological and karyological approaches. Living material was sampled in sites including the *loci classici*. Morphological measurements were made using characters of vegetative parts (bulb, leaf) and reproductive structures (umbel, perigone, stamen, pistil and capsule). Karyomorphometric measurements, karyotype formulas and chromosomal asymmetry parameters were established. The two studied species share many morphological similarities as their small size, usually hairy leaves, and fibrous bulb tunics with species from *A. cupanii* group (sect. *Brevispatha*). Karyological data characterized the two endemic species, *Allium trichocnemis* and *A. seirotrichum*, as distinct taxa that were well separated from the related *A. cupanii* and *A. hirtovaginatum*. The tetraploid chromosome number 2n = 4x = 32 is reported here for the first time for the two endemics. Our results point to the relation between polyploidy and threatened narrow endemics. That is what challenges us to further cytogenetic and phylogenetic research for more comprehensive evolutionary trends of the genus *Allium* at the whole Mediterranean area.

P.0799 Neglected diversity in the Balkans: Sesleria skipetarum (Poaceae) is a morphologically and genetically distinct species

Nevena Kuzmanović[1], Peter Schönswetter[2], Božo Frajman[2], Tijana Đenader[1], Romeo Di Pietro[3], Ivana Stevanoski[1], Dmitar Lakušić[1]

1 Faculty of Biology University of Belgrade, Belgrade, Serbia. 2 Faculty of Biology University of Innsbruck, Innsbruck, Austria. 3 Faculty of Architecture, Sapienza University of Rome, Roma, Italy.

Sesleria is one of the most species-rich grass genera on the Balkan Peninsula. It is taxonomically complicated due to the frequent hybridisation and polyploidisation. According to the most recent phylogenetic study, within *Sesleria* sect. *Argenteae* three well defined groups were singled out: Argentea group, Latifolia group and Robusta group. Members of the Latifolia group are distributed in Mediterranean, sub-Mediterranean and supra-Mediterranean areas from the Apennine Peninsula to the Caucasus. The most enigmatic species in this group is *Sesleria skipetarum*, described in 1959 based on the material collected by Doerfler on ultramafic rocky grasslands near Bardanjolt in Albania. It was identified by Degen as Balkan endemic, *S. tenuifolia,* due to the presence of reticulate old basal leaf sheaths and an interrupted inflorescence. The species was neglected in Flora Europaea, while in most recent checklists (Euro+Med, World Checklist of Vascular Plants) it was synonymized with *S. insularis*. We reconstructed relationships among populations of *S. latifolia* from the central part of the Balkan Peninsula, populations from ultramafic bedrock in Albania corresponding to *S. skipetarum*, and a population of *S. insularis* from Sardinia using Amplified Fragment Length Polymorphisms (AFLPs). Our data revealed that the populations growing on ultramafic substrates in Albania are more closely related to *S. latifolia*, but are nevertheless distinct and should be recognized as separate species. The genetic differentiation was reflected in morphological differentiation, which led to the confirmation of the specific status of *S. skipetarum*. It is an obligate serpentinophyte and an endemic Balkan species distributed in northwestern Albania.

P.0800 Malesherbia Ruiz & Pav. (Passifloraceae): discovery of an unexpected distributional gap in the Mediterranean-Temperate transition

Kester Bull-Hereñu[1], Carla Novoa Sepúlveda[2]

1 Laboratorio Flores, Fundación Flores, Santiago, Chile. 2 Bavarian State Collection for Botany, Bavarian Natural History Collections, Munich, Germany.

We report the extension of the distributional range of two *Malesherbia* species in Chile based on the revision of the plant collection of Professor Jürke Grau stored at the Munich Herbarium. We noticed the existence of unknown vouchers of *M. linearifolia* (Cav.) Pers. and *M. lirana* Gay that evidence for the first time the occurrence of these species in the Maule region in Chile at around 35°S. The new locations are situated about 100 and 200 km beyond the species' previous known southern limit, respectively. Interestingly enough, a third species of *Malesherbia*, *M. humilis* Poepp., is known for presenting an analogous distribution with also one southernmost population in the Maule region and a similar gap towards the north of about 300 km. It is still not clear whether this distributional gap is the consequence of a diminished collection effort in the area or a natural biogeographic disjunction. However, the latter explanation seems plausible as 34-36ºS marks the transition between Mediterranean (to the north) and temperate (to the south) climates in Chile. Given that *Malesherbia* species are adapted to dry environments, it is reasonable that 34ºS would represent a natural climatic barrier for the genus, whereas unusual xeric spots in the Maule region at 35-36ºS could facilitate the establishment and persistence of *Malesherbia* individuals there. These alleged extraordinary arid conditions in the Maule region could in turn be orographically related to the locally more pronounced longitudinal extent of the Andes, which would provide enhanced rain shadow to the precipitations incoming from the west and allow a westwards introgression of the South-american 'arid diagonal' from Argentina. Remarkably, the here addressed southernmost isolated *Malesherbia* populations could also represent relict communities that locally survived after the climate transition in the early Holocene when more arid conditions dominated in the region.

P.0801 Taxonomic revision of Berberidaceae in Ecuador

Carmen Ulloa Ulloa[1], Nora H. Oleas[2]

1 Missouri Botanical Garden, St. Louis, USA. 2 Centro de Investigación en Biodiversidad y Cambio Climático, Universidad Tecnológica Indoamérica, Quito, Ecuador.

The family Berberidaceae comprises shrubs, rarely trees, and also perennial herbs, exhibiting both evergreen and deciduous characteristics. It consists of 13–19 genera and approximately 700 species. While the family is well represented in the North Temperate Zone, only one genus, *Berberis*, extends into tropical Africa, Asia, and South America. *Berberis* stands as the largest genus within the Berberidaceae, with approximately 500 species. This poster presents the latest taxonomic revision of *Berberis* in Ecuador. We review specimens collected from across Ecuador's distribution range and deposited in herbaria and digital databases, we aim to address the limited understanding of this group. We identified 15 species, seven of which are endemic to Ecuador. Additionally, we provide a key to differentiate these species.

P.0802 The Festuca stricta/ valesiaca complex in the Alps and Appenines: filling in the gaps with integrative taxonomy.

Pallanza Mattia[1,2], Foggi Bruno[3], Šmarda Petr[4], Rossi Graziano[1], Orsenigo Simone[1,2]

1 Department of Earth and Environmental Sciences, University of Pavia, Pavia, Italy. 2 National Biodiversity Future Center, Palermo, Italy. 3 Department of Biology, University of Florence, Florence, Italy. 4 Department of Botany and Zoology, Masaryk University, Brno, Czech Republic.

Festuca subgenus *Festuca*, commonly known as fine-leaved fescues, is a diverse group of grasses that dominates various xerophytic and alpine communities across Europe. The shared xerophytic and cryophytic adaptations of this group make individual taxa very similar, giving fine-leaved fescues the status of one of the taxonomically most critical groups in Southern Europe. These characteristics also make fine-leaved fescues important in ecological restoration, particularly in relation to grassland environments. In Italy and neighboring territories, many have dedicated their efforts to unravel the taxonomy and systematics of fine-leaved fescues. However, the *stricta/ valesiaca* complex remained inadequately addressed. The stricta/valesiaca complex comprises nine naturally occurring taxa in the Alps and Appenines [*F. valesiaca* Gaudin, *F. pseudodalmatica* Domin, *F. stricta* Host subsp. *stricta*, *F. stricta* subsp. *trachyphylla* (Hack.) Pils, *F. stricta* subsp. *sulcata* (Hack.) Pils], 4 of which are endemic to the Alps [*F. bauzanina* (Pils) S. Arndt, *F. bauzanina* subsp. *rhaetica* S. Arndt, *F. guinochetii* (Bidault) S. Arndt, *F. ticinensis* (Markgr.-Dann.) Markgr.-Dann.]. Species of this group are characterized by three separate sclerenchyma strands in tiller leaves (*F. valesiaca*, *F. stricta* subsp. *sulcata*) which in some species can conflue and form even and unevenly thickened sclerenchyma ring (*F. stricta* subsp. *trachyphylla*, *F. stricta* subsp. *stricta*). Our aim so far has been to revise these taxa and identify clear boundaries between them utilizing an integrative taxonomy-based approach that combines morphometry and ploidy level analysis. While most of the morphological data is still under processing, preliminary ploidy level analyses reveal significant gaps in our current knowledge. Flow cytometry analyses have underscored discrepancies between the actual and expected ploidy levels, highlighting numerous misidentifications of the taxa, particularly in the Apennines subregion.

P.0803 Leaf architecture and anatomy of Tilia L. (Malvaceae): a numerical approach

Marysol Ramírez-Díaz[1,2], Jorge Gutiérrez[3], Teresa Terrazas[1]

1 Instituto de Biología, Universidad Nacional Autónoma de México, Mexico City, Mexico. 2 Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Mexico City, Mexico. 3 Universidad Autónoma Chapingo, Mexico State, Mexico.

Systematic anatomy and leaf architecture have supported the separation of species by using leaf morphological and anatomical characters, such as, the arrangement of vascular bundles or the venation pattern. The genus *Tilia* (Malvaceae) consists of approximately 23 species with unclear boundaries between some of them. The purpose of this work was to find leaf morpho-anatomical characters that contribute to *Tilia* species delimitation. Leaves of 11 taxa were collected and their architecture was described using cleared-leaves and their anatomy using transverse and paradermal sections. Multivariate analyses and agglomerative clustering analysis were performed to recognized species or species groups. Results showed that leaves are variable in shape with first and second order teeth, secondary venation mostly craspedodromous and well-developed areole. Leaves were hypostomatic and heterobaric, with three types of midvein. Multivariate analyses revealed that number of teeth per cm, tooth base width and the length of the trichome arms with four arms were important characters for species separation. The combination of characters favored the recognition of species. For example: *T. platyphyllos* subsp. *platyphyllos* is characterized by teeth with narrower bases, *T. mongolica* is the only species with a deltoid lamina and without domatia and *T. caroliniana* subsp. *occidentalis* is separated by lamina with 3 teeth per cm and four-armed stellate trichomes with a length of 296 µm. The characteristics of the leaf lamina should not be the only ones used in the taxonomy of the genus; it is proposed to explore the inflorescence and the fruits.

P.0804 Morphology and nomenclature within Dianthus ciliatus s.l. (Caryophyllaceae)

Ivana Rešetnik[1], Ana Terlević[1], Ivica Ljubičić[2], Sandro Bogdanović[2]

1 Faculty of Science, University of Zagreb, Zagreb, Croatia. 2 Faculty of Agriculture, University of Zagreb, Zagreb, Croatia.

Dianthus L. is the second largest genus in Caryophyllaceae and comprises more than 330 species distributed in Eurasia and Africa. The genus represents one of the fastest radiations of flowering plants, with high diversity in the Mediterranean Basin, which is a hotspot of European biodiversity. Many *Dianthus* species are endemic within this region, and among themare several morphologically and taxonomically well-defined groups. One of them is the endemic amphi-Adriatic *D. ciliatus* s.l., which occurs in the Apennine and the Balkan Peninsulas. Presently, the taxonomic classification designates it as a single species with three morphologically very similar subspecies: the nominal *D. ciliatus* Guss. subsp. *ciliatus*, *D. ciliatus* subsp. *dalmaticus* (Čelak.) Hayek and *D. ciliatus* subsp. *medunensis* (Beck & Szyszył.) Trinajstić. Despite this classification, numerous validly published names exist within *D. ciliatus* s.l., and the morphological variability within these populations remains largely unexplored. This study presents a comprehensive morphometric analysis of twenty-seven populations spanning the entire distribution range. Petal limb shape and denticulation, the woody base of the plant, epicalyx scale’s length and height of the epicalyx itself turned out to be the most informative characters in distinguishing the investigated populations of *D. ciliatus* s.l. Based on significant differences in morphological characters, a new identification key is offered. Moreover, the typification of five names belonging to *D. ciliatus* s.l. is provided.

P.0805 Integrative taxonomy approach of the genus Oxalis L. (Oxalidaceae) in Argentina

Agostina B. Sassone[12], Sonia Rosenfeldt[3], Marta Bianchi[4], Marisa G. Bonasora[5], M. Lis Echeverría[1], Alicia López Méndez[1,6]

1 Facultad de Ciencias Agrarias, Universidad Nacional de Mar del Plata, Balcarce, Argentina. 2 Leibniz Institute of Plant Genetics and Crop Plant Research, Leipniz, Germany. 3 Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Buenos Aires, Argentina. 4 Facultad de Ciencias Agrarias, Universidad Nacional de Rosario, Zavalla, Santa Fe, Argentina. 5 Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina. 6 Consejo Nacional de Investigaciones Científicas y Técnicas, Argentina.

The genus *Oxalis* L. (Oxalidaceae) is cosmopolitan and includes ca. 500 species that live from sea level to the snow line and in all climates, including annual herbs, woody shrubs, cushions, and vines. They may have tubers, rhizomes, or bulbs. Currently, in Argentina, 67 species are recognized. We are bringing together diverse sources of evidence to achieve a large-scale diversity analysis of the genus *Oxalis*. Our final aim is to generate a stable classification that reflects the evolutionary relationships of the *Oxalis* taxa currently distributed in Argentina, using an integrative taxonomy approach to make inferences about the evolutionary history and make contributions to the biogeographic history of the genus. So far, we reunited new data on 1. micro-morphology of pollen grains (5 sp.), and orbicules (15 sp.), and 2. herkogamy (6 sp., 22 populations) and, 3. cytogenetics (cytomixis in 1 sp). As preliminary results, 1. the study of pollen and orbicules reinforces the hypothesis of the current sections; .2. within the analyzed populations, the three morphotypes and, to a lesser extent, plants with semihomostyly were recorded. In some populations, there are significant differences among the frequencies of floral forms. The low frequency of some of the morphotypes, together with the presence of intermediate morphotypes (semihomostyly), would indicate a transition process from tristyly to distyly in some populations; 3. the alternation of normal interfaces with irregular divisions, together with cytomixis, could limit the diversity of reports for the number of chromosomes and constitute one of the probable mechanisms of polyploidization within the genus, so its study is of interest in the context of the integrative taxonomy. We continue to collect data and analyze the results combining all the sources of information to make inferences about the evolutionary history and make contributions to the biogeographic history of the genus.

P.0806 Preliminary insights into the diversity of Pampean Zephyrantes (Amaryllidaceae)

Juan M. Goyenetche[1], Cecilia M. Acosta[1], Rosa L. Scaramuzzino[1], Silvia C. Arroyo-Leuenberguer[2], Agostina B. Sassone[3,4]

1 Facultad de Agronomía, Universidad Nacional del Centro de la Provincia de Buenos Aires, Azul, Argentina. 2 Instituto de Botánica Darwinion (CONICET-ANCEFN), Buenos Aires, Argentina. 3 Facultad de Ciencias Agrarias, Universidad Nacional de Mar del Plata, Balcarce, Argentina. 4 Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany.

Subfamily Amaryllidoideae is one of the three within the family Amaryllidaceae and is of great economic importance. The genus *Zephyranthes* Herb. includes ca. 170 species, currently circumscribed to 7 subgenera. Most of the species and subgenera have a controversial taxonomy, and taxa circumscription has been a source of confusion for various reasons. We have focused our studies on species of the subgenera *Zephyranthes*, *Habranthus* (Herb.) Nic. García, and *Neorhodophiala a* Nic.García & Meerow, sympatrically distributed in the Pampas grassland of South America. The final aim of this research is to present a multidisciplinary study of Pampean *Zephyranthes* to define the number of species, contributing to a better knowledge of the genus. Morphological and genomic analyses were conducted. We performed phenetic analyses including 81 specimens on the base of 28 vegetative and reproductive morphological characters (three qualitative and 25 quantitative) analyzed with Principal Coordinates analysis. Furthermore, 25 individuals were gathered, and we inferred their phylogeny and genomic structure based on GBS (Genotyping-by-sequencing) loci. Our morphological results show that the analyzed species can be differentiated on the base of the selected features. also included different populations to investigate variation within species but no clear morphological features were found among them. When exploring genomic data, Z. *barrosiana* (Hunz. & DiFulvio) S.C.Arroyo, *Z. bifida* (Herb.) Nic.

García & Meerow, *Z. minima* Herb, and *Z. tubispatha* (L'Hér.) Herb. resulted monophyletic. As regards, genomic structure, *Z. bifida* may be genetically different from the rest of the analyzed species, and the other species show some level of admixture. Our next step is to continue collecting data at species and population levels from the species distributed in the Pampas region.

P.0807 The rediscovery of Reichardia intermedia (Sch. Bip.) Samp. in the Canary Islands

Guillermo Sicilia-Pasos[1, 2], Yurena Arjona[2], Miguel A. Padrón-Mederos[3], J. Alfredo Reyes-Betancort[3], Louis S. Jay-García[1, 2], Javier Tuero-Septién[2], Ángel García[4], Jairo Patiño[1,2]

1 Instituto de Productos Naturales y Agrobiología (IPNA-CSIC), La Laguna, Spain. 2 Departamento de Botánica, Ecología y Fisiología Vegetal. University of La Laguna (ULL), La Laguna, Spain. 3 Jardín de Aclimatación de La Orotava, Instituto Canario de Investigaciones Agrarias (ICIA), Puerto de La Cruz, Tenerife, Spain. 4 Parque Nacional de Garajonay, La Gomera. 6 San Sebastián de La Gomera, La Gomera, Spain.

The Canary Islands currently host four species of the genus *Reichardia*, three of which are endemic to the archipelago (*Reichardia crystallina, R. famarae* and *R. ligulata*), and one is considered as non-endemic native (*R. tingitana*) according to data compiled by the Biodiversity Data Bank of the Canary Islands. Upon revisiting the historical context, it has been observed that there are additional taxa that have been cited in the past for the archipelago but are not currently considered present, such as *Reichardia intermedia*. In the description of this species' basionym, *Picridium intermedium*, the presence in the archipelago is mentioned but no locality is specified. Subsequent authors also mentioned the occurrence of this species for the islands of La Palma, La Gomera, Tenerife and Gran Canaria. To complete its historical record, the identity of *R. intermedia* and its potential confusion with other species of the genus is not clear in some cases, possibly due to its broad morphological variability. Despite the various citations in the past regarding this species, the revision of the genus conducted by Gallego et al. (1980) did not include this taxon in the context of the Canary Islands. In this study, we present phylogenetic and morphological evidence from a population found on the island of La Gomera, confirming the identity of *R. intermedia.* We also review the historical context of this taxon in the Canary Islands. Building upon these findings, we propose to re-incorporate this species as an additional taxon within the *Reichardia* genus in the Canary Islands.

References: Gallego, M. J., Talavera Lozano, S., & Silvestre Domingo, S. (1980). Revisión del género *Reichardia* Roth (Compositae). *Lagascalia, 9 (2), 159-217.*

P.0808 A systematic study of Coriandreae (Apiaceae) tribe in Turkey

Sefa Sönmez[1,2], Emine Akalın3, Sabiha Esra Sönmez[4]

1 Institute of Graduate Studies in Health Sciences, Istanbul University, Istanbul, Turkey. 2 DUAGEM, Natural Products Research and Development Center, Altinbas University, Istanbul, Turkey. 3 Faculty of Pharmacy, Istanbul University, Istanbul, Turkey. 4 Prof. Dr. Cemil Tascioglu City Hospital, Istanbul, Turkey.

The aim of this study is current systematic investigation of the Coriandreae tribe in Turkey. The tribe consists of two genera and five species worldwide, with two species in the *Coriandrum* genus and two species in the *Bifora* genus that are native to Turkey. *Bifora americana* (DC.) A.Gray is the only species not found in this tribe in Turkey. Plant materials are collected in different regions of Turkey. Classic and modern techniques in systematic are used in this study. In morphological analysis, basal and stem leaves, fruit measurements are used. Cross-section of fruits are photographed and investigated. In addition to morphological and anatomical studies, molecular analysis is conducted. DNA was isolated from the fruit or leaf. Molecular analyses were conducted, with a focus on the ITS gene region of the isolated DNA. After amplification and sequencing, a phylogenetic tree was constructed. *Coriandrum* species are identified by difference on stem leaves and ray numbers on umbels. *Coriandrum sativum* L. have ovate segmented basal leaves and linear segmented stem leaves. *Coriandrium tordylium* (Fenzl) Bornm. have ovate segmented leaves both in basal and stem. 2-6 rays in *C. sativum* and 6-12 rays in *C. tordylium* have founded. *Bifora* species are identified by fruit numbers and fruit apex types. *Bifora radians* M.

Bieb. have many fruits in umbel and *B. testiculata* (L.) Spreng. have 2-3 fruits in umbel. In anatomical analysis, *Coriandrum* species have 2 commissural and 5 dorsal vittae. Conversely, *Bifora* species have numerous dorsal vittae and 2 commissural vittae. Dorsal vittae of *Bifora* species has a different structure. Molecular analysis results support the morphological and anatomical analysis.

P.0809 Environmental niche comparison between diploid and tetraploid cytotypes of Dianthus ciliatus s.l. (Caryophyllaceae)

Martina Temunović[1*], Ana Terlević[2], Ivica Ljubičić[3], Božo Frajman[4], Ivana Rešetnik[2], Sandro Bogdanović[3]

1 Faculty of Forestry and Wood Technology, University of Zagreb, Zagreb, Croatia. 2 Faculty of Science, University of Zagreb, Zagreb, Croatia. 3 Faculty of Agriculture, University of Zagreb, Zagreb, Croatia. 4 University of Innsbruck, Innsbruck, Austria.

Polyploidisation is one of the main evolutionary forces in flowering plants, often followed by niche evolution of polyploids in relation to their diploid progenitors. We here inferred ploidy levels, their geographic distribution, and relative genome size (RGS) variation in three subspecies of the amphi-Adriatic *Dianthus ciliatus* s.l. (Caryophyllaceae): *D. ciliatus* subsp. *ciliatus, D. ciliatus* subsp. *dalmaticus* and *D. ciliatus* subsp. *medunensis*. We analysed a total of 84 populations, of which 67 were included in the RGS analysis. We identified 24 diploid (2*x*) and 60 tetraploid (4*x*) populations of *D. ciliatus*, with diploids confined to the Balkan Peninsula. We further compared environmental niches between pooled diploid and tetraploid populations, as well as pairwise between the three subspecies. In particular, we tested for niche conservatism pattern, the tendency of polyploids to preserve niche traits of their diploid ancestors, which is more expected for autopolyploids than for allopolyploids. Niche overlap between pooled di- and tetraploids was low (26.3%), with diploid niche nested almost completely within the wider tetraploid niche. In pairwise comparisons between the subspecies, the results suggested different environmental requirements of each subspecies. Niche conservatism was not confirmed between diploids and tetraploids globally. However, niche conservatism was significant between diploid and tetraploid *D. ciliatus* subsp. *ciliatus*, suggesting autopolyploid origin of tetraploids that showed 76% of niche expansion in relation to the ancestral diploids. Significant niche conservatism was also detected between diploid *D. ciliatus* subsp. *ciliatus* and *D. ciliatus* subsp. *medunensis*, suggesting their close relatedness, whereas in other pairwise comparisons niches were not conserved. Our results thus suggest allopolyploid origin of tetraploid *D. ciliatus* subsp. *dalmaticus.* In conclusion, wider niches of polyploids likely facilitated their dispersal and establishment in novel environments marginally occupied by their progenitorsand likely facilitated their expansion to the Apennine Peninsula.

P.0810 Senecio ser. Otopteri (Asteraceae): new molecular hypotheses

Florencia T. Mendoza[1], Susana E. Freire[2], Raúl E.Pozner[1], Stephan Beck[3], Estrella Urtubey[1]

1 Instituto de Botánica Darwinion, San Isidro, Argentina. 2 Museo Argentino de Ciencias Naturales, Buenos Aires, Argentina. 3 Herbario Nacional de Bolivia, La Paz, Bolivia.

Series *Otopteri* (*Senecio*) comprises 14 species: *S. attenuatus, S. bangii, S. belenensis, S. deferens, S. herrerae, S. kosterae, S. lorentzii, S. otites, S. otopterus, S. pensilis, S. pseudotites S. sepium, S. sinapoides* and *S. tucumanensis* mainly distinguished by its lower leaves with well-differentiated petiole, usually auriculate or decurrent along the stem. Previous molecular studies of *Senecio* using ITS marker, only included *S. bangii, S. deferens*, and *S. otites* in the phylogeny of Senecioneae, in which *S. deferens* remains included in *Senecio* s. str. and *S. bangii* and *S. otites* are remotely related to the core of *Senecio*. Our investigation using 8 of the 14 species of series *Otopteri* and markers (ITS and ETS) shows: 1. *Senecio deferens, S. otopterus* and *S. sepium* belong to series *Otopteri*; 2. *Senecio lorentzii, S. pensiles, S. pseudotites* would be excluded from this series but belong to *Senecio* s. str.; 3. The exclusion of *Senecio otites* and *S. bangii* (= *Lomanthus bangii*) from *Senecio* s. str. was confirmed by our results. Finally, we propose *S. otopterus* as the type species for series Otopteri.

P.0811 Repeatome diversity in the Myrtaceae family

Magdalena Vaio[1], Natali Baz[1], Mathias Mangino[1], Héctor Oberti[1], Sebastián Pita[2], Clara Pritsch[1]

1 Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay. 2 Facultad de Ciencias, Universidad de la República, Montevideo, Uruguay.

Myrtaceae is one of the largest plant families (5,500 species, 15 genera, 17 tribes). Genome size in the family is fairly small (200-600 Mbp) and basic chromosome number is constant with x=11. Repetitive DNA sequences (or repeatome) are one of the main components of all plant genomes. Transposable elements and satellite DNAs from repeatome, are key players on evolutionary changes of genome organization and function. Despite its relevance, the Myrtaceae repeatome has been poorly analysed. The aim of this study was to annotate and compare the repeatome of four tribes of Myrtaceae. We analysed 15 species assigned to tribe *Myrteae* (9), tribe *Eucalypteae* (4), tribe *Melaleuceae* (1) and tribe *Metrosidereae* (1). For the analyses, we randomly sampled raw reads from short-read libraries extracted from either public databases or built in our study. To characterize the repeatome composition and abundance, we used RepeatExplorer2 while satellite DNA was identified with TAREAN. The repeatome ranged from 15 up to 37%. LTR retrotransposons were the most abundant repeats (5- 26%). The lineages Tekay, Ogre, Ikeros and SIRE, were the most relevant in explaining the observed abundance differences. Differences in repeatome composition were also detected even between botanical varieties (*Psidium cattleyanum*). Satellite DNAs ranged from 8 % (*Melaleuca alternifolia*) to P.4 % (*Metrosideros polymorpha*). We identified for the first time in Myrtaceae, 58 DNA satellite families, with 1 to 10 families/species with monomer sizes from 55 to 1800 bp. Also, we detected a number of within-genus (*Eucalyptus*) and within-tribe (*Myrteae*) shared DNAsat families. Our results showed a high diversification of Myrtaceae repeatome despite both genome size and chromosome stability.

P.0812 Unveiling the rapid radiation of the subgenus Eriocarpum (genus Helianthemum) through target capture sequencing

María Valerio de Arana[1], Sara Martín-Hernanz[1,2], Juan Viruel[3], Polina Volkova[4], Zhihao Su[5], Encarnación Rubio[1], Amelia Shepherd-Clowes[3], Rafael G. Albadalejo[1], Abelardo Aparicio[1]

1 Universidad de Sevilla, Seville, Spain. 2 Universidad Complutense de Madrid, Madrid, Spain. 3 Royal Botanic Gardens Kew, London, United Kingdom. 4 Russian Academy of Sciences, Borok, Russia. 5 Xinjiang Normal University, Urumqi, China.

Understanding the ecological and evolutionary drivers of biodiversity is essential to prevent its loss. The genus *Helianthemum* is an ideal lineage to decipher the role of three main events in plant evolution and speciation that took place in the Mediterranean Basin and adjacent areas (the Messinian salinity crisis, the establishment of the Mediterranean climate and the Pleistocene climate changes). Previous phylogenetic reconstructions of the genus at species level confirmed its monophyly and its division in three monophyletic subgenera: *Eriocarpum, Plectolobum* and *Helianthemum*. Further studies of each subgenus could expand our understanding of these paleoclimatic events as well as the relationships between species. Here we focused on the subgenus *Eriocarpum*, integrated by fruticose deserticolous plants inhabiting arid and semi-arid ecosystems from the Macaronesian archipelagos, the Maghreb to the Middle East and the Horn of Africa until Central Asia. Since previous phylogenetic approaches have been very sample-limited, we have newly generated target capture data for 29 species (> 90%) and c. 80 populations of the subgenus using the universal Angiosperms 353 kit. Our preliminary phylogenetic reconstructions confirm the monophyly of the two largest sections within subgenus *Eriocarpum* (i.e., sect. *Pseudomacularia* and sect. *Eriocarpum*), and the existence of major disjunctions between the Mediterranean, Saharo-Arabic and Iranian-Turanian regions. However, within sect. *Eriocarpum*, some widespread species are not monophyletic (*H. lippii, H. stipulatum* and *H. ellipticum*). This likely reflects a taxonomic problem rather than a complex evolutionary history, where there is a lack of consensus on the diagnostic characters on which the flora of each region is based. Furthermore, the species *H. dagestanicum* clustered in the section *Pseudomacularia* whereas it previously belonged to the subgenus *Helianthemum*. Overall, our results suggest a deep restructuring of the systematics of this subgenus and provide a solid basis for further downstream analyses.

S.087. INTERDISCIPLINARY APPROACHES IN THE VISUAL ARTS AND THE BOTANICAL SCIENCES

P.0813 Greening lost worlds: paleoart for the vegetation landscape of early hominins in Europe

Gabriela Amorós[1], José S. Carrión[1], Victoria Sánchez-Giner[1], Ariadna Amorós[1], Juan Ochando[2, 1], Manuel Munuera[3], Ana Belén Marín-Arroyo[4], Juan Manuel Jiménez-Arenas[5]

1 University of Murcia, Murcia, Spain. 2 University of La Sapienza, Roma, Italy 3 University Polytechnic Cartagena, Cartagena, Spain. 4 University of Cantabria, Santander, Spain. 5 University of Granada, Granada, Spain.

There is a notable scarcity of pictorial reconstructions specifically centered on Iberian vegetation during the Quaternary. However, our paleobotanical understanding of the region has substantially improved in recent decades, providing a solid scientific foundation that can serve as a source of inspiration. Here we present results of paleoartistic research aimed at visually reconstructing the vegetation landscapes surrounding the Orce Archaeological Zone (OAZ), dated between 1.6 and 1.2 Ma in the Early Pleistocene of the Guadix-Baza Basin in southern Spain. The OAZ is a depression surrounded by forested areas of the Betic cordillera, but the present-day landscape is characterized by badlands and a largely treeless vegetation. However, during the Early Pleistocene, the region featured wetlands when the large Baza Lake was active and cyclically receded, giving rise to freshwater springs, ponds, and pools. Within this context the remains of numerous mammals, are located. Notably, OAZ includes human remains among the oldest in western Eurasia for the *Homo* genus. The scientific foundation supporting the artwork relies on fossil pollen data from three OAZ sites: Venta Micena 1, Barranco León, and Fuente Nueva 3. We pay due attention to the potential distribution of vegetation zones, the taxonomic and structural diversity of the vegetation, including taxa with widely disparate current biogeographic definitions, taxa that have become extinct in the Iberian Peninsula in later phases, or those that had previously gone extinct in higher latitudes in the European continent. This paleoartistic essay also aims to visualize the coexistence of mesophytic, thermophytic, and xerophytic plant communities during the early Pleistocene at this meeting point in the southwestern corner of the European continent.

P.0814 Floral morphology as a modern signature tool in therapeutics

Kester Bull-Hereñu[1]

1 Laboratorio Flores, Fundación Flores, Santiago, Chile.

Flowers obviously generate a reaction in the subject when looked at and have thus always been a mean for human communication, improvement of life quality and health. Ample and diverse is the history of cultural meanings of flowers and strong is the evidence of the various physiologic reactions of the psyche to them. Dr. Edward Bach alleged in the 1930's that flowers may alleviate uncomfortable states of mind by changing the mood of the person in question. Under his view, twelve angiosperm species (i.e. 'the twelve healers'), arranged in groups of three species each, deal with four main mood states. In this work I try to diagnose floral attributes common to each one of these groups that could possibly stand for the respective alleged therapeutic reactions. The first group is represented by the yellow color in flowers of *Mimulus* (Phrymaceae), *Agrimonia* (Rosaceae) and *Cistus* (Cistaceae), which tend to ease fearful states of mind. The second group is characterized by flowers with rather stiff parts arranged in a funnel shape as the case of *Scleranthus* (Caryophyllaceae), *Clematis* (Ranunculaceae) and *Ceratostigma* (Plumbaginaceae), which help to center a dispersed mind. The third group presents flowers with apparent elevating hairy structures such as the fimbriate corolla of *Gentiana* or curled styles of *Centaurium* (Gentianaceae) and *Chicorium* (Asteraceae), that relieve a general state of bitterness. The last group shows pink to violet flowers that tend to generally calm the mood as the case of *Hottonia* (Primulaceae), *Verbain* (Verbenaceae) and *Impatiens* (Balsaminaceae). In sum, it is possible to identify general floral attributes that could be understood and further be tested as plausible mood modulators when contemplating at them. This opens the possibility of conceiving the floral morphology as part of a therapeutic-signature field that operates balancing the state of mind.

P.0815 Conception and destiny of Dr Louis Auzoux's botanical models

Diane Courtin[1]

1 Muséum national d'Histoire naturelle, Paris, France.

The botanical models of Dr Louis Auzoux (1797-1880) are papier-mâché objects designed in the 1860s to facilitate the instruction in natural sciences. Since their creation, they have been appreciated by teachers for the solutions they provide and their adaptability to a wide range of plant-related topics. Exhibited in a variety of contexts throughout their history, they are also well known to the general public, who praise their aesthetic and technical qualities. After several decades of neglect due to the development of new teaching aids, they are gradually becoming part of our cultural heritage. Their resurgence has been made possible by a change in perception of their status. They are no longer seen simply as educational tools, but as ancient objects of historical and artistic interest. As a result, they are being preserved in educational establishments and museums. In this poster, we look back at the history of these pedagogical models. Louis Auzoux was a doctor and a businessman, but he also taught comparative anatomy. His reasons for creating such botanical objets remain unclear, but the public's perception of them reveals creative intentions that go beyond the merely practical.

P.0816 The use of photography in plant conservation involving communities in the Brazilian Atlantic Forest

José Augusto de Andrade Souto Maior[1], André V. Suzuki[2], Joelcio Freitas[3], Elton J. de Lírio[1,2,4]

1 Conservação de Espécies Ameaçadas da Mata Atlântica, São Paulo, Brazil. 2 Universidade Federal do ABC, São Paulo, Brazil. 3 Instituto Nacional da Mata Atlântica, Santa Teresa, Brazil. 4 Universidade de São Paulo, São Paulo, Brazil.

Certain plants have the ability to capture people's attention, stimulating curiosity and encouraging them to learn more. It can occur due to the visual connection established when using photographs, which plays an important role integrating the community in the conservation of threatened plants. We used photographs in a conservation approach with seven threatened species from the Brazilian Atlantic Forest. We visited and photographed the habitat where these species occur as well as the specimens found. Among the captured pictures, we highlight an individual of Cariniana legalis (Pink Jequitibá) with more than 47 m and with an estimated age of 800 years in the Espírito Santo state. The pictures were used to produce an identification guide with the seven threatened species that is virtually available and also was distributed to local people in a printed version. The guide and the pictures were used to engage people through social media (Instagram, 414 followers) and in practical lectures in local schools in the municipality of Santa Teresa, in Espírito Santo. Besides, we produced a scientific/artistic exhibition at the Instituto Nacional da Mata Atlântica (Santa Teresa, Espírito Santo). Many of the threatened species may be closer to people than they think. However, lack of knowledge often prevents this connection. The image can help overcome this obstacle, allowing people to identify species that are around them and awaken interest in their conservation.

P.0817 Wood identification of the coffin-reliquary of the holy Serbian king Stefan of Dečani (14th century)

Milan Gavrilović[1], Dragana Rančić[2], Alexei Oskolski[3,4], Miljana Matić[5], Milodarka Kocev[6], Aleksa Jelikić[6], Pedja Janaćković[1]

1 Faculty of Biology, University of Belgrade, Belgrade, Serbia. 2 Faculty of Agriculture, University of Belgrade, Belgrade, Serbia. 3 Department of Botany and Plant Biotechnology, University of Johannesburg, Auckland Park, Johannesburg, South Africa. 4 Komarov Botanical Institute, Russian Academy of Science, St. Petersburg, Russia. 5 Museum of the Serbian Orthodox Church, Belgrade, Serbia. 6 Institute for the protection of cultural monuments of Serbia, Belgrade, Serbia.

The coffin-reliquary for the relics of the holy Serbian king Stefan Uroš III of Dečani (r. 1322–1331) is made around 1343 as a rectangular chest with a gable cover. It originally stood at the Dečani church of Christ Pantokrator, in front of the templon, and today is situated at the Serbian Orthodox Church Museum in Belgrade. The dimensions of the coffin-reliquary are 197 × 60 × 43.5 cm (the chest of the coffin-reliquary is 197 cm long, 60 cm wide and 43.5 cm high, and the lid is 196 cm long, 61.5 cm wide and 20 cm high). The lid, the front and the right side of the coffin-reliquary are decorated with the use of woodcarving technique, gilding and various colors, dominated by red. The inside of the coffin-reliquary is undecorated. For the purpose of wood identification three samples were anatomically studied. The wood of all three samples is anatomically identical. Combination of key characters: diffuse-porous wood, radially orientated vessels multiplies and clusters, distinct spiral thickenings in vessels, simple perforation plates, 3- to 4-seriate noded rays and diffuse-in-aggregates apotracheal axial parenchyma occur only in the genus *Tilia* (Malvaceae). However, based on the anatomical characteristics of the wood, it cannot be determined with certainty to which of the three species (*T. cordata* Mill., *T. platyphyllos* Scop. and *T.* x *europaea* L.), which occur in Europe, the sample belongs. It can be assumed that linden wood was used due to the ease of processing and that it is considered one of the sacred trees in Serbian culture.

P.0818 History and importance of the Iberian flora scientific illustration

González L[1,3], Montero Muñoz Iris[2], Cardiel JM[1,4]

1 Departamento de Biología, Facultad de Ciencias, Universidad Autónoma de Madrid, Ciudad Universitaria de Cantoblanco, Madrid, Spain. 2 Real Jardín Botánico de Madrid, CSIC, Madrid, Spain. 3 Basque Centre for Climate Change, Lejona, Spain. 4 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Ciudad Universitaria de Cantoblanco, Madrid, Spain.

The botanical diversity of the Iberian Peninsula has promoted the interest of botanists since ancient times. From the 16th century to the present, works dealing with Iberian plants have evolved at the same time as the scientific advances, including the tools employed such as the creation of botanical collections and the use of scientific illustrations. Botanical scientific illustration is an indispensable tool for representing plant species with a visual, precise, clear, and objective approximation, that allows us to understand common features among all individuals and helps in the description and classification of the taxa. Over the centuries, illustrations of the Iberian flora have changed, not only in its knowledge and technical aspect but also due to the pictorial and engraving trends that were conditioned by the historical events of each century. The work here presented compiles and analyze the illustrations of the Iberian flora from the 16th century until the most recent volumes of the *Flora iberica* by Castroviejo (1986-2021), discussing tools and techniques employed over about 450 years. The extensive work *Flora iberica* probably contains the largest number of illustrations published of any other modern flora to date.

P.0819 Illustrating the botanical richness of Sierra Nevada: selection of endemic alpine flora

Ana M. Mingorance-Paredes[1]

1 Department of Drawing. University of Granada, Granada, Spain.

Sierra Nevada, the only alpine mountain in southern Iberian Peninsula, is recognized as a biodiversity hotspot that boasts over 2,350 plant species, among which approximately 4% are endemic. This project is developed within the framework of the ongoing research of the PhD thesis 'Endemic flora of Sierra Nevada. Illustrated botanical guide', which aims to present a compendium of the endemic flora of this mountain range, highlighting the interrelationship between Art and Science, and promoting the use of scientific illustration as a dissemination tool. This artistic discipline, which through a series of strategies allows to configure archetypes capable of being universally understood, becomes an ally to raise awareness about the importance and fragility of nature, particularly of this unique flora, much of which is threatened. Out of the 62 endemic species that can be found in the alpine zone, 23 have been selected. Fieldwork for the study of these plants has been based on the collection of documentation in their natural habitat and in the Hoya de Pedraza Botanical Garden. Working with various samples of fresh material, with the aid of a binocular microscope, both to achieve the most accurate visual message possible. As a result, we have obtained detailed and high quality watercolour representations for these species that have been included in two publications entitled 'Unique flora of Sierra Nevada; a natural treasure' that take part of the Smart EcoMountains project associated with the European Research Infrastructure LifeWatch-ERIC. One of them is a brochure that serves as a field guide with essential information for the species identification, and the other is a set of illustrated prints where the composition is distributed based on the vegetation's colour, creating a collection of artistic and scientific value. Also, we emphasize the crucial value of this type of images for dissemination and awareness.

P.0820 Art as an exploratory tool of science: a synergy between Botany and creative expression

Iván Pérez-Lorenzo[1,2], Pol Fernández[1,2], Paula Bruna[1,3]

1 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 2 Laboratori de Botànica, Facultat de Farmàcia i Ciències de l'Alimentació, Universitat de Barcelona, Barcelona, Spain. 3 CREAF-CSIC-UAB, Cerdanyola del Vallès, Spain.

Art has enormous potential to generate and convey knowledge through senses and emotion, complementing and enriching scientific production. In this work, three artistic manifestations grounded in botanical experimentation are explored. The graphs generated when studying the composition of repetitive elements in a genome allow us to identify genetic variations, thus aiding in the identification of hybrids and cryptic species. These graphs, constructed from the similarity between DNA sequences, bear resemblance to compositions in abstract art, prompting reflection on the inherent beauty in data structure. The study of invasive plants and herbarium conservation techniques forms the scientific backdrop of the artistic installation "A Modern Dance." In it, pressed specimens of *Araujia sericifera* Brot. and *Kalanchoe × houghtonii* D.B.Ward are presented as "phyto-monsters" dancing to the rhythm of modernity in a choreography of zombies exhibiting their superiority over humans. The work, combining science, art, and fiction, invites consideration of ecological conflicts from non-human perspectives to reconsider their management from less anthropocentric viewpoints. Finally, nocturnal monitoring of plant-animal interactions revealed unexpected diversity in the number of species visiting *Achillea millefolium* L. when the human eye is unable to see. Based on the recordings obtained, the video installation "Noctes Achilleienses'' was created, a large-scale projection allowing viewers to immerse themselves in the nocturnal stories of arthropods visiting the synflorescences.

S.088. INVENTORYING THE PLANT DIVERSITY OF THE EUROMEDITERRANEAN AREA: INTEGRATING TAXONOMIC PROGRESS INTO DYNAMIC WEB CHECKLISTS AND ELECTRONIC FLORAS

P.0821 Some endemic plant taxa growing in Cungus District of Diyarbakır province in Turkey

A. Dogan Karahan[1], Mehmet Basbag[2]

1. Dicle University Institute of Science and Technology, Diyarbakir, Turkey. 2. Dicle University Faculty of Agriculture Department of Field Crops, Diyarbakir, Turkey.

This study was conducted in four different directions of Savrucak Mountain in Çungus District of Diyarbakır Province in 2021 and 2022. In the research, a total of 12 taxa belonging to 7 families were found as endemic, all of these taxa are perennial and are in the invasive group in terms of meadow-pasture forage plants. Among the families, the Astracea family (*Gundelia cappadocica*, *Helichrysum arenarium* subsp. *aucheri*, *Tanacetum cadmeum* subsp. *orientale*, *Tanacetum densum* subsp. *cadmeum*, *Achillea pseudoaleppica*) had the highest number of taxa, followed by Boraginaceae (*Alkanna megacarpa*, *Paracaryum cristatum* subsp. *cristatum*), Araceae (*Arum rupicola* var. *rupicola*), Brassicaceae (*Isatis aucheri*), Lamiaceae (*Phlomis linearis*), Liliaceae (*Tulipa sintenisii*) and Plantaginaceae families (*Linaria genistifolia* subsp. *praealta*), respectively. When we examine endemic taxa according to their botanical compositions; *Helichrysum arenarium* subsp. *aucheri* 15.26% in the east direction, 8.81% in the south direction, 2.46% in the west direction and 1.59% in the north direction; *Phlomis linearis* 1.91% in the west, 0.64% in the south, 0.62% in the east and 0.40% in the north; *Gundelia cappadocica* 0.96% in the south and 0.16% in the east; *Tanacetum cadmeum* subsp. *orientale* is 4.05% in the east and 0.55% in the west; *Tanacetum densum* subsp. *cadmeum* 2.34% in the eastern direction; *Tulipa sintenisii* 0.96% in the south; *Linaria genistifolia* subsp. *praealta* was detected at a rate of 0.16% in the eastern direction. As a result, in order for these endemic taxa to continue their generation, it is extremely important to protect them both in-situ and in gene banks (ex-situ).

P.0822 Determination of forage quality values of some flax genotypes (Linum spp.) in meadow-pasture and natural vegetation in the Southeastern Anatolia region of Turkey

Mehmet Basbag[1], Sema Basbag[1]

1 Dicle University, Faculty of Agriculture, Department of Field Crops, Diyarbakir, Turkey.

In this study, some forage quality characteristics were examined in herbage samples taken from 6 genotypes of 3 different flaxes (*Linum* spp.) species collected from meadow-pasture and natural vegetation of the Southeastern Anatolia Region of Turkey in 2023.According to the results obtained, crude protein (HP) in the genotypes was 14.66-23.54%, dry matter (DM) was 89.68-91.84%, acid detergent fiber (ADF) was 19.38-29.53%, neutral detergent fiber (NDF) was 28.38-36.32%, acid detergent protein (ADP) 0.33-0.79%, digestible dry matter (DDM) 65.89-73.81%, dry matter intake (DMI) 3.30-4.23%, relative feed value (RFV) 168.8-241.7, potassium (K) 2.05-3.70%, calcium (Ca) 1.63-1.89%, magnesium (Mg) 0.29-0.51%, phosphorus (P) 0.24-0.39%, Ca/P 4.40-7.21 and K/(Ca+Mg) 0.96-1.82. The highest value in terms of crude protein, which is one of the most important criteria in terms of animal nutrition, was obtained from *Linum hirsutum* subsp. *pseudoanatolicum* genotypes and *Linum usitatissimum* species, while the lowest value was obtained from *Linum mucronatum* subsp. *armenum* genotypes. As a result, although these genotypes, which grow naturally in the region's meadow-pasture and natural vegetation, show statistical differences from each other in terms of the examined characters, it has been observed that all of them can be useful in animal nutrition in terms of the forage values they contain.

P.0823 Contribution to the knowledge of Morocco flora by the Emirates Center for wildlife propagation

Mathieu Chambouleyron1, Jean-François Léger[2]

1 Reneco North Africa, Rabat, Morocco. 2 Reneco IWC, Abu Dhabi, United Arab Emirates.

Ranked among the top Mediterranean countries in terms of plant biodiversity, and the first in North-Africa, Morocco still has a high potential for floristics and chorological discoveries. Among its least known regions, Eastern Morocco is being studied since the 2000's by the Emirates Center for Wildlife Propagation / Reneco. These thorough plant studies have enabled to add 200+ taxa to local inventories, including seven taxa new for Africa and 16 for Morocco. Additional results are in preparation, with the objective to produce an up-to-date checklist of Eastern Morocco flora. Whether they concern common or rare taxa, the numerous discoveries done confirm that the knowledge of Eastern Morocco flora is still unsatisfactory and highlights the need for further studies. These studies have led to the descriptionof five taxa new for science. In parallel, systematic revisions of selected little-known plant groups are underway or planned. One of these revisions is given as an example. It concerns the study of the Stipeae (Poaceae) of North Africa, carried out in partnership with one of the specialists of this group, F.M. Vázquez Pardo (Centro de Investigaciones Científicas y Tecnológicas de Extremadura - Spain). The monograph in preparation, based on the study of 2,000+ herbarium vouchers, provides an updated taxonomy, original descriptions and illustrations, distribution maps and an identification key for the 49 taxa recognised. The results include the description of a new species, seven new combinations and 14 typifications. Though a partnership with the Conservatoire et Jardin Botaniques de Genève, these results are used to update and expand the African Plant Database (https://africanplantdatabase.ch/en).

P.0824 Contributions to the knowledge of the biodiversity of León province (Spain)

Ángel Penas1, Saúl Blanco Lanza[3], María Borrego Ramos[3], Raquel Alonso-Redondo[1], Alejandro González-Pérez[1], Aitor Álvarez-Santacoloma[1], Giovanni B. Ferreiro-Lera[1], Norma Y. Ochoa-Ramos[1], Sara del Río González [2]

1 Department of Biodiversity and Environmental Management. Faculty of Biological and Environmental Sciences, University of León, León, Spain. 2 Department of Biodiversity and Environmental Management. Faculty of Biological and Environ-mental Sciences. University of León. Institute of Mountain Livestock (CSIC-Ule), León, Spain. 3 Diatomology Laboratory, Institute of Environment, Natural Resources and Biodiversity, University of León, León, Spain. sblal@unileon.es; mborr@unileon.es; sriog@unileon.es; apenm@unileon.es; ralor@unileon.es; gferl@unileon.es; agonp@unileon.es; aalvas@unileon.es; nochor00@estudiantes.unileon.es; blopem02@estudiantes.unileon.es; mherng09@estudiantes.unileon.es.

A deeply examination was conducted on the living organisms within the León Province (Spain), covering Algae (Prokaryotes and Eukaryotes), Fungi (Ascomycota, including Lichens, and Basidiomycota), Bryophyta, Vascular Flora (including native, alloctonous, and introduced), and plant communities, following a comprehensive bibliographical review and incorporating personal contributions from the authors. This study establishes a novelty contribution to the overall "plant" biodiversity of León Province. To ensure systematic consistency, the most widely recognized taxonomy for each group was adopted. Algae taxonomy stuck to the classification proposed by https://www.algaebase.org/; Fungi and Lichens followed the taxonomy outlined in https://www.indexfungorum.org/names/names.asp; Bryophytes were classified according to Flora Briofítica Ibérica (J. GUERRA, (ed), vascular flora referenced information from https://www.emplantbase.org/home.html (Euro+Med Plantbase), with certain exceptions made for specific taxa. Plant communities were classified following the proposal of S. RIVAS-MARTÍNEZ & AL. (2002). In brief, this study aimed to delineate the biodiversity within the study area, bearing a total of taxa as follows: 743 for Algae, 2412 for Fungi (including lichens), 543 for Bryophyta, 3408 for Vascular Flora, and 449 for plant communities. These taxonomic groups were further divided into representative subgroups and the Shannon index was used to measure their diversity.

References: Guerra, J. (ed.). (2007, 2015, 2006, 2010, 2014, 2018). Flora Briofítica Española. Volumen I, II, III, IV, V, VI. Ed. UMU & SEB. ISBN: 978-84-697-9126-4 (Ed. UMU & SEB). ISBN (I, II, III, IV, V, VI)): 978-84-611-8462-0.; 978-84-608-2198-4; 978-84-609-9097-4; 978-84-614-1023-1; 978-84-616-8434-2; 978-84-697-9126-4; Rivas-Martínez S. et al. (2002). Vascular plant communities of Spain and Portugal. Addenda to de syntaxonomical checklist of 2001. Itinera Geobotanica 15: 1-922. León (España).

P.0825 Maianthemum bifolium (L.) F. W. Schmidt and Satureja thymbra L., two new species to flora of Albania

Marjol Meço[1*], Lefter Kashta[2], Alfred Mullaj[2]

1 Department of Biology, Faculty of Natural Sciences, University of Tirana, Albania. 2 Research Center of Flora and Fauna, Faculty of Natural Sciences, University of Tirana, Albania. leka.kashta@yahoo.com, alfredmullaj@gmail.com.

Albania is a small country but with rich and interesting flora. The new documented findings of the last 20 years are greatly increasing the number of plant species in the country. *Maianthemum bifolium* (Asparagaceae) and *Satureja thymbra* (Lamiaceae) are two new records to the flora of Albania. *Maianthemum bifolium* was found in the herb layer of a mixed forest with *Fagus sylvatica* and *Picea abies* that lies on a stabilized gravel substrate along the Valbona River, Tropojë, N Albania. It is the first species of *Maianthemum* genus reported in Albania. This finding represents the most southern extension area of the species in Balkan. *Satureja thymbra* was found on the southwestern hills slope of Thumanë, northern part of central Albania. It occurs in some disturbed degraded low shrubland, on limestone substrate. This finding represents the most northern extension area of the species in Balkan and increases the number of *Satureja* species in Albania to four.

P.0826 An updated distributional database for the Balearic and Iberian Spanish vascular flora

Ignacio Ramos[1,2], Alejandro Alonso[1], Jaime Boyano[1], Elvira Castillo-Almansa[1], Marina Coca de la Iglesia[1], Angélica Gallego-Narbón[1], Moisès Guardiola[3], Manuel Marquerie[1], Rubén G. Mateo[1,2], Andrés V. Pérez Latorre[4], Llorenç Sáez[3], Estrella Saiz[5], Carlos Salazar Mendías[6], Lluis Serra[7,8], Virginia Valcárcel[1,2], Juan Carlos Moreno Saiz[1,2]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Biodiversity & Global Change Research Center (CIBC-UAM), Madrid, Spain. 3 Universitat Autònoma de Barcelona, Bellaterra, Spain. 4 Universidad de Málaga, Málaga, Spain. 5 Universidad de León, León, Spain. 6 Universidad de Jaén, Jaén, Spain. 7 Generalitat Valenciana, Alicante, Spain. 8 Font Roja Natura UA Scientific Station, San Vicente del Raspeig, Spain.

Within the Mediterranean hotspot, the Iberian Peninsula and the Balearic Islands stand out as a center of biodiversity (6,456 native species and subspecies) and endemism (30%) of vascular plants. The AFLIBER database, published with open access (Ramos-Gutiérrez *et al.*, 2021), made 1,824,549 unique plant occurrence records available to managers and researchers. These records are distributed among 6,316 UTM grid cells of 10 km side-resolution. To ensure the database remains current, the Spanish Botanical Society (SEBOT) has established a working group tasked with periodic updates. This involves incorporating non-digitized publications, obtaining additional databases with public or restricted access, and rectifying errors detected in the previous version. The outcomes of the SEBOT working group will be published in a data paper, and the distributional information will be freely accessible on the society's website. The latest update comprises 141,000 citations (88,000 after removing repetitions). Notably, only 18,800 occurrences (20%) are new to the dataset, emphasizing the high completeness of the AFLIBER database. However, these new additions are crucial for filling gaps in areas that were previously less sampled, particularly in the inland plateaus of Iberia. Medium-term challenges faced by the SEBOT working group include: i) updating the taxonomy and nomenclature of the database, taking advantage of the checklist currently under development within SEBOT; ii) incorporating the Spanish bryophyte flora; and iii) increasing the detail of chorological information with citations for the 1 km-sided grid cell.

References: Ramos-Gutiérrez, I. *et al.* (2021). Atlas of the vascular flora of the Iberian Peninsula biodiversity hotspot (AFLIBER). *Global Ecology and Biogeography* 30, 1951–1957. https://doi.org/10.1111/geb.13363

P.0827 The current knowledge about the distribution of Pteridium taxa (Dennstaedtiaceae) in Europe

Mykyta Peregrym[1,2], Ingrid Turisová[3], Peter Turis[3], Olesya Bezsmertna[4], Heorhii Bondarenko[5]

1 Luhansk Taras Shevchenko National University, Myrhorod, Ukraine. 2 University of Oulu, Oulu, Finland. 3 Matej Bel University in Banská Bystrica, Banská Bystrica, Slovakia. 4 Taras Shevchenko National University of Kyiv, Kyiv, Ukraine. 5 V.N. Karazin Kharkiv National University, Kharkiv, Ukraine.

The genus *Pteridium* Gled. ex Scop. has been considered as a monotypic one with the cosmopolitan species *P. aquilinum* (L.) Kuhn. for many years. However, morphological divergences observed in various regions since the 1940s have led to the description of new species, subspecies, and varieties. Molecular investigations, while not conclusively settling taxonomic debates, have underscored the extensive genetic diversity within the genus, affirming the status of several previously described species and subspecies globally. This wealth of data has prompted revisions of the *Pteridium* genus in regional floras, with Northern Eurasia serving as a central arena for such studies in the last 30 years. While no final agreed-upon conception exists, recent data suggest that the European flora comprises a single species, *P. aquilinum*, with two subspecies, *P. aquilinum* subsp. *aquilinum* and *P.a.* subsp. *pinetorum* (C.N.Page & R.R.Mill) J.A.Thomson. But, their distribution within the continent remains unclear. To address this uncertainty, our study aims to analyze herbarium, literature, and citizen science data regarding the distribution of *Pteridium* taxa in Europe, seeking to establish their current ranges. As a result, the eastern border of *P. aquilinum* subsp. *aquilinum* has been clarified, as well as the southern and eastern borders of the spreading of *P. aquilinum* subsp. *pinetorum* was set. Furthermore, it is clearly evidenced the presence of *P. aquilinum* subsp. *pinetorum* within the Netherlands, Austria, Czechia, Slovakia, Hungary and Romania for the first time.

S.089. KEY MORPHOLOGICAL INNOVATIONS IN FLOWER EVOLUTION

P.0828 Bract formation in Houttuynia cordata f. viridis

Mizuho Endo[1], Akitoshi Iwamoto[1]

1 Kanagawa University, Kanagawa, Japan.

Houttuynia cordata usually has apetalous flowers consisting of three stamens and one pistil and forms a spike inflorescence. Flowers usually develop inconspicuous small bracts in their axils, but four bracts subtending the first four flowers in an inflorescence become large and white petaloid. In *H. cordata* f. *viridis,* it has been reported that all bracts also become white petaloid, and some of them become green. Our preliminary observation on this form, *H. cordata* f. *viridis*, revealed that some bracts become not only green but also foliage leaf-like in shape. In this study, we observed the inflorescence development of this form with SEM, focusing on the variation of bract formation. We confirmed three types in the inflorescences of this form as follows. Type 1: Only the first four bracts in inflorescence become large and white petaloid as in the normal *H. cordata*. Type 2: All bracts of inflorescence become large and white petaloid, and some of them partly become green. Type 3: Bracts become foliage leaf-like organs, and white large petaloid bracts develop at later stages in the same inflorescence. The morphology of the primordium of foliage leaf-like organ in Type 3 was completely different from that of normal foliage leave. The phyllotaxis of the foliage leaf-like organs was spiral, which was common in bracts, while that of foliage leaves was dichotomous. On the other hand, the foliage leaf-like organs didn't subtend any flower in their axils, but developed vegetative buds. These results suggest that the foliage leaf-like organs should be intermediate between bracts and leaves to be named as "intermediate leaves". We will elucidate the identity of all types of bracts in this enigmatic form of *H. cordata* including the intermediate leaf with in situ hybridization to assess the expression of related genes for floral, leaf, and bract development.

P.0829 Spots, stripes, rosettes or checkerboard patterns. Solving shape formation with plant species

Pierre Galipot[1]

1. UMR CNRS 6553 ECOBIO, Campus Beaulieu, Université de Rennes, Rennes, France

Shapes and colors diversity is tremendous in Eukaryotes and serve many biological functions. Here we propose to illustrate how plant species are perfect to decipher morphogenetic processes. First, we will present how *Nigella damascena* (Ranunculaceae) elaborate petals allowed us to show the links between micro-patterns (cell number and sizes) and macro-patterns (petal shape and size). Then, we will show what are and how diverse are PGTCPs (Putative-growth Turing-like Color Patterns) in Eukaryotes and how *Scutellaria rubropunctata* (Lamiaceae) allows us to study their formation. Finally, we will present how rounds are changed into squares to form checkerboard patterns in *Fritillaria* (Liliaceae) tepals. Together, this shows the importance to explore the biodiversity of plants to select the best possible models to solve morphogenetic questions.

P.0830 Evolution and diversification of MADS-box genes in Scutellaria (Lamiaceae): focusing on five representative genomes

Jeongwoo Seo[1], Sangtae Kim[1]

1 Sungshin Women's University, Seoul, Republic of Korea.

MADS-box genes are transcription factors that control eukaryote development and growth, particularly in regulating flower development in plants through the ABC(D)E model. Revealing the functions of MADS-box genes and their regulatory network, together with other related genes, will play a key role in understanding the evolution of angiosperms. *Scutellaria* is the second largest genera in the Lamiaceae, encompassing over 460 species. This genus is morphologically distinct from other genera in the family by having scutellum, a skull-cup-like specialized upper calyx. Some species in the genus, such as *S. baicalensis* and *S. barbata*, have been widely used as medicinal plants in Asia. We identified a complete set of MADS-box genes in five *Scutellaria* genomes, three of which (*S. cypria, S. insignis,* and *S. strigiliosa*) from newly sequenced genomes in this study using both long-read (Nanopore) and short-read (MGI) sequenced, and two of them from a previously reported genome (*S. baicalensis* and *S. barbata*). The three newly sequenced genomes, ranging from 0.26 to 0.33 Gbps, are of high quality (83 to 475 contigs and > 96.3% of BUSCO values). We addressed lineage-specific deletion, addition and duplication events of MADS-box genes in *Scutellaria* based on phylogenetic analyses of genes detected from genomes in five *Scutellaria* species, *Solanum lycopersicum* (the closest high-quality genome published to *Scutellaria*), *Arabidopsis thaliana* (a representative of the dicots) and *Amborella trichopoda* (a sister to all other angiosperms). Expressions of MADS-box genes were addressed using RNAseq of each floral organ. This study shows the evolution, diversification, and expression of MADS-box genes in *Scutellaria* and provides insights into the relationship between these genes and the floral morphology of *Scutellaria*.

S.090. KIN DISCRIMINATION AND KIN SELECTION IN PLANTS

P.0831 Kin recognition influences sex allocation in Moricandia moricandioides

Camilo Ferrón[1,*], José María Gómez[2,**]
John R. Pannell[3], Rubén Torices[1,***]

*1 Área de Biodiversidad y Conservación, Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos, Móstoles, Spain. 2 Departamento de Ecología Funcional y Evolución. Estación Experimental de Zonas Áridas, Consejo Superior de Investigaciones Científicas, Almería, Spain. 3 Department of Ecology and Evolution, University of Lausanne, Lausanne, Switzerland. *camilo.ferron@urjc.es,**jmgreyes@eeza.csic.es, ***ruben.torices@urjc.es*

Plants may potentially enhance the pollination success of other neighbours in the same patch through a ‘magnet effect’. This effect indicates that a plant’s investment in attractive floral structures may increase pollinator visits to its own flowers and those of its neighbours, leading to benefits at both the individual and group level. This phenomenon is observed in Moricandia moricandioides, a self-incompatible and hermaphroditic species, which exhibits larger floral displays when surrounded by kin compared to non-kin. This increased investment in attraction when growing among relatives could be a result of selection due to its impact on inclusive fitness. However, it is not yet clear whether plants might modify their sex expression based on the kinship of their local neighbours. We hypothesized that the greater investment in pollinator attraction seen when growing with kin should lead to a male-biased sex allocation if the increased advertising effort enhances male fitness returns. To test this, we examined floral sex allocation in plants under various experimental neighbourhood conditions where the number and mother identity of the neighbours were controlled. Contrary to our hypothesis, plants growing with kin produced significantly more ovules but not pollen grains, indicating an increase in plant femaleness. This finding supports the potential existence of kin recognition in this species and its influence on reproductive strategies. Nevertheless, additional research is required to determine whether the adjustment of floral sex allocation to the neighbourhood is prevalent in other populations of this species or in other species that exhibit a positive pollination effect in dense plant clusters.

P.0832 Inosculation and cooperative dynamics in conspecific mature tree communities

Anna Finke[1]

1 Minimal Intelligence Lab, Department of Philosophy, University of Murcia, Spain.

Inosculation, the fusion of tree parts, represents a broad spectrum of interactions including root grafting, and serves as a crucial but undervalued indicator of kin selection and cooperative dynamics within tree communities. I posit inosculation as a key adaptive behavior fostering resilience and alliances among conspecific adult trees, with genetic similarity enhancing the probability of such unions. I suggest that this phenomenon has largely been overlooked as in modern managed forests, inosculation is less prevalent due to human intervention and the relative short rotation of tree stands, signaling a significant gap in our understanding of forest ecology. Mature trees engaged in inosculatory behaviors display a reduction in competitive tendencies, preferring instead to establish resource-sharing networks indicative of a cooperative existence. This mutualistic interaction, particularly evident in root grafting, contrasts with the competitive isolation experienced by younger, solitary trees and underscores a shift from competitive to cooperative behavior and the importance of communal networks in mature stands. The shared resources and stability afforded by these connections confer a collective competitive advantage, challenging the long-held belief that competitive exclusion is the predominant interaction within tree canopies, especially in forests dominated by few species. The implications of this research are profound, proposing a more frequent occurrence of cooperation among adult conspecifics than previously recognized. It calls into question the traditional interpretations of tree competition and dominance, potentially prompting a significant reevaluation of forest management and conservation practices. In light of these considerations, inosculation emerges as a potentially transformative element in our understanding of forest communities, and could catalyze a paradigm shift in the ecological management of forests.

P.0833 Root exudates composition within and among four genetic clusters of Arabidopsis thaliana from the Iberian Peninsula

Harihar Jaishree Subrahmaniam[1]*, F. Xavier Picó[2], Thomas Bataillon[3], Camilla Lind Salomonsen[4], Marianne Glasius[4], Bodil K. Ehlers[1]

1 Department of Ecoscience, Aarhus University, Aarhus C, Denmark. 2 Departamento de Biología Evolutiva, Estación Biológica de Doñana, Sevilla, Spain. 3 Department of Molecular Biology and Genetics, Bioinformatics Research Centre, Aarhus University, Aarhus C, Denmark. 4 Department of Chemistry, Aarhus University, Aarhus C, Denmark.

Root exudates are a critical yet understudied component of terrestrial ecosystems, playing important roles in nutrient acquisition, microbial symbiosis, and inter-organism communication. Despite their significance, comprehensive insights into the natural variation and eco-evolutionary factors driving the composition of root exudates are scarce. Our study addressed this gap by exploring the chemical diversity of root exudates from 105 *Arabidopsis thaliana* accessions of the Iberian Peninsula. Employing ultra-high performance liquid chromatography coupled with mass spectrometry, we identified 373 putative chemical compounds, unveiling the complex chemical ecology of root exudates. Our findings reveal a significant influence of the genetic structure of Iberian accessions on root exudate composition, with 25 compounds showing notable heritability estimates. We observed variation in the mean abundances of nine compounds across the four genetic clusters, suggesting unique metabolic signatures tied to specific genetic clusters. This finding hints at the potential of root exudates in facilitating differential interactions among plants, including kin recognition. A genome-wide association study illuminated specific single nucleotide polymorphisms located in or near 26 known genes with diverse functions, encompassing metabolism, defense, signaling, and nutrient transport, hinting at the multifaceted roles of root exudates in mediating plant physiological processes and ecosystem functioning. Integrating genetic, environmental, geographic, and life-history trait variation among accessions, we identified significant correlation between genetic distance and terpenoid composition distance. Our study offers the first comprehensive exploration of root exudate variation at an ecologically large scale, providing first insights into the potential roles of these exudates in below-ground plant-plant interactions. Understanding the genetic and physiological underpinnings of root exudates is crucial for predicting plant responses to environmental changes and resource dynamics. Our findings emphasize the need for multidisciplinary exploration in this field integrating ecology, genomics and chemistry to fully comprehend the ecological and evolutionary facets of root exudates.

S.091. LARGESCALE GENERATION AND UTILISATION OF REFERENCEQUALITY GENOMES FROM PLANTS

P.0834 Evolution of splice site choice in eukaryotes

Craig I Dent[1,11], Stefan Prodic[1,12], Aiswarya Balakrishnan[1], James Georges[1], Aaryan Chhabra[1], Sourav Mukherjee[1], Jordyn Coutts[1], Michael Gitonobel[1], Rucha D Sarwade[1], Joseph Rosenbluh[2], Mauro D'Amato[3, 4, 5], Partha P Das[6, 7], Ya-Long Guo[8], Alex Fournier-Level[9], Richard Burke[1], Sridevi Sureshkumar[1], David Powell[10], Sureshkumar Balasubramanian[1]

1 School of Biological Sciences, Monash University, Clayton, Australia. 2 Biomedicine Discovery Institute, Monash University, Clayton, Australia. 3 De-

partment of Medicine and Surgery, LUM University, Casamassima, Italy. 4 Gastrointestinal Genetics Lab, CIC bioGUNE – BRTA, Derio, Spain. 5 Ikerbasque, Basque foundation for Science, Bilbao, Spain. 6 Department of Anatomay and Developmental Biology, Monash University, Clayton, Australia. 7 Development and Stem Cells Program, Monash Biomedicine Discovery Institute, Clayton, Australia. 8 State Key Laboratory of Systematic and Evolutionary Botany, Institute of Botany, Chinese Academy of Sciences, Beijing, China. 9 School of Biosciences, University of Melbourne, Parkville, Monash University, Clayton, Australia. 11 Max-Planck Institute for Plant Breeding and Genetics, Cologne, Germany. 12 The Centre for Computational Biomedical Sciences, John Curtin School of Medical Research, Australian National University, Canberra, Australia.

Splicing is a key gene regulatory process in which certain sections of the synthesised RNA referred to as introns are removed with the joining of the adjacent exons. There is extensive variability in splicing that can result in different proteins being produced by the same gene. Sequence variation can cause variability in splicing. Given the functional relevance of splicing, it becomes an important evolutionary mechanism through which phenotypic variability could be achieved both within and between species. Typically, splicing is looked at an individual species level or at a molecular level, but there are relatively few studies, who take a global approach and compare distinct species on their splicing variability and choice. We have exploited large scale genome wide transcritomes and GWAS to decipher patterns of splicing and reveal some of the basic features that govern splice site choice. Comparision of GWAS hits reveal potential mechanisms of phenotypic variation from flowering to human disease. Our studies provide experimentally verifiable principles of splice site selection from yeast to plants to humans. Our latest comparative analysis and their evolutionary significance would be discussed.

P.0835 Comparative analysis of simple sequence repeats in the chloroplast genomes of selected Dracaena species

Konrad Celiński[1], Luiza Wolska[1], Joanna Sikora[1], Justyna Wiland-Szymańska[1]

1 Adam Mickiewicz University, Poznań, Poland.

Simple sequence repeats (SSRs), also known as microsatellites, are very important DNA segments that play a key role, i.a. in genome evolution and gene expression. They are also widely used in DNA profiling, genetic linkage or kinship analysis, and in forensic identification. SSRs provide a broad resource for developing molecular markers necessary for species monitoring and conservation. Due to high reproducibility and high polymorphism with many alleles per locus and the possibility of transfer between species, SSR markers have found wide application in genetic diversity studies and population structure analysis. The genus *Dracena* L. *sensu stricto* (Asparagaceae) collects ca. 116 species distributed in Africa, Asia, Australia and Central America. Many of its members are recognized ornamental plants e.g., *D. fragrans* (L.) Ker Gawl., while others are used for medicinal purposes and social functions e.g., *D. cinnabari* Balf.f. These variable plants inhabit different habitats from equatorial forests to semideserts, but their taxonomy, pollination and dispersal modes as well as distributions are not fully known. Some of them are quite widespread, while others are restricted to small areas. The wild species of *Dracaena* are actual wild relatives for ornamental varieties and an important source of income for collectors of “dragon’s blood”. The survival of some species is threatened by the overexploitation of natural populations and climate change. The main aim of the study was to analyze the distribution and diversity of simple sequence repeats in the chloroplast genomes of selected species of the *Dracaena* genus. The obtained results expand knowledge about microsatellites and may help in both understanding the phylogeny of these taxa and in their conservation.

P.0836 Towards a comprehensive reference genome for Reseda genus: unravelling the genomic landscape for conservation and evolutionary study

Degli Alberti, Martina[1,2], Martínez-García, Irene, Martínez-Nieto, Isabel[3], Soriano, Pilar[3], Bombarely, Aureliano[2], Manrique, Silvia[1]

1 Instituto Universitario para la Conservación y Mejora de la Agrodiversidad Valenciana, Universidad Politécnica de Valencia, Valencia, Spain. 2 Instituto de Biología Molecular y Celular de Plantas (IBMCP) Primo-Yufera, Consejo Superior de Investigaciones Científicas (CSIC)- Universidad Politécnica de Valencia, Valencia, Spain. 3 Jardín Botánico, Universidad de Valencia, Valencia, Spain.

Reseda is a genus of flowering plants containing more than 60 species, native to the temperate region of the north hemisphere. The genus has a biodiversity hotspot in the Mediterranean area, with three related species native to the Iberian Peninsula with interesting evolutionary properties. *R. hookeri,* critically endangered, and *R. barrelieri* are hypothesized as tetraploid species adapted to coastal cliffs and limestone habitats, respectively. These two species coexist with *R. alba,* a wide-range species, described as octoploid. Despite their significance in ecosystems, the genomic resources for *Reseda* species remain limited. Here, we present our ongoing efforts towards generating high-quality reference genomes for *R. alba*, *R. hookeri* and *R. barrelieri* to progress in the characterization and conservation of these species. For that, we have explored best practices for the obtaining of good quality, high-molecular-weight DNA from these plants, a mandatory first step for the posterior sequencing with the newest long-read sequencing platforms, such as PacBio Revio. Through this, we aim to overcome the inherent complexities associated with polyploidy within the *Reseda* genomes. The establishment of a high-quality reference genome will serve as a foundational resource for advancing research in the *Reseda* genus. Our initiative represents a significant step towards unlocking the genomic mysteries of the Reseda genus, paving the way for comprehensive genomic and translational studies aimed at harnessing the biodiversity and evolutionary innovations of these remarkable plant genus.

P.0837 Progress on the plant side of the Canada BioGenome project

Sean W. Graham[1], Marco Todesco[1,2], Samantha Jones[3], The Land-Plant Panel of the Canada BioGenome Project[4], Steven Jones[3,5]

1 Department of Botany, University of British Columbia, Vancouver, Canada. 2 Michael Smith Laboratories, University of British Columbia, Vancouver, Canada. 3 BC Cancer Research Centre, Vancouver, Canada. 4 Multiple Canadian Academic Institutions 5. Department of Medical Genetics, University of British Columbia, Vancouver, Canada.

The Canada BioGenome Project (CBP) is part of the Earth BioGenome Project, which aims to sequence the genomes of all the eukaryotic biodiversity. The project is relevant to scientific exploration and conservation of Canadian species. CBP is currently generating the first set of high-quality genome assemblies of ~400 Canadian species, including over 100 Canadian land plants, to demonstrate how genomics can aid in conservation, biodiversity research, restoration, and species monitoring. Species selection was coordinated in consultation with stakeholders and experts to select species of relevance to Canada. We focused on species that are either native or invasive/established. Selection criteria include economic importance (crops, weeds), conservation status, cultural significance, and scientific interest to Canadian researchers, with a special interest in Arctic plants. While the focus for vascular plants is on diploid plants with small genomes, we are including several polyploids and/or plants with large genomes as proof-of-concept for future phases of CBP. The goal is to produce high-quality (haplotype-resolved, chromosome-level) assemblies that are publicly available to researchers and other stakeholders. The project also aims to develop genomic information and bioinformatic tools to inform policy, conservation and monitoring. We provide an update on the status of the selected Canadian species, development of collection protocols, and progress on test species—including axenically grown bryophytes.

P.0838 Plants of the Tree of Life Programme: past, present and future

Benjamin Jackson[1], Adam Bates[1], Isabelle Clayton-Lucey[1], Amy Denton[1], Juan Pablo Narvaez Gomez[1], Jessie Jay[1], Graeme Oatley[1], Priyanka Sethu Raman[1], Elizabeth Sinclair[1], Abitha Thomas[1], Halyna Yatsenko[1], Caroline Howard[1]

1 Tree of Life Programme, Wellcome Sanger Institute, Cambridgeshire, UK.

The Darwin Tree of Life Programme is a collaboration of scientific partners producing high-quality reference genomes for all 70,000 known eukaryotic species of animals, plants, fungi and protists in Britain and Ireland. Having publicly released 1,000 reference level genome assemblies in October 2023, and with thousands more in the pipeline, the development of bespoke procedures has proven crucial in meeting the demands of simultaneously processing phenotypically diverse species rapidly and efficiently. A key challenge has been the isolation of pure, high-quality and high molecular weight genomic DNA; a prerequisite to generating adequate long-read sequencing data. For plants, the exceptional heterogeneity observed amongst species at all taxon levels has presented a unique set of challenges that each require bespoke solutions. For example, the abundance of inhibitory sugars, oils and other endogenous biochemicals present in the tissues of recalcitrant plants often impede the extraction of DNA and its aligned procedures. Whilst the array of resilient structures often owed to the extracellular matrix of plants necessitates the use of laborious, mechanical cryogenic disruption procedures. Meanwhile, further complexities are introduced by the abundance of species with exceptionally large genome sizes, such as *Viscum album* (ca. 90 gigabase pairs), or species with specimens of exceptionally small size, such as non-vascular plants. Reaching 100 complete plant genome assemblies in January 2024, with over 800 species being actively processed, the laboratory team continues to systematically innovate and optimise its methodologies to meet ever more complex challenges. A suite of modular procedures has been developed focusing on the reception, preparation and homogenisation of specimens, along with the extraction, purification and processing of nucleic acids. This poster will investigate ToL's plant extraction pipeline within the context of long-read sequencing for reference level genome assembly, challenges and obstacles met along the way, and methods for standardising these approaches at scale.

P.0839 A chromosome-scale genome assembly and recombination map of Pedicularis cranolopha reveals determinants of genetic diversity

Jason Leung[1], Jianjun Jin[1], Patrick McKenzie[2], Jared Meek[1], Deren Eaton[1]

1. Department of Ecology, Evolution, and Environmental Biology, Columbia University, New York, USA 2. Department of Organismic and Evolutionary Biology, The Arnold Arboretum, Harvard University, Cambridge, USA

The genus *Pedicularis* (Orobanchaceae) is a diverse clade of hemiparasitic flowering plants that has radiated throughout temperate and alpine regions of the northern hemisphere, most notably the Qinghai Tibetan Plateau and Hengduan Mountains of China, where >300 species are endemic. Here we present the first chromosome-scale genome assembly and recombination map of *Pedicularis cranolopha* as a new genomic resource for this clade. Using genome-wide re-sequencing data from *P. cranolopha,* and RAD-seq data from ~100 additional species, we examine genome-wide patterns of diversity and divergence in sliding windows along chromosomes. We examine correlates of diversity across the genome, including gene content, repetitive elements, and recombination rate. Windows with high recombination in *P. cranolopha* exhibit greater diversity and divergence both within *P. cranolpha* (across populations) as well as across the diversity of species examined. This suggests that the recombination map is relatively conserved across this clade, and that patterns of diversity across genomes may be influenced more by genome structure than adaptation.

P.0840 Optimization of nuclei isolation for high-molecular weight DNA extraction from wild plants

Irene Martínez-García[1]; Martina Deglialberti[2]; Aureliano, Bombarely2; Mario Xavier Ruiz-González[1]; Santiago Vilanova[1]; Silvia Manrique[1]

1 Instituto Universitario para la Conservación y Mejora de la Agrodiversidad Valenciana, Universidad Politécnica de Valencia, Valencia, Spain. 2 Instituto de Biología Molecular y Celular de Plantas Primo-Yufera, Consejo Superior de Investigaciones Científicas -Universidad Politécnica de Valencia, Valencia, Spain.

Obtaining high-quality, high-molecular-weight (HMW) DNA is mandatory for constructing reference genomes, yet it remains a significant challenge, particularly for non-model plant species. Many plants contain polysaccharides and secondary metabolites such as polyphenols and tannins, which hinder DNA extraction. Exposure to multiple environmental stresses along their lives exacerbate this issue in wild plants collected from nature, as they may synthesize additional compounds that impair DNA extraction. This study investigates the efficacy of various DNA extraction protocols on four recalcitrant plant species—*Pistacia lentiscus*, *Phyllirea angustifolia*and *Limbarda crithmoides*—each possessing unique traits complicating DNA extraction (e.g., succulence, lignification, coloration). Samples were collected from El Saler (Valencia), and multiple protocols for nuclei isolation and DNA extraction were tested. The results were systematically evaluated to compile a comprehensive best practices guide, aiding researchers in selecting optimal methods tailored to their species of interest. This guide serves as a valuable resource for future endeavours in genome research, facilitating advancements in understanding and conservation efforts for diverse plant species.

P.0841 The Darwin Tree of Life project: progress in sequencing the whole genomes of the flora of Britain and Ireland

José I. Márquez-Corro[1], Ilia J. Leitch[1], Michelle L. Hart[2], Maarten J.M. Christenhusz[1], Alex Twyford[2,3], David Bell[2], Laura L. Forrest[2], Sahr Mian[1], Andy Griffiths[2], Markus Ruhsam[2], Peter Hollingsworth[2], Paul Kersey[1]

1 Royal Botanic Gardens, Kew, Richmond, UK. 2 Royal Botanic Garden, Edinburgh, UK. 3 Institute of Evolutionary Biology, University of Edinburgh, Edinburgh, UK.

Under the umbrella of the Earth Biogenome Project (earthbiogenome.org), whose ambition is to sequence the genomes of all eukaryotic life on earth, the Darwin Tree of Life consortium is a collaborative project between biodiversity, genomics and analysis partners from across Britain and Ireland. The overall aim is to generate platinum-grade chromosome-level genome assemblies of the ~70,000 eukaryotic organisms that inhabit the archipelago of islands that constitute Britain and Ireland.

With a focus on the ~2,700 native land plants (comprising ~1,600 vascular plants and ~1,100 bryophytes), the Royal Botanic Garden Edinburgh and Royal Botanic Gardens Kew (the Plant Working Group) coordinate the collecting of plants. These are then sequenced, assembled, curated and released into the public domain by the Wellcome Sanger Institute in Cambridge, UK. Since the start of the project in 2019 the Plant Working Group has collected >1,100 plants, of which >100 have been fully sequenced and are now publicly available (see portal.darwintreeoflife.org). These include some of our most emblematic species, such as the orchard apple (*Malus domestica*) and the shamrock (*Trifolium dubium*), as well as other ecologically important species such as common ivy (*Hedera helix*) and twisted bogmoss (*Sphagnum contortum*). In addition, a complete chromosome-level genome assembly of the parasitic mistletoe *Viscum album* has been released. With a genome size of ~90 Gb and therefore ~30x the size of a human genome, this represents the largest genome assembled so far. The genomic information retrieved from the high-quality genomes will be invaluable for helping to understand the origins and future of plant biodiversity and how species are best preserved in the face of climate change. It provides key resources to enable step-changes in the fields of conservation, biology, medicine and biotechnology.

P.0842 Development of genomic resources in Mexican Bursera (section Bullockia: Burseraceae)

Yessica Rico[1], Gustavo P. Lorenzana[2], Bode A. Olukolu[3]

1 Red de Diversidad Biológica del Occidente Mexicano, Instituto de Ecología, Michoacán, Mexico. 2 School of Forestry, Northern Arizona University, Arizona, USA. 3 Department of Entomology and Plant Pathology, University of Tennessee, Tennessee, USA.

Bursera comprises ~100 tropical shrub and tree species with the center of species diversification in Mexico. Genomic resources developed for the genus are scarce and have limited the study of gene flow, local adaptation, and hybridization dynamics. In this study, based on ~155 million Illumina paired end reads per species, we performed a *de novo* nuclear genome assembly and annotation of three *Bursera* species of the *Bullockia* section: *B. bippinata, B. cuneata,* and *B. palmeri*. We also characterized their complete chloroplast genome structure and functional annotation. The total length of the genome assemblies was 253, 237, and 229 Mb for *B. cuneata*, *B. palmeri* and *B. bippinata*, respectively. The assembly of *B. palmeri* retrieved the most complete and single-copy BUSCOs (87.3%) relative to *B. cuneata* (86.5%) and *B. bipinnata* (76.6%). The *ab initio* gene prediction identified between 21,000–32,000 protein-coding genes.

For the chloroplast (Cp) genome sizes, they ranged from 159,824 to 159,872 bp in length. The three Cp genomes consisted of 135 genes, of which 90 were functional, 37 tRNAs, and 8 rRNAs. A comparison of the three Cp genomes revealed that they were relatively conserved, with the LSC region exhibiting the greatest nucleotide divergence. Moreover, for both the nuclear and chloroplast genomes, we identified simple sequence repeats (SSRs). Phylogenetic relationships within Burseraceae using Bayesian inference confirmed that *Commiphora* is the sister taxa of *Bursera*. Our work contributes to the development of *Bursera*'s genomic resources for taxonomic, evolutionary, and ecological studies.

P.0843 Rates of nuclear, plastid, and mitochondrial evolution are linked in land plants

Yasmin Asar[1], Hervé Sauquet[1,2,3], Simon Y.W. Ho[1]

1 University of Sydney, Sydney, Australia. 2 Botanic Gardens of Sydney, Mount Annan, Australia. 3 University of New South Wales, Sydney, Australia.

Mutation rates in plants can be affected by factors such as UV irradiation, temperature, rate of growth, and the efficiency of DNA repair systems. A link between evolutionary rates across the nuclear, chloroplast, and mitochondrial genomes would indicate that these genomes respond to mutagenic factors in similar ways, or that they share systems of DNA repair. By using the most accurate and powerful methods to date, we tested whether the evolutionary rates of nuclear and organellar genomes are coupled in plants. We sampled major clades from land plants (Embryophyta), including angiosperms, gymnosperms, ferns, and bryophytes, as well as three parasitic angiosperm clades (*Rafflesia*, Orobanchaceae, and Opiliaceae). We found that evolutionary rates of nuclear and chloroplast genomes were linked in each group of land plants we tested, except for the parasitic angiosperms. Overall, rates of nuclear, chloroplast, and mitochondrial evolution were linked in plants, but these patterns are less pronounced for mitochondrial markers. We found that mitochondrial genes displayed the highest rate variation across lineages, followed by nuclear and then chloroplast genes. Overall, these findings indicate that nuclear, plastid, and mitochondrial genomes in land plants are similarly affected by factors that alter rates of mutation, despite considerable variation in life history strategies among clades. The results of this study also have practical implications for phylogenetic analyses of combined plant organellar genomes, as plant mitochondrial genomes are usually excluded from phylogenetic inference due to their slow rates of evolution and disparate evolutionary dynamics.

P.0844 Biogeography of the Cape Clade of Indigofera: Exploring patterns that resulted in an immense radiation in the GCFR

Brian du Preez [1,2], Brian D. Schrire [3], Léanne L. Dreyer [2], Charles H. Stirton [1], Samson B.M. Chimphango [1], A. Muthama Muasya [1]

1 Bolus Herbarium, Department of Biological Sciences, University of Cape Town, South Africa. 2 Department of Botany and Zoology, Stellenbosch University, South Africa. 3 Honorary Research Associate, Accelerated Taxonomy Department, Royal Botanic Gardens, Kew, Richmond, Surrey, UK.

The genus *Indigofera* L. is globally distributed, comprising over 750 species. Three of the four main globally recognized clades display intercontinental distributions, while the Cape Clade (140 species) is restricted to southern Africa. Most species in this clade are endemic to the Greater Cape Floristic Region (GCFR), a small area in the south-western corner of South Africa that is characterized by a winter rainfall regime and unique Fynbos Biome flora. The Cape Clade has an inferred origin in the Succulent Biome at the southern edge of the Namib Desert approximately 22 mya, with *I. nudicaulis* representing the earliest diverging lineage, predating other extant Cape Clade lineages by ca. 10 my. Lineages within the Cape Clade, classified as sections and subsections, show remarkable biogeographic patterns, based on biome preference and associated edaphic and climatic conditions. Sections *Digitatae* and *Oligophyllae*, which have Succulent Biome origins, are most diverse, but are not restricted to this biome, with multiple shifts into Temperate and grass-rich Subtropical Thicket and Grassland Biomes taking place. Section *Juncifoliae* appears to represent an early dispersal into the Temperate Fynbos Biome, particularly in seasonally wet areas. Sections *Productae* and *Brachypodae* are recent and diverse radiations derived from a Succulent Biome ancestor, that are endemic to Fynbos, but not in seasonally wet areas. The only areas that have mixing of Succulent and Temperate lineages are along the coast of the

Temperate Biome, typically in Fynbos and Strandveld vegetation types. Lineages from the three other global clades show similar patterns, having origins in the Succulent or grass-rich Biomes, before dispersing into Temperate Fynbos. This suggests that the Temperate Fynbos Biome is a sinkage area for multiple *Indigofera* lineages, that have adapted to the edaphic conditions of the region to such an extent, that they are unable to disperse back into other biomes.

S.092. LEGUME SYSTEMATICS: FROM COLLABORATIVE NETWORKS TO GENOME SEQUENCING

P.0845 The significance of repeatome differentiation of Albizia s.l. (Leguminosae) in Neotropical colonization

Géssica S. Santos[1,2], Lucas Costa[1], Magdalena Vaio Scvortzoff[3], Ana Paula Moraes[4], Gustavo Souza[1], Maria J. G. de Andrade[2]

1 Universidade Federal de Pernambuco, Recife, Brazil. 2 Universidade do Estado da Bahia, Paulo Afonso, Brazil. 3 University of the Republic, Montevideo, Uruguay. 4 Universidade Estadual Paulista Júlio de Mesquita Filho, Botucatu, Brazil.

The repeatome corresponds to the most dynamic portion of plant genomes, due to its rapid evolution, and its activity can be impacted by environmental aspects. Albizia s.l. encompasses ~140 species with conflicting phylogenetic relationships. Recently the group has undergone taxonomic changes, including the relocation of neotropical taxa into a new genus, Pseudoalbizia. We comparatively analyzed the repeatomes of 31 taxa of Albizia s.s., and representatives of closely related genera covering different continents and aimed to discuss possible biogeographic implications in repeat evolution. We used RepeatExplorer to characterize the lineages of repeats in a temporal and phylogenetic context. For this, we constructed a dated phylogenetic tree based on complete plastomes. This topology showed strong support for two main clades: A (Pseudoalbizia + Hydrochorea obliquifoliata – 10.5 Mya) and B (Albizia s.s. – 7.5 Mya). Transposable elements (TEs) represented the most abundant portion of the all repeatomes, especially the Ty3-Gypsy and Ty1-Copia superfamilies of LTR retrotransposons. High abundances and variability in the Tekay (52% - 17%), Athila (46% - 17%), and SIRE (9.4% - 0.22%) lineages suggest they contributed to genomic diversification in the group. A clear differentiation was revealed between the repeatomes of neotropical taxa compared to others, with genomic synapomorphies including the sharing of unique clusters of TEs, and DNA satellite (satDNA). While specific satDNAs were detected in Old World species. Our data suggest that the plesiomorphic geographic distribution of Albizia s.s. (Africa and Asia) is associated with more similar repeatomes, while the colonization of the Neotropical region appears to have been accompanied by strong differentiation in this genomic fraction. This scenario corroborates with fossil records that highlight Asia as the center of origin for Albizia. Suggesting that colonization of a new environment with differentiation in ecological conditions can impact repeat evolution.

P.0846 Does adaptive radiation impact repeat evolution? Comparative genomic analysis of Acacia subg. Phyllodineae (DC) Ser. (Leguminosae)

Géssica S. Santos[1 2], Yennifer Mata-Sucre[1], Lucas Costa[1], Maria José Gomes de Andrade[2], Andrea Pedrosa-Harand[1], Gustavo Souza[1]

1 Universidade Federal de Pernambuco, Recife, Brazil. 2 Universidade do Estado da Bahia, Paulo Afonso, Brazil.

Plant genomes composition shows high variability, especially due to the diversity of repetitive elements and their abundance fluctuations across evolutionary time. However, it is unclear how certain evolutionary events, such as adaptive radiation, impact the evolution of the repeatome. Acacia subg. Phyllodineae (1,084 species) underwent adaptive radiation in Australia about 5 Mya. Most of the subgenus belong to the Pilbara clade, which had an increased rate of diversification in dry environments. The main repetitive DNA classes of 50 taxa of the subgenus Phyllodineae were characterized through a comparative genomic analysis. Low coverage (genome skimming) reads were comparatively analysed and the repeat evolution was interpreted under a full plastome phylogeny. Overall, the repetitive fraction comprised (15 - 48%) of the genomes, with a higher proportion of LTR Ty1/copia/SIRE retrotransposons in most species. Approximately 90% of the clusters included transposable elements (TEs) and most of these were shared between species, with a small variation in abundance among genomes. In contrast, satellite DNAs (satDNAs) were highly dynamic, with low phylogenetic reach. The early diverging lineages had the highest diversity of satDNA families, with some being subclade-specific. The Pilbara clade showed a lower diversity of satDNAs, as well as more conserved TEs abundances. Our results support the satellite library hypothesis as an explanation for the evolution of these repeats. Compared with plastome topology, this clade showed no phylogenetic resolution in both repeat abundance or similarity topologies. The low rates of repeat evolution identified here could be related to the recent age and arboreal habit of the Pilbara clade. In this scenario, the homogeneity in the repetitive genomic fraction can be explained by mutation/drift, but the generated patterns of repeat abundance/similarity were insufficient for phylogenetic reconstruction. Thus, despite the ecological/morphological diversification, our data suggest that adaptive radiation is not necessarily accompanied by repeatome diversification.

P.0847 Phylogenomics of Genisteae (Fabaceae) and implications for the distribution of quinolizidine alkaloids

Sarah Hunter[1], Brian Sedio[1], Domingos Cardoso[2], Tracey A. Ruhlman[1], Robert K. Jansen[1]

1 University of Texas at Austin, Austin, USA. 2 Jardim Botanico, Rio de Janeiro, Brazil.

Genisteae is a legume tribe whose members are known for producing quinolizidine alkaloids (QAs). These compounds act as a natural defense mechanism against pests, and can be very beneficial for crop species. One of the major challenges to understanding the evolution of QAs is that there still has not been a comprehensive phylogeny of Genisteae; thus, many relationships remain unresolved among the genera. This study aims to build a phylogeny for Genisteae and then use it as a framework for assessing the distribution and major classes of QAs. We have sampled 41 species representing 24 genera of Genisteae. This contains representatives from nearly every genus with the exception of *Argyrocytisus*, which was unavailable. The plastomes have been assembled and have an average size of 152,153 base pairs, and 1,546 low-copy nuclear genes have been retrieved using PhyloHerb. Phylogenies were constructed for both the plastome and nuclear data using maximum likelihood (ML), coalescence, and Bayesian methods. The resulting trees were then compared for congruence using several topology testing methods, including RELL approximation, Kishino-Hasegawa (KH), Shimodaira-Hasegawa (SH), expected likelihood weight (ELW), and approximately unbiased (AU). The phylogenetic trees identified several monophyletic groups, including the *Lupinus* clade, the *Cytisus-Genista* complex, the *Argyrolobium* group, and the *Anarthrophyllum* group. The *Argyrolobium* group is in its predicted position at the base of Genisteae and the newly identified *Anarthrophyllum* group, containing *Anarthrophyllum, Polhillia,* and *Sellocharis,* is sister to the remaining genera of the tribe. Alkaloids were extracted and analyzed using liquid chromatography-tandem mass spectrometry. QAs were then plotted on the plastome and nuclear trees to examine their phylogenetic distribution. QAs are present in almost all the taxa, which agrees with existing literature. Intermediate compounds have also been found in almost all taxa, including taxa without QA compounds present, which may suggest a partially present biosynthetic pathway.

P.0848 Unraveling the evolution of Arthroclianthus and Nephrodesmus: New Caledonia's only endemic Leguminosae

Zalko J[1], Deroin T[2], Favre A[3], Jabbour F[2], Malem J[4], Vandrot H[5], Sarthou C[2]

1 Université Paris-Saclay, INRAE, CNRS, AgroParisTech, Génétique Quantitative et Evolution-Le Moulon, IDEEV, Gif-sur-Yvette, France. 2 Institut de Systématique, Evolution, Biodiversité, Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Universi-

té des Antilles, Paris, France. 3 Regional Nature Park of the Trient Valley, Salvan, Switzerland. 4 Okinawa Institute of Science & Technology Graduate University, Tancha, Onna-son, Okinawa, Japan. 5 Institut Agronomique Néo-Calédonien (IAC), UMR AMAP - Botanique et Modélisation de l'Architecture des Plantes et des Végétations, Nouvelle-Calédonie.

In the Pacific archipelago of New Caledonia, the combination of a specific geological history and diverse landscapes has favored a rich and unique flora with almost 75% of endemic vascular plant species. *Arthroclianthus* Baill. and *Nephrodesmus* Schindl. form the only endemic group of Leguminosae of the archipelago. They exhibit distinct morphological characters and their specific delineation is challenging. While supporting the *Arthroclianthus*-*Nephrodesmus* clade, previous phylogenetic reconstructions based on nuclear and chloroplastic markers questioned the monophyly of each genus and dated the diversification of the group within the last 10 million years. In this study we aim to elucidate the phylogenetic relationships within the group using Next-Generation Sequencing (NGS) data. We retrieve various loci, including full chloroplast genomes for all the 17 morphological species in the group and we explore new diagnostic morphological characters, with a particular focus on understudied fruit morphology. We identify morphological groups supported by the phylogenetic reconstructions, yet incongruences between chloroplast and nuclear markers suggest introgression events, potentially influenced by shared ecological preferences within sympatric populations. The observed diversity in the group is likely influenced by the unique ecological and geographic conditions in New Caledonia.

P.0849 Structural and phylogenetic analysis of plastid genomes in Loteae (Leguminosae): the first results

Tatiana Kramina[1], Yury Kopylov-Guskov[1], Tahir Samigullin[1]

1 Lomonosov Moscow State University, Moscow, Russia.

The subfamily Papilionoideae of Leguminosae is characterized by numerous rearrangements of the plastid genome, especially in the IRLC (Inverted Repeat Lacking Clade). The tribe Loteae includes 16 genera and about 280 species of herbs, semi-shrubs and shrubs, common in Eurasia, Africa, Australia, Oceania, North and South America. In the phylogenetic tree of legumes, the tribe Loteae is located close to the IRLC. The genera *Robinia* and *Sesbania*, phylogenetically close to Loteae, showed the presence of large rearrangements in the LSC (large single copy) region of the plastid genome: 36 kb inversion in *Robinia* and 50 kb reversion in *Sesbania*. The slow evolution of plastid sequences has led to a lack of proper resolution in the relationship between the large evolutionary branches within Loteae by plastid markers, which can be overcome by whole genome sequencing. The main objectives of the study include: 1. Complete reading and annotation of ca.15 plastid genomes of representatives of large genera of the tribe Loteae. 2. Conducting structural and phylogenetic analyses of the plastomes. All plastomes were sequenced using Illumina platform. To date, we have 22 plastid genomes (including six from GenBank), which belong to 20 species from six genera of the tribe Loteae (*Acmispon, Anthyllis, Coronilla, Hippocrepis, Hosackia* and *Lotus*), as well as *Sesbania cannabina* and *Robinia pseudoacacia* as ougroups. The results obtained and preliminary conclusions: 1. The plastomes of representatives of the tribe Loteae have a conservative structure with only minor rearrangements, unlike those of the closest related groups (*Robinia* and *Sesbania*). 2. The genome-wide plastid data showed a good phylogenetic signal, which allowed to resolve the relationship between the large evolutionary branches of the tribe, such as *Hippocrepis*, *Coronilla* and *Anthyllis*.

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P.0850 Characterization and phylogenetic analysis of the complete chloroplast genome of Colutea triphylla (Fabaceae: Coluteae)

Mahtab Moghaddam[1], Shahrokh Kazempour-Osaloo[1], Atsushi Ohta[2], Motoki Shimizu[3], Ryohei Terauchi[2]

1 Tarbiat Modares University, Tehran, Iran. 2 Kyoto University, Japan, 3 Iwate Biotechnology Research Center, Japan.

The chloroplast genome (plastome) is an essential organelle in photosynthetic cells, playing a vital role in maintaining life. Plastome typically has a circular quadripartite structure composed of two almost identical copies of inverted repeat regions (IRa and IRb) separating large single-copy region (LSC) and small single-copy region (SSC). Compared with the nuclear and mitochondrial genomes, the plastome across seed plants are highly conserved in gene structure and composition. However, different rearrangements have been reported at the genome and gene levels of some angiosperm lineages. Fabaceae (legumes), the third largest angiosperm family, demonstrate extreme structural variations in the plastome. Inverted repeat lacking clade (IRLC) with 52 genera and over 4,000 species and nine tribes, is the largest legume lineage which the plastomes of most important genera of this clade (at least one species) have been sequenced to date. Thus, it is essential to investigate representatives from other taxa to better understand plastome evolution within the IRLC, and more broadly within legumes. In this context, the genus *Colutea* which is poorly studied, is a good candidate for sequencing the plastid genome and investigating plastome evolution in the IR-loss clade. Here we report the first complete chloroplast genome of *Colutea triphylla* Bunge ex Boiss. is sequenced using Illumina Hiseq 2000 platform. This species with shrubby/sub-shrubby habit, is endemic to Iran.The whole chloroplast genome is 123,929 bp in length and contains 110 genes, including 76 protein coding genes, 30 tRNA genes, and 4 rRNA genes. In addition, the *atp*F intron was absent. The overall GC content of the whole genome is 34.1%. Phylogenetic analysis based on protein sequences of 34 chloroplast genomes indicated that *C. triphylla* and *Sphaerophysa salsula* were closely related, which is congruent with previous studies. This study provides valuable information to the molecular phylogenetic and genetic diversity in future.

P.0851 Genomic insights into the drought adaptation of Caragana korshinskii (Fabaceae), a forage shrub widely planted in drylands

Shengdan Wu[1]

1 State Key Laboratory of Herbage Improvement and Grassland Agro-ecosystems, College of Ecology, Lanzhou University, Lanzhou, China.

The highly drought-tolerant Korshinsk peashrub (*Caragana korshinskii*) is commonly planted in arid and semi-arid regions to restore locally degenerated vegetations and serves as a forage shrub. To understand the genomic basis underlying its drought-tolerant adaptability, we produced a chromosomal-scale genome assembly and annotation for *C. korshinskii*. Our synteny analyses rejected the occurrence of a genus-specific whole-genome duplication (WGD) event that was proposed by the recent transcriptome analyses of this species and other congeners. Despite the lack of a WGD, more than 3,000 gene families expanded their copy numbers in *C. korshinskii*, among which numerous ones respond to drought stress and elevate their expressions. These genes increase their expressions during drought and are involved in abscisic acid biosynthesis, osmotic balance, reactive oxygen species scavenging, and cellular protection and damage repair. Additionally, we demonstrate that the overexpression of eight tandemly duplicated *dehydrin* genes greatly improves the survival rates of *C. korshinskii* seedlings under drought stress. Therefore, these tandem duplications likely contribute to drought-tolerance by increasing gene dosage. Together, our results provide new insights into how this legume shrub has obtained long-term drought adaptation in desert regions. Ultimately, the stress-responsive gene repertoire in *C. korshinskii* may serve as a potential genetic source for genetically breeding drought-tolerant crops.

S.093. LET PEOPLE COME TO BOTANY II: IMPROVING FLORA KNOWLEDGE THROUGH INATURALIST

P.0852 Introduction of citizen science using iNaturalist for teaching at higher education

José Blanco-Salas[1], Míriam Hernández-Del-Barco[2], Isaac Corbacho-Cuello[3], Jesús Sánchez-Martín[3]

1 Área de Botánica, Facultad de Ciencias, Universidad de Extremadura. Badajoz, Spain. 2 Departamento de Física y Matemáticas, Facultad de Educación, Universidad de Alcalá. Madrid, Spain. 3 Área de Didáctica de las Ciencias Experimentales, Facultad de Educación y Psicología, Universidad de Extremadura. Badajoz, Spain.

Botany has traditionally been seen by students as a boring and difficult subject, although it is crucial for understanding ecosystems and biology. Citizen science is a method used in science education to engage students with botany. The *Biomarathon of Spanish Flora* is a successful example of this. The aim of this work is to describe, analyse and offer a teaching strategy for teaching botany in higher education, emphasising the value of citizen science projects. The study was developed at the University of Extremadura (Spain) with 61 prospective teachers (80.3 % of the students enrolled). The sample was chosen intentionally among students in the fourth year of the Degree in Primary Education, enrolled in the subject of "Knowledge of the Natural Environment" who voluntarily decided to participate in the activity. This activity involves observing and recording information of different botanical using a mobile application (iNaturalist). The participants made a total of 1829 observations, of which 148 have so far reached "research grade", which means that they are scientific contributions with potential use for scientific purposes. Remarkably, one of the observations has already been confirmed as a chorological novelty for a Spanish province. The evaluation of the students by the teacher, which was carried out by means of a rubric, gave very positive results for this activity. The success achieved in evaluating and qualifying the students confirms that using iNaturalist in higher education, with prior training and a defined and clear objective, can serve to generate quality scientific data. This can also help to ensure that citizen science is given the value that it deserves. Of course, it is necessary to supervise and check the contributions of the participants. But the validation of these contributions will allow them to be considered for what they are: scientific data with real applicability.

P.0853 InvaPlant: citizen science for the detection of invasive alien flora in Spain

Adrián García Rodríguez[1], Sara Santamarina[1], Andrea Fernández Gómez[1], Jorge Miguel Isabel Rufo[1], Carmela Capistrós Bitrián[1], Marta Viu Cuerda[2], Noelia Vallejo Pedregal[2]

1 Department of Natural Environment, TRAGSATEC, Madrid, Spain. 2 Directorate-General of Biodiversity, Forests, and Desertification, Ministry for Ecological Transition and the Demographic Challenge, Madrid, Spain.

Invasive alien flora presents a threat to biodiversity. Citizen science is a valuable tool to raise awareness and engage society to confront this challenge. In line with this, the Ministry for Ecological Transition and the Demographic Challenge of Spain launched "InvaPlant" in 2023, a citizen science initiative for the detection and monitoring of invasive alien flora in the national territory. Target species, referred to as "invaplants," are flora taxa from the Spanish Catalog of Invasive Exotic Species (Royal Decree 630/2013) and those from the List of Invasive Alien Species of Union Concern (Commission Implementing Regulation (EU) 2016/1141) detected in Spain. Presence records are automatically collected through an iNaturalist collection project (https://www.inaturalist.org/projects/invaplant). Users may contribute by taking clear photographs of representative parts of specimens, facilitating identification, and capturing the surrounding environment to estimate abundance and improve knowledge of invasion-prone environments. Hundreds of members got involved with InvaPlant in its first year and over 2000 observers have contributed to the initiative. "Invaplanters" have revealed provincial and regional chorological novelties in Spain, highlighting their key role in early detection. Validated data from iNaturalist will contribute to meet Spain's conservation legal commitments. Increased social engagement has boosted the detection of invasive alien plants in Spain. If you wish to contribute to the search for "invaplants" join the iNaturalist project and encourage your colleagues to explore their environment interactively, promoting environmental awareness about this issue. You can find more information on our social media channels (@InvaPlant).

P.0854 In the head of Asteraceae: Citizen science data as a tool to study plant-arthropod interactions

Iván Pérez-Lorenzo[1,2], Luis Palazzesi[3], Neus Nualart[1], Jeanne de Montaigne de Poncins[1,4], Teresa Garnatje[1,5], Jaume Pellicer Moscardó[1,6], Oriane Hidalgo[1,6]

1 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 2 Laboratori de Botànica, Facultat de Farmàcia i Ciències de l'Alimentació, Universitat de Barcelona, Barcelona, Spain 3 Museo Argentino de Ciencias Naturales, CONICET, División Paleobotánica, Buenos Aires, Argentina 4 AGRAPOLE - ISARA LYON, Lyon, France. 5 Jardí Botànic Marimurtra - Fundació Carl Faust, Blanes, Spain. 6 Royal Botanic Gardens, Kew, Richmond, United Kingdom.

The growing use of citizen science platforms enables scientists to obtain large amounts of quality data, optimizing sampling efforts to cover increasingly larger spatial and temporal extensions. This research focuses on characterizing plant-arthropod interactions, and more specifically those that may impact reproductive success (e.g., pollination, pollen feeding), for one of the most diverse botanical families, the Asteraceae, through the use of iNaturalist. We took advantage of the fact that arthropod observations often show the animal on a plant, to screen those on Asteraceae species. Out of approximately 37,500 verified arthropod observations (insects and crab spiders) from our study area encompassing the Pyrenees and surrounding territories, 2305 records of Asteraceae-arthropod interactions were gathered. They span altitudes from 116 to 2903 m and a time range from 1982 to 2023. The objectives of this study were: (1) to assess the completeness of the sampling by using species accumulation curves, (2) to examine the diversity of capitulum visitors across different groups of Asteraceae using rarefaction-extrapolation estimates based on sampling coverage and effective number of taxa and (3) to analyze the interaction patterns through bipartite network properties. A list of 366 floral visitor species from 68 families is reported and grouped as "pollinators", "phytophagous", "insect predators", "complex relationship" and "apparently neutral interactors". 48 species of Asteraceae have been identified in these interactions, with the remaining observations identified at the genus or tribe level. The properties of the interaction network were compared to a null model to study the effect of randomness on the results obtained. Finally, iNaturalist data were compared with those obtained from our own field observations to discuss the usefulness, bias and limits of citizen science as a source of information for the study of plant-arthropod interactions.

S.095. MALVACEAE: PROGRESS & PROSPECTS IN EVOLUTIONARY RESEARCH IN THE COTTON & CACAO FAMILY

P.0855 Effect of organic fertilizer applications on yield and fiber quality in cotton (Gossypium hirsutum L.)

Suat Daskin[1], Sema Basbag[2]

1 Dicle University Institute of Science and Technology, Diyarbakir, Turkey. 2 Dicle University Faculty of Agriculture, Department of Field Crops, Diyarbakir, Turkey.

Failure to replace the decreasing plant nutrients in the soil with mineral and organic fertilizers leads to losses in soil fertility and consequently in the product. The use of environmentally friendly organic fertilizers that can be an alternative to the use of chemical fertilizers is of great importance for the realization of sustainable agriculture. This study, which was carried out to determine the effect of different doses of organic fertilizer (liquid seaweed) application on yield and fiber quality in cotton, was established in the 2018-2019 cotton growing season in Dicle University, Faculty of Agriculture, Field Crops Experimental areas according to the Split Plots Experimental Design in randomized blocks with 3 replications. In the study, varieties (BA440, BA119, Gloria) constituted the main plots and treatment doses (Control, 300ml, 200ml, 100ml) constituted the sub-plots. The treatments were carried out during the cotton combing period. The effects of organic fertilization on plant yield and fiber quality were examined. The effects of organic fertilizer doses on yield, fiber durability, ginning yield, first fruit branch internode height and boll number were found to be significant. In the study, the highest values of cotton mass yield were obtained from 300 ml/da dose application of BA119 variety with 493.69 kg/da; the highest ginning yield was obtained from 300 ml/da dose application of BA119 variety with 44.91%; the highest number of bolls was obtained from 300 ml/da dose application of BA119 variety with 14.4 pcs/plant; the most resistant fibers were obtained from 100 ml/da dose application of Gloria variety with 36.3 g/tex.

P.0856 Phylogeny of the Pachira sensu lato clade (Bombacoideae, Malvaceae) with new infrageneric classification based on DNA sequences

Vania N. Yoshikawa[1], Júlia S. Siqueira[1], William S. Alverson[2], Alexandre W. S. Hilsdorf[1], Letícia R. Morais[1], Flávia F. Pezzini[3], Marília C. Duarte[1,*]

*1 University of Mogi das Cruzes, Mogi das Cruzes, Brazil. 2 University of Wisconsin, Madison, USA. 3 Royal Botanic Garden Edinburgh, Edinburg, UK, *mariliacd@umc.br.*

The *Pachira* s.l. clade (Bombacoideae, Malvaceae) comprises ca. 73 species and includes the genera *Eriotheca* and *Pachira*. *Pachira* is the richest genus within the subfamily Bombacoideae, with ca. 45 species mainly in the Neotropical region. *Eriotheca* contains ca. 26 species, most of them occurring in Brazil, predominantly in Atlantic Rainforest and Cerrado biogeographic regions. In previous phylogenetic analyses, *Pachira* emerged as paraphyletic, in two distinct lineages: an Amazonian *Pachira* clade, and its sister clade comprising *Eriotheca* and Extra-Amazonian *Pachira*. However, those results were based on a sample of less than 50% of all species in *Pachira* s.l. clade. This study explores relationships within the *Pachira* s.l. clade, specifically testing the monophyly of the genera *Eriotheca* and *Pachira*, and investigates the biogeographic history of the clade. In this current study, we sampled ca. 70% of the species diversity in the clade and used nuclear and chloroplast molecular markers to infer new phylogenetic hypothesis under Maximum Likelihood and Bayesian frameworks. We inferred ancestral morphological states and areas/biogeographic regions. Our analysis indicates that neither *Eriotheca* nor *Pachira* is monophyletic. However, the subgenera described by Robyns (1963) are monophyletic as are the clades of *Pachira* proposed by Carvalho-Sobrinho (2016). The ancestral areas reconstruction showed that the expansion of Dry Diagonal may have been a catalyst that drove the evolution of clades within *Pachira* s.l. Our analysis of morphological traits also supported the monophyly of seven subgenera. The "Amazonian *Pachira* clade" has two-colored free part of stamens as synapomorphy; the "Extra-Amazonian *Pachira* clade" is characterized by green petals; *Pachira calophylla* constitutes a monospecific subgenus, by its longest petiolule among *Pachira*; and all subgenera and species of *Eriotheca* are now combined under *Pachira*, which now has ca. 73 species.

P.0857 An overview of digital collection of preserved specimens of the Sida cuneifolia complex (Malvaceae, Malvoideae) from Paleotropics

Rafaela P. Camargo[1*], Flávia F. Pezzini[2], Vania N. Yoshikawa[3], Marília C. Duarte[1]

*1 University of Mogi das Cruzes, Mogi das Cruzes, São Paulo, Brazil. 2 Royal Botanic Garden Edinburgh, Scotland, Edinburgh, UK. 3 University of São Paulo, São Paulo, Brazil. *rafaela-camargo12@hotmail.com*

Sida is one of the largest and most complex genus in Malvaceae with about 200 species divided into 11 sections, including section *Malachroideae,* with 23 species distributed in Brazil, Africa, India and Sri Lanka. *Sida cuneifolia* Roxb., included in the sect. *Malachroideae*, was described in Flora Indica as a small, irregular, shrubby species with wedge-shaped leaves. Because of its similarity to the African species *Sida schimperiana* A. Rich., they were treated as the same taxon, until Vollesen in 1986 described the *Sida cuneifolia*-complex with six species, including *S. schimperiana*, and *S. cuneifolia* as endemic to India. There has been no revision of this group since then, and there seems to be no consensus on treating *S. cuneifolia* and *S. schimperiana* as separate species, as some databases consider them the same. Therefore, we created a dataset of occurrence records of herborized species of the *S. cuneifolia* complex using global digital repositories. We curated 129 records of six species and verified their identifications. The most abundant species was *S. tenuicarpa* (56 records), followed by *S. schimperiana* (47), *S. massaica* (8), *S. tanaesis* (6), *S. shinyangensis* (6), and *S. cuneifolia* (6). Except for *S. cuneifolia,* which is restricted to India, the other species occur in Kenya, Tanzania, Ethiopia, Congo, Rwanda, Somalia, and Uganda. *Sida massaica* is found only in Kenya and *S. shinyangensis* in Tanzania. Almost all the material was collected in the 20th century as part of local flora, the most recent being in 2001, therefore, mostly lack coordinate information. Thus, further update in current records of African flora in global repositories is needed, and to encourage more studies on endemic species. Our study contributes to a better understanding of the paleotropical flora and can be used to advance taxonomic, ecological, phylogenomic and evolutionary studies in *Sida.*

P.0858 Floral merosity variation, taxonomy, and evolution of the Neotropical genus Mollia Mart. (Malvaceae, Grewioideae)

Maria Tereza R. Costa[1], Massimo G. Bovini[1], Elsie Franklin Guimarães[1], Javier Fuertes Aguilar[2]

1 Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Real Jardín Botánico - CSIC, Madrid, Spain.

Mollia Mart. is an almost exclusively Amazonian genus with 17 species described. The genus belongs to the subfamily Grewioideae of Malvaceae, and is characterised by rudimentary stipules, simple leaves, androecium divided in two distinct whorls, capsule bilocular with loculicidal dehiscence, and seeds distributed in two rows. The genus lacks a recent taxonomic revision, so we have revised its taxonomy using molecular phylogenetic and morphological analyses of individuals from natural populations and herbarium specimens. We concluded that the current number of species that deserves recognition is 19. From a morphological perspective, the species of the genus can be grouped into two main groups: one with leaves completely serrate, globular capsules, and seeds winged; and other with leaves with margin entire to serrate at the apex, sulcate capsules winged or not, and seeds non-winged. In our phylogenetic study, plastid and ribosomal genes suggest the presence of two main lineages, although not completely congruent with those previously defined by morphological characters. The most striking finding was the detection of some populations in a large extent of occurrence about 1752 km², in the north of Manaus (Brazil), by individuals which consistently presented flowers with a reduction in the number of pieces of the calyx, corolla and outer androecium whorl from 5 to 3. The number of pieces by whorl tends to be a constant trait within genera of Malvaceae. Although there some cases of within-species variation in corolla and/or calyx between 4-6, there are a few cases among members of Grewioideae of a shift in the number of pieces from pentamerous to trimerous whorls (e.g. *Entelea arborescens*). This taxon has been recently recognized as a new species, *M. trimera*.

P.0859 Occurrence of Waltheria glabribracteata (Malvaceae) in Colombia: first record and description of brevistylous flowers

Miguel A. F. Jimenez[1], Arthur Macedo[2], Thales S. Coutinho[3]

1 Nacional University of Colombia, Bogotá, Colombia. 2 Botanic Garden of the University of Coimbra, Universidade de Coimbra, Coimbra, Portugal. 3 Federal University of Mato Grosso, Cuiabá, Brazil.

Waltheria L. is a genus of the Malvaceae family with approximately 60 species, mainly distributed in the Neotropical region. It is characterized by its heterostylous flowers, penicillate stigma and 1-carpelar ovary. In Brazil, novelties have been published in the last years, as *Waltheria glabribracteata* T.S. Coutinho & M. Alves. This species was described recently only with longistylous flowers, occurring only in limited areas from Brazil and Bolivia. During the floristic search of *Waltheria* in Colombia carried out by the first author, a distinct species was recorded, and based on morphological analysis and specific literature this taxon was determined as *W. glabribracteata*, especially by its glabrous bracts and bracteoles, unique character in the genus. This record represents the first occurrence of this species to Colombia. The morphologic description was based on samples housed in COL, COAH and FMB herbaria, and the conservation status was accessed with geographic data from its total distribution (Brazil, Bolivia, and Colombia). In Colombia, *W. glabribracteata* occurs in rocky outcrops, habiting transition areas between Savanna and Amazonian Forest, similarly in Brazil and Bolivia (type areas). When described, *W. glabribracteata* had rounded blade leaves, however, in Colombia different morphotypes were presented, with ovate to lanceolate blade leaves, but with glabrous bracts and bracteoles persistent. Besides, the first description to brevistylous flowers is presented, being similar to longistylous flowers but with staminal tube longer than gynoecium and free filaments. *Waltheria glabribracteata* is now accessed as Least Concern according to IUCN criteria, due to its Extent of Occurrence of 290,000,000 km². This record highlighted the importance of botanical collection in taxonomic or floristic searches, with novelties to local flora and providing new data about distribution, morphological variation, and conservation.

P.0860 Comparative proximate and chemical analysis of two species of Corchorus olitorius (Malvaceae)

Joy Ifunanya Odimegwu[1], Olalekan Yusuf[1], Akinyemi, Dorcas Obabi [1], Fagbemide, Opemipo Mary[1], Okonkwo Uchenna[1], Coker, Herbert[2]

1 Department of Pharmacognosy, Faculty of Pharmacy, University of Lagos, Nigeria. 2 Department of Pharmaceutical Chemistry, Faculty of Pharmacy, University of Lagos, Nigeria.

Corchorus olitorius is a staple vegetable in the sub-Saharian African region. It is consumed for nutrition and also has varied medicinal properties. There are scientific reports of its blood-boosting and antihypertensive effects. Numerous chemical analyses of the leaves showed significant amounts of folates, iron and proteins. In Western Nigeria, it was observed that two morphologically different plants bear the same common names and are even identified as the same at a University Herbarium. One of the plants has distinct serrated leaf (SL) edges and the other has smooth leaf (ML) edges. This study aims to compare the chemical constituents of the two plants using phytochemical assays, proximate mineral analysis, vitamin contents assays and Gas Chromatography-Mass Spectrometry to ascertain their Chemotaxonomy and if possible differentiate the two plants concretely. Also, the results of the chemical analysis will confirm the lore of the plant's blood-boosting and hypertension-modulating properties. Preliminary chemical analysis showed that SL and ML both do not have cadmium and only ML has lead. They both had varying amounts of Arsenic, Copper, Zinc, Manganese and Cromium. SL had 0.201 ppm, 1,311 ppm, 1.093 ppm, 2.045 ppm and

1.461 ppm while ML had, 0.503 ppm, 0.813 ppm, 1.107 pm, 3.001 ppm and 1.342 ppm, respectively. These findings suggest differences in the chemical components of both plants and it is necessary to verify which of the two is the original *Corchorus olitorius*.

P.0861 Unraveling Okra's adaptive strategies: insights from SWEET17 expression in response to dehydration stress

Hagar T. Elhefnawi[1], Diaa Abd el-Moneim[2], Mahmoud Magdy[1,3]

1 Department of Genetics, Faculty of Agriculture, Ain Shams University, Cairo, Egypt. 2 Department of Plant Production (Genetic Branch), Faculty of Environmental Agricultural Sciences, Arish University, El-Arish, Egypt. 3 Department of Plant Biology, Faculty of Biology, Murcia University, Murcia, Spain.

Okra (*Abelmoschus esculentus*), a member of the Malvaceae family, renowned for its culinary and nutritional value, possesses inherent resilience to dehydration stress, making it a valuable crop in regions prone to water scarcity. In our study, we investigate the molecular mechanisms underlying okra's natural tolerance to dehydration stress, focusing on the regulated patterns of gene expression. Utilizing RNA sequencing (RNAseq) technology revealed a significant upregulation of SWEET17 in response to dehydration, indicating its pivotal role in mediating water stress tolerance in okra plants. A member of the SWEET family (Sugars Will Eventually be Exported Transporters), a group of transporters responsible for the efflux of sugars across cellular membranes in plants. They play crucial roles in various physiological processes, including phloem loading, nectar secretion, seed filling, and stress responses. To validate the involvement of SWEET17 in the dehydration response, ongoing experiments employ CRISPR technology and overexpression transformation. These endeavors aim to conclusively establish SWEET17's function in okra's adaptive response to water scarcity, providing valuable insights into the genetic basis of stress tolerance in this resilient crop. The discovery of SWEET17's upregulation in dehydrated okra plants not only enriches our understanding of plant adaptation mechanisms but also holds promise for enhancing crop resilience against environmental challenges, such as drought. By unraveling the role of SWEET genes in stress tolerance, researchers can pave the way for targeted breeding strategies to develop drought-tolerant okra varieties, thus ensuring food security in water-limited regions. Moreover, these findings extend beyond okra, potentially influencing research in related crops within the Malvaceae family, such as cotton and cacao. Understanding the genetic underpinnings of stress tolerance in okra can inform comparative genomics studies across diverse plant species, facilitating the identification of conserved pathways and candidate genes for enhancing resilience in agriculturally important crops.

P.0862 A review of digitized herbarium collections of the genus Spirotheca Ulbr. (Malvaceae, Bombacoideae)

Vania N. Yoshikawa[1]*, Flávia F. Pezzini[2], Matheus Colli-Silva[3], William S. Alverson[4], Marília C. Duarte[5], José R. Pirani[1]

*1 University of São Paulo, São Paulo, Brazil. 2 Royal Botanic Garden Edinburgh, Scotland, Edinburgh, UK. 3 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 4 University of Wisconsin-Madison, Madison, USA. 5 Universidade de Mogi das Cruzes, Mogi das Cruzes, São Paulo, Brazil. *vania_nobuko@hotmail.com.*

Spirotheca Ulbr. (Malvaceae, Bombacoideae) is a neotropical genus with six species found in Andean rainforests, Central America, and Brazil. Unique in the family by its hemiepiphytic habit and spirally arranged anthers (each with two superposed pairs of thecae), the most recent revision was in 2006. In view of this nearly two-decade informational gap, we constructed a dataset of occurrence records from preserved specimens stored as of 2023, relying on global biodiversity repositories. We reviewed taxonomic determinations and georeferencing procedures to yield maximum spatial accuracy. Downloads of 1,147 records allowed us to review, curate, and clean the data, guided by literature and author expertise. The most recorded species include *S. rosea* (582 records), followed by *S. rivieri* (262), *S. awadendron* (52), *S. elegans* (20), *S. michaeli* (9), and *S. mahecae* (2). Most specimens (713) were collected in the 20th century, funded by US and European projects that facilitated South American fieldwork. Since the 21st century, local support prevailed for new collections (305 specimens), with Brazil leading (281), likely due to the *Flora of Brasil* project. We found that

76 specimens are identified only to genus, 52 are identified with basionyms, and 117 with synonyms. Conservation assessments categorize *S. mahecae* as Critically Endangered, *S. rosea* as Least Concern, with other species unevaluated. Regarding to geographic precision, 559 records (48.7%) have coordinates and 15 (1.3%) have zero coordinates. Our study underscores the significance of enhancing South American research for a deeper understanding of Neotropical flora. This collaboration holds potential for advancing taxonomic, ecological, phylogenomic, and evolutionary studies in *Spirotheca*.

S.096. MECHANICAL FORCES IN PLANT GROWTH AND DEVELOPMENT

P.0863 The effect of mechanical stress on the anatomy and morphology of Urtica dioica L.

Urszula Zajączkowska[1], Dominika Dmitruk[2], Alicja Dołkin-Lewko[1], Barbara Łotocka[2]

1 Department of Forest Botany, Warsaw University of Life Sciences, Warsaw, Poland. 2 Department of Botany, Warsaw University of Life Sciences, Warsaw, Poland.

Anatomical, morphological, and gene expression changes in *Urtica dioica* plants subjected to mechanical stress were examined. The mechanical impact was simulated using a specially designed device in which a sheet of paper was attached to a 40 cm long rotating link. The paper was constantly moving and making gentle contact with the surface of the plants. The overall anatomical composition of the touched plants was similar to that of the control plants. There was a noticeable variation in the shape of the internode cross-section. The stress-treated plants initially had a four-ribbed structure. However, as the internodes advanced, their shape gradually changed into a rectangular configuration. The epidermis of the control plants was decorated with different types of trichomes, including simple setulose, glandular, and stinging trichomes. However, the touched plants lacked stinging trichomes and the callose accumulated more heavily on the setulose trichomes. Cell wall lignification was observed at an earlier stage in stress-treated plants than in the older internodes of control plants. According to genetic analysis, UdTCH1 expression was significantly upregulated in contacted plants compared to control plants, suggesting that the UdTCH1 gene is involved in the mechanical stress response of plants. In contrast, the UdERF4 and UdTCH4 genes showed down-regulation of expression under stress conditions. According to our findings, mechanical stress induces a variety of anatomical, molecular, and morphological changes in nettle plants. However, additional interdisciplinary research is needed to understand better the functional effects and mechanisms underlying these changes.

P.0864 Investigating the presence of calcium oxalate crystals in the Magnoliales order

S. Aristidou[1], R.H.J. Erkens[1,2], G. Perversi[1]

1 Maastricht Science Programme, Faculty of Science and Engineering, Maastricht University, Maastricht, The Netherlands. 2 System Earth Science, Faculty of Science and Engineering, Maastricht University, Venlo, The Netherlands.

Calcium Oxalate (CaOx) is a crystalline biomineral found in various plants. It occurs in five distinct morphologies, which are hypothesised to be regulated by genetic processes. CaOx presence is recognised in magnoliid species but little is known about their phylogenetic distribution. Here we studied CaOx morphologies within Magnoliaceae and Annonaceae to find out more on this. To extract the crystals, 5 dried and 37 freshly collected magnoliid species were subject to a heavy liquid solution protocol which utilised the densities of Caesium Chloride and Calcium Chloride, to collect the crystals. Extracted crystals were identified by bright field microscopy. This extraction process was further conducted on Magnoliaceae leaves of varying ages and a branch from the same tree, to assess potential differences in crystal morphologies with leaf aging, and whether the presence of crystals in the leaves differed to those in the branches. Results revealed the pres-

ence of CaOx crystals in all sampled species. In general, there is no significant difference in a crystal morphology between any two clades of the magnoliid, possibly due to the small sample sizes that were used in each category. As leaves aged, the abundance of CaOx crystals increased accompanied by the development of additional distinct crystal morphologies. Furthermore, crystal morphologies differed between leaves and branches, suggesting tissue-specific influences on crystal growth. We did not reconstruct a clear phylogenetic pattern, when using the latest magnoliid phylogenetic tree. So far there is, therefore, no evidence that CaOx crystals can reliably serve as markers for determining a plant's phylogenetic position.

P.0865 Needles in the angiosperm haystack- where do calcium oxalate raphides hide?

N.S. Lawrie[1], N. Medrano Cuetos[1], F. Sini[1], G.A. Salam[1], H. Ding[1], A. Vancolen[1], J.M. Nelson[1], R.H.J. Erkens[1,2], G. Perversi[1]

1 Maastricht Science Programme, Faculty of Science and Engineering, Maastricht University, Maastricht, The Netherlands. 2 System Earth Science, Faculty of Science and Engineering, Maastricht University, Venlo, The Netherlands.

Calcium oxalate (CaOx) crystals are biominerals present in a wide variety of plants. Formation of these crystals is a biomineralization process occurring in vacuoles within specialized cells called crystal idioblasts. This process is dependent on two key components: deprotonated oxalic acid, and calcium ions ($Ca2+$), and can result in multiple crystal morphologies. Raphides are needle-like CaOx crystals found in various plant organs and tissues. Though their function is highly debated, they can potentially store calcium, sequester heavy metals, protect against herbivory and possibly programmed cell death. The last review of the taxonomic and anatomical distribution of raphides across the plant kingdom dates back to 1980, in a review by Franceschi and Horner, prompting an updated systematic review of raphides in plants. We conduct a broad literature search to record plant taxa and tissue locations containing raphides. We provide an overview of raphide-forming plant taxa, discussing phylogenetic distribution of raphides at the order level, and report on the specific locations of raphides within plants. Our review reveals raphide occurrence has been studied in 33 orders, 76 families and 1305 species, with raphides presence confirmed in 24 orders, 46 families and 797 species. These taxa represented less than 1 % of known species per family. Leaves are the most prominent raphide-containing primary location in all three major angiosperm clades investigated: Eudicots, Magnoliids, and Monocots. Roots are least reported to contain raphides. The collation of such information lays the groundwork to unveil the genetic origin and evolution of raphides in plants, and highlights targets for future studies of the presence and role of plant raphides.

P.0866 Lace plant: a novel model system to study programmed cell death in plants

Arunika Gunawardena[1]

1 Department of Biology, Faculty of Science, Dalhousie University, Halifax, NS, Canada.

Programmed cell death (PCD) plays a significant role in plant development and defense. One fascinating example of developmentally regulated PCD is perforation formation in the leaves of an aquatic lace plant (Aponogeton madagascariensis) in the family Aponogetonaceae. The formation of complex leaf shape through PCD is a rare event across vascular plants and occurs only in a few species of Monstera and in the lace plant. The evolutionary significance of leaf perforations remains unknown, although several hypotheses have been proposed. During early development, the lace plant leaf forms a pattern of equidistantly positioned perforations across its surface, giving it a lattice-like appearance. Lace plant leaves emerge from the corm in a heteroblastic series. The first 3–4 leaves that emerge are called juvenile leaves and do not produce perforations as they mature. Early-stage adult leaves are tightly furled and red due to anthocyanins and show no visible signs of cell death. As the leaves unfurl, PCD is initiated in the center of areoles, located between the longitudinal and transverse veins. The first visible sign of PCD is the disappearance of anthocyanins at the center of each areole, which then develops outwards and stops 4-5 cell layers from the veins. These peripheral cells that do not undergo PCD are named NPCD (non-PCD) cells. Many unanswered questions remain. Why does cell death always start at the center of areoles? Why does cell death stop from 4-5 cells from the veins? Why do cells display substantially different responses to PCD signals? At the mature stage of leaf development, perforation formation is complete, cells no longer undergo PCD, and mesophyll cells at the perforation border transdifferentiate as epidermal cells. The lace plant's suitability as a novel model to study PCD in plants will be discussed, covering plant morphology, evolutionary and molecular biology, and biophysics.

P.0867 Iridescence in Hibiscus: understanding the mechanics of nanoridge formation

Bhavani Natarajan[1], Beverley J. Glover[1]

1 University of Cambridge, Cambridge, UK.

Iridescence is a form of structural colour found in various organisms. In *Hibiscus trionum*, iridescence is produced due to interference of light by nanoridges present on the petal epidermal cells. Nanoridges are formed by buckling of the cuticle, and mechanics plays an important role in this. A mathematical model from previous work in the lab had identified five parameters crucial for nanoridge formation, namely cuticle thickness, cuticle stiffness, extracellular matrix stiffness, cell elongation, and turgor-induced deformation. In this work, we aim to experimentally test this model. We plan to modify nanoridges – and thereby iridescence – by producing transgenic *H. trionum* plants defective in cuticle biosynthesis, as well as by treating buds with hormones and drugs. To check if iridescence has any role in pollinator attraction, we will conduct experiments with bumblebees and assess their preference for wild type and transgenic lines. Overall, these approaches would be the first to test the mechanical model of nanoridge formation in any organism.

P.0868 Force-triggered floral rapid movement via a mechanosensitive channel

Xuan Zhou[1], Tetsuya Higashiyama[2], Shihao Su[1]

1 School of Agriculture, Sun Yat-sen University, Shenzhen, China. 2 Department of Biological Sciences, The University of Tokyo, Tokyo, Japan.

Plants have evolved various approaches and mechanisms to move. Rapid movement of floral stigmas triggered by mechanical force has been documented since Darwin. Those stigmas often consist of multiple lobes, which are sensitive to touch and can close rapidly within seconds. Previous studies explored the adaptive significance of stigma movement; however, the genetic nature of sensitive stigmas remains mysterious. Here, we investigate *Torenia fournieri* that possesses typical sensitive stigmas. We monitored the cytosolic calcium ($[Ca^{2+}]_{cyt}$) dynamics using a Ca^{2+}sensor. Mechanostimulation that deforms the stigma lobe leads to a rapid increase of $[Ca^{2+}]_{cyt}$ on the touched lobe followed by movement, which can be blocked by Ca^{2+} channel inhibitors. To characterize potential genes involved in mechanosensation, we further performed RNA-Seq and identified a candidate gene, *JUE1*, which encodes a mechanosensitive ion channel specifically expressed in stigma parenchyma cells. Stigma of*jue1*mutantsshows no response to force whereas can be triggered by wound or electrical shock, suggesting the function of JUE1 as a mechanical sensor. We finally demonstrate that JUE1 is required for force-triggered $[Ca^{2+}]_{cyt}$ signature. To conclude, we report a molecular genetic basis for force-triggered organ rapid movement via a mechanosensitive channel in plants.

S.097. MECHANISMS AND CONSEQUENCES OF DISPERSAL IN LAND PLANTS: TOWARDS A MORE UNIVERSAL UNDERSTANDING

P.0869 PAICE, an innovative tool to estimate inter-island colonization events accounting for sampling bias

Alberto J. Coello[1, 2], Mario Fernández-Mazuecos[2, 3], Ruben H. Heleno[4], Pablo Vargas[5]

1 National Museum of Natural History, Smithsonian Institution, Washington, D.C., USA. 2 Universidad Autónoma de Madrid, Madrid, Spain. 3 Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Madrid, Spain. 4 University of Coimbra, Coimbra, Portugal. 5 Real Jardín Botánico (CSIC), Madrid, Spain.

Colonization is a central topic in ecology and one of the cornerstones of island biogeography. However, it is difficult to evaluate how successful an organism is in colonizing across oceanic archipelagos. Scholars have traditionally assumed that plant species without dispersal syndromes are not successful colonizers, but recent studies using floristics and genetic data have revealed more complex patterns. One source of uncertainty is the estimation of colonization events without considering appropriate sample sizes, namely: a significant number of samples for both individuals/populations and DNA regions sequenced. Specifically, an increase in the number of individuals and DNA sequences studied increases the number of detected colonization events, hindering comparisons among studies and organisms. With PAICE (Phylogeographic Analysis of Island Colonization Events), we propose a new tool to estimate the number of colonization events across islands of the same archipelago accounting for these sampling bias. PAICE is developed in R and available as a package in CRAN (https://cran.r-project.org/package=PAICE). To estimate the number of inter-island colonization events, PAICE uses rarefaction curves for both genetic and field sample sizes. The first analyses with PAICE resulted in sample-unbiased estimations that allow the comparison among organisms. This tool will be useful for future analyses comparing island colonization success among a great variety of organisms (e.g., analysis for the whole flora of an archipelago) and it will be fundamental to test classical hypothesis, including consideration of sampling bias (e.g., are plant species with long-distance dispersal syndromes more successful colonizers?).

P.0870 When the going gets tough, the tough get going: Factors that drive the distribution of North American Ephedra species

Petra Führding-Potschkat[1], Stefanie Ickert-Bond[2]

1 Frontier Botany, University of Alaska Fairbanks, Yukon Drive, Fairbanks, USA. 2 University of Alaska Fairbanks, Fairbanks, USA.

The genus *Ephedra* are mainly dioecious, profusely branched shrubs with photosynthetic stems distributed in arid biomes, differing primarily in the nature of the strobilus bracts, which have been documented to be associated with different dispersal syndromes. The strobilus bracts in Asia, Europe, North Africa, and South America are either fleshy and red (rarely white or orange) or dry and papery-winged. Only in North America (southwestern USA and Mexico), an intermediate coriaceous dry bract type evolved in addition to the previous two. Thirteen species occur mainly across the North American Deserts, Great Plains and Southern Semi-arid Highlands, temperate forests and sierras, and Mediterranean California. We aim to understand which factors differentiate the ranges of North American *Ephedra* species. We hypothesize that precipitation, temperature, the resulting water availability to the plant, and the particular strobilus type play an important role. We used 562 expert records of twelve species as calibration data and 6,602 GBIF records as test data. The habitats were analyzed using 19 bioclimatic variables (CHELSA), plant-available water, and strobilus type. We used GLM and MaxEnt to predict the species' spatial distribution drivers. The study showed a low impact of the annual mean temperature (bio1) on eight *Ephedra* species and a moderate effect on two species (R^2: 0.51 to 0.75). Also, the annual precipitation (bio12) moderately impacted all species with a fleshy strobilus (R^2: 0.53 to 0.59), and the precipitation of the driest month (bio14) showed a moderate impact on *E. californica* (R^2: 0.64). Data uncertainties like false-positive localities in the GBIF data may have contributed to the low to moderate R^2s. We suggest identifying the false positives, fine-tuning the climate variables, and testing further factors, e.g., soil types, influencing the distribution of North American *Ephedra*.

P.0871 Zoochoric trees, anemochoric vines, and autochoric herbs and shrubs: a Caatinga pattern that persists in different substrates

Grênivel M. Costa[1], Ligia S. Funch[2], Abel A. Conceição[2]

1 Universidade Federal do Recôncavo da Bahia, Cruz das Almas, Brazil. 2 Universidade Estadual de Feira de Santana, Feira de Santana, Bahia, Brazil.

The timing and the mode of plant dispersal in arid and semiarid regions are particularly influenced by environmental factors, highlighting a general anemochory predominance. Our study evaluated the proportion of vascular plant species per habit and seed dispersal syndromes in two physiognomies of caatinga (Seasonally Dry Tropical Forests in the crystalline basement and Woodlands in the sedimentary basin), in Tucano, Bahia State, Brazilian northeastern. We determined the dispersal syndromes and the plant habits of all species collected in each physiognomy. We sampled 201 species in the crystalline basement, while in the sedimentary basin were sampled 172 species. In the crystalline basement, autochory predominated among shrubs (54%) and herbs (59%), zoochory among trees (49%), and anemochory among vines (45%). In the sedimentary basin, autochory prevailed among shrubs (48%) and herbs (57%), anemochory and autochory among vines (40%), and zoochory among trees (69%). The contrasting substrates, but similar patterns among habit and dispersal modes (zoochoric trees, anemochoric vines, and autochoric herbs and shrubs) may be related to niche partitioning between the herbaceous and arboreal components, mainly related to water availability and different micro-environmental conditions. In the caatinga, herbs and sub-shrubs are typically annuals, so the fruit development and the seed release are fast, creating a seed bank from many autochoric fruits. On the other hand, the trees are perennial and in general have deep roots for water acquisition, so they have time and resources to produce zoochoric fruits. Climbing vines are found mainly at edges or ascending into the canopy, with anemochoric fruits exposed to wind. Despite having different floristic compositions and structures depending on the substrate, the predominance of the same dispersal modes by habit in different substrates reinforces the important role of water availability, morphological features, and vegetation stratification on fruit and seed dispersal in the caatinga.

P.0872 'Out-of-Australasia' again? An investigation into the distinctive biogeography of Libertia and Orthrosanthus (Iridaceae)

Sophie C. Newmarch[1], Richard C. Winkworth[1], Dan J. Blanchon[3], Joanne L. Birch[4], Nicolás García[5], Jennifer A. Tate[1,2].

1 School of Natural Sciences, Massey University, Palmerston North, New Zealand. 2 MPN Herbarium, Massey University, Palmerston North, New Zealand. 3 Auckland War Memorial Museum, Auckland, New Zealand. 4 MEL Herbarium & Faculty of Science, University of Melbourne, Melbourne, Australia. 5 Herbario EIF & Facultad de Ciencias Forestales y de la Conservación de la Naturaleza, Universidad de Chile, Santiago, Chile.

Taxa with disjunct distributions have long fascinated biologists and have provided important insights into biological evolution, particularly patterns of dispersal. Based on molecular phylogenies, it has been suggested that the Iridaceae came 'out-of-Australasia' despite the majority of the family's diversity occurring in the Americas. Less well understood is the biogeography of *Libertia* and *Orthrosanthus*, two understudied genera that are the only members of Iridaceae (~70 genera) disjunct between Australasia and the Americas. Both groups occur naturally in Australia and South America; *Libertia* is also found in New Zealand and New Guinea with *Orthrosanthus* also occurring in Central America. Previous studies have suggested that *Libertia* and *Orthrosanthus* are sister within the tribe Sisyrinchieae, which likely arose in South America ~21.6 million years ago. Because these studies included just one species from each genus, their historical biogeography remained uncertain. We present biogeographical analyses based on whole plastome and Angiosperms353 nuclear phylogenies with comprehensive species-level sampling of *Libertia* and *Orthrosanthus*. We investigated maximum likelihood and Bayesian approaches, broadening the sampling in some analyses to account for the biogeographic context and the notoriously poor fossil record of the Iridaceae. The results provide novel insights into the biogeography of *Libertia* and *Orthrosanthus*, aligning with patterns seen for other plant groups in the southern hemisphere and extending our understanding of the biogeography of Iridaceae. Going forward, these findings will also serve as a foundation for studies into polyploidy and floral evolution in these two genera.

P.0873 The biogeography of fruit colour in the Iberian Peninsula

María Sánchez-Gracia[1], Francisco Rodríguez-Sánchez[2]

1 Universidad Pablo de Olavide, Sevilla, Spain 2 Universidad de Sevilla, Sevilla, Spain.

The ecological and evolutionary drivers behind fleshy fruit types and characteristics have attracted extensive research, mainly in the context of disperser agents and adaptative hypotheses. Many studies have analysed fruit characteristics (morphology, chemistry, colour, scent, etc.) in relation to frugivores; abiotic variables have perhaps received less attention. In this study we investigate the geographical distribution of fruit colour across the Iberian Peninsula in relation to several climatic variables that can affect fruit development and colour. After compiling an exhaustive list of 206 native plant species producing fleshy diaspores across the Iberian Peninsula and Balearic Islands, we examined the role of winter temperatures, growing season length, and accumulated heat sum along the year on the prevalence of the two most common fruit colour categories: black/dark and red/pink/orange. We found that black fruits are more abundant in regions with warm winters and mild summers, while red fruits are associated with northern, cooler regions with shorter growing seasons. We also found strong phylogenetic inertia in the probability of producing black fruits; for red fruits, phylogenetic inertia was considerably weaker. Our results are congruent with other studies performed at global, macroecological scales that have also established a relationship between fruit colour and different climatic variables – but do so by contributing with information at a smaller scale and high resolution. Our work reinforces the idea that factors influencing fruit characteristics are not restricted to their disperser environment but can also include environmental abiotic factors, phylogenetic constraints and evolutionary history.

S.098. MECHANISMS UNDERLYING PLANT DIVERSITY PATTERNS IN THE EAST ASIAN–AUSTRALASIAN REGION

P.0874 Tree species composition of two kerangas forest in southern part of Sarawak, Malaysia

Nur Safinas Binti Jelani[1], Meekiong Kalu[2], Yahud Bin Wat[1], Yazid Bin Kalbi[1], Halipah Binti Bujang[1], Mohizah Binti Mohamad[1], Noorhana Binti Mohd Sapawi[1], Stafannie Nilla Anak Marshall Rio[1], Dami Anak Jude[1], Michiko Nakagawa[3]

1 Research and Development Division, Forest Department Sarawak, Sarawak, Malaysia. 2 Faculty of Resource Science and Technology, University Malaysia Sarawak, Sarawak, Malaysia. 3 Graduate School of Bio-Agricultural Sciences, Nagoya University, Aichi, Japan.

Heath forest, also known as kerangas, is one of the forest types in Borneo and is described as having very poor, acidic soils that are typically podsolic and composed of course, white sand covering, to different depths, a thick, hard, severely acidic pan. The diversity of tree species in Sarawak's heath forest is a subject of ongoing research; however, comparisons between the sites are rarely made. This study evaluates the tree species in two heath forests in southern Sarawak, namely, Samunsam Wildlife Sanctuary (SWS), and Kelingkang Forest Reserve (KFR). A 1-hectare plot with 100 10 m × 10 m quadrats was established. The total basal area of both sites, which consisted of 1,251 trees with a diameter of at least 10 cm, was calculated to be 26.78 m^2ha^{-1} for SWS and 14.08 m^2ha^{-1} for KFR, respectively. With a mean diameter for trees at both sites of about 18.00 cm, Dipterocarpaceae predominated as the highest group. In the kerangas forest, KFR and SWS shared species such as *Whiteodendron moultonianum* and *Hopea kerangasensis*. Endemic species like *Dryobalanops fusca* and *Vatica adenanii* were identified during this plot assessment. Despite the poor soil qualities, it is crucial to conserve the kerangas themselves; hence, more species need to be studied.

P.0875 Characterization of a flower of fossil genus Sahnianthus by micro-CT and placement in Lythraceae

Chandana Karumanchi[1], Ashley Hamersma[2], Steven Manchester[2]

1 Department of Microbiology and Cell Sciences, University of Florida, Gainesville, USA. 2 Florida Museum of Natural History, University of Florida, Gainesville, USA.

The Deccan intertrappean beds of India are a series of sedimentary layers deposited between volcanic events from the Late Cretaceous (Maastrichtian) to Paleocene (Danian) as the Indian subcontinent drifted northward over a mantle plume or hotspot in the present-day location of Réunion Island. The intertrappean cherts of the locality produce abundant morphologically and anatomically preserved fossil woods, as well as plant reproductive material including fruits, seeds, and flowers. Paleobotanical study of this locality is important in order to provide high-resolution insight into the rapid climatic and biotic change brought on by repeated and extensive volcanism. Extensive research has been carried out spanning several decades (1940s-2010s) on the fossils of the Deccan plateau. The fossil genus *Sahnianthus* has been recorded from the Deccan intertrappean beds and is represented in the University of Florida collections. It has been hypothesized to belong to the family Lythraceae, and this project seeks to use new techniques to confirm that placement. Prior research has been focused primarily on characterizing the fossil flowers through thin-section and light microscopy, techniques that while standard may exclude some information that we seek to recover through microcomputed tomography scanning (micro-CT). Specimens for this study have been studied with micro-CT and reconstructed digitally to further characterize their morphology, and existing thin sections have been studied with light microscopy to characterize anatomy. In addition, scanning electron microscopy (SEM) has been used to visualize pollen grains from fossils. This study contributes to the understanding of overall paleoclimatic and paleogeographic change in the area, and confirms the affinity of reproductive material to the family Lythraceae, expanding the known fossil record and geography of the family.

P.0876 The macrofossil flora investigation and the research progress in Taiwan

Y.-P. Lo[1], J.-M. Hu[1,2] *

*1 Institute of Ecology and Evolutionary Biology, National Taiwan University, Taipei city, Taiwan. 2 NTU Herbarium (TAI), National Taiwan University, Taipei city, Taiwan *jmhu@ntu.edu.tw*

Taiwan is located in the East Asia island arcs, neighboring China, Japan and the Philippines, and the unique natural history of Taiwan was shaped by its mixture of temperate and tropical elements from the surrounding regions. The highest peak in Taiwan reaches nearly 4000 m, thus providing extremely diverse habitats that house more than 4000 vascular plants with 26% of endemic species. Many relic lineages of plants survived in Taiwan after they migrated from the Himalayas and Japan, even though the geological age of the island formed only a few million years ago. The research of paleontology in Taiwan began in the 19th century. Most of the investigations so far are focused on animal fossils, and plant fossils research is mainly concentrated on microfossils, like spores and pollens, which are from lake sediments. Plant macrofossils from Taiwan were scarce because of common fragmentation and difficulty in identification. We made thorough literature reviews and a few field expeditions to excavate more plant macrofossil specimens, particularly from the Miocene (Tertiary) and Pleistocene (Quaternary) in Taiwan. There are less than 20 reports of plant macrofossils and most of them were published after 1960. Only a few reports contain more completed specimens and information (all specimens are from the Miocene formation) are as follows: the Miocene fossil vegetation in northern Taiwan published in 1968, the leaves and cone fossil records of *Metasequoia occidentalis* (Cupressaceae) published in 1972, the petrified wood of *Taxodioxylon sequoianum* (Cupressaceae) published in 1999, the petrified woods of *Bischofia* (Phyllanthaceae) and *Camellia* (Theaceae) published in 2003, and the petrified wood of *Podocarpoxylon nageioides* (Podocarpaceae) published in 2021. As more macrofossils of plants are discovered, we hope to use these data, along with the microfossils, to reconstruct the paleovegetation and paleoenvironment in Taiwan.

S.099. METAL HYPERACCUMULATORS: NEW ADVANCES ON A BOTANICAL CURIOSITY

P.0877 Features of thallium tolerance and accumulation in metallicolous and non-metallicolous accessions of Silene latifolia

Ilaria Colzi[1], Gaia Regini[1], Isabella Bettarini[1], Beatrice Chiavacci[1], Marco Dainelli[1], Federico Selvi[2], Antony van der Ent[3], Cristina Gonnelli[1]

1 Department of Biology, University of Florence, Florence, Italy. 2 Department of Agriculture, Food, Environment and Forest Sciences, University of Florence, Florence, Italy. 3 Laboratory of Genetics, Wageningen University and Research, Wageningen, The Netherlands.

Thallium (Tl) is one of the most toxic elements on Earth and has recently been attracting more and more attention because it is considered both an emerging pollutant and a valuable element for the ecological transition. The possibility to exploit natural technologies for the remediation of polluted soils (phytoextraction) and even the recovery of Tl from the plant biomass would be, therefore, desirable. The species *Silene latifolia* has recently been indicated as a potential Tl-hyperaccumulator, and therefore as a plant suitable for phytoextraction purposes. Since a complete characterization of the Tl-tolerance strategies of this species has never been carried out, the aim of this work was to compare the tolerance and accumulation capacity of metallicolous plants from a Tl-rich mine dump (Saint-Laurent-le-Minier, France) and non-metallicolous plants from a non-contaminated area (Barraux, France). Seeds from both sites were sown in peat soil and seedlings were exposed to a range of $TlNO_3$ concentrations (0-60 μM) in hydroponic culture for seven days. At the end of the treatment, different growth (e.g. leaf area, root length increment) and physiological (e.g. chlorophyll a fluorescence and pigment content indices) parameters were analysed as indicators of plant Tl-tolerance. Plants from the metallicolous site had an exceptional higher growth ability when exposed to Tl compared to non-metallicolous ones, which showed a significantly lower EC50 parameter (2.5 ± 0.3 vs 22.5 ± 0.8 μM of metallicolous plants). The reduced growth of non-metallicolous plants was partly explained by the significant negative effect of Tl on photosynthetic parameters and pigment content. Our results show that *S. latifolia* metallicolous plants have evolved Tl tolerance and ongoing analysis of Tl accumulation in roots and shoots will reveal whether such tolerance is linked to the metal hyperaccumulation. Moreover, further accessions from Italian Tl-rich mine dump are now under study to widen the comparison.

P.0878 Effects of elevation on growth, photosynthetic and Ni-accumulation responses in Bornmuellera emarginata (Brassicaeae)

Ilaria Colzi[1], Nadia Bazihizina[1], Isabella Bettarini[1], Federico Selvi[2], Cristina Gonnelli[1]

1 Department of Biology, University of Florence, Florence, Italy. 2 Department of Agriculture, Food, Environment and Forest Sciences, University of Florence, Florence, Italy.

Bornmuellera emarginata is a Balkan Ni-hyperaccumulator indicated as a promising candidate for agromining practices. Here, two elevation-contrasting accessions (250 m, Low Elevation plants LE, and at 1600 m, High Elevation plants, HE) were compared in terms of growth, photosynthetic activity, and Ni accumulation in controlled conditions to assess possible differences exploitable in practical applications. After two months of pot cultivation on garden and serpentine soil, plant biomass, gas exchanges and Ni concentrations were evaluated. Plants grown on serpentine soil showed reduced biomass as compared to those from garden soil, without any difference between LE and HE. In both accessions, growth in serpentine soil resulted in photochemical/biochemical limitations and reduction in stomatal conductance, especially in LE. HE showed low stomatal conductance in all the conditions, despite a greater stomatal density. Shoot Ni accumulation was higher in HE (~1600 µg Ni g^{-1} d.w. and 1200 µg Ni g^{-1} d.w. in HE and LE respectively), thus resulting in a significantly higher metal content per plant in respect to LE (~120 and ~85 µg $plant^{-1}$ in HE and LE respectively). Furthermore, a hydroponic trial with increasing $NiSO_4$ concentration was performed to evaluate Ni tolerance and accumulation. In this case, HE possessed higher Ni tolerance and accumulation in respect to LE. In conclusion, underlying the higher shoot metal amount of HE, Ni tolerance seemed to play a pivotal role, overtaking possible negative effects of reduced transpiration rates compared to LE. Our results point to the opportunity of exploring and exploiting the variation in accumulation level among *B. emarginata* accessions for the implementation of environmental restoration and metal cropping practices.

P.0879 Assessment of morphology and heavy metals (lead and copper) in selected mangrove species in Malaguit river, Camarines Norte

Andrea L. Gamboa[1], AJ Lexee O. Gonzales[1], Jannah Czerlin A. Palomar[1], Ana Dominique M. Quibot[1], Alyssa Marie A. Lola[2,3]

1 Department of Biological Sciences, Far Eastern University, Sampaloc, Manila, Philippines. 2 Graduate School of Science, Tokyo Metropolitan University, Tokyo, Japan. 3 Plant Sciences Laboratory, University of Santo Tomas, Philippines.

Mangroves are commonly found in the coastal barangays of Camarines Norte. However, limited data about the assessment of heavy metals on the different mangrove species from this locality have been published. Certain mangroves can accumulate heavy metals in their environment that can induce physiological changes in plants. This study aims to assess the presence of lead (Pb) and copper (Cu) in mangrove species and their environment in Malaguit River, Camarines Norte, and assess their morphological characteristics. Pneumatophores (root above ground), roots below the ground, and leaves were subjected to wet digestion before undergoing the Flame Atomic Absorption Spectroscopy (FAAS) to determine their heavy metal concentration. The mangrove species found in the Malaguit River were determined as *Rhizophora stylosa*, *Ceriops tagal*, *Aegiceras corniculatum*, and *Bruguiera sexangula*. Among all the samples, Pb was predominantly observed in leaves and Cu was concentrated in the roots below. In a comparative analysis, the *B. sexangula* accumulated more Pb, whereas *C. tagal* accumulated more Cu. The overall observation of the mangrove species present in the study site tends to accumulate higher concentrations of Pb than Cu. Bioconcentration factor (BCF) values resulted in all samples' low ability to accumulate Pb and Cu from their external environment. *R. stylosa* and *C. tagal* also displayed the ability to translocate Pb from their roots to leaves based on their translocation factor (TF) values. This is the first study on heavy metal analysis of mangroves from Camarines Norte. It showed the potential environmental risk to the mangroves due to their inability to hyperaccumulate such heavy metals. Therefore, regulatory and restoration activities are necessary to protect these species from contaminated urban and industrial areas.

P.0880 Allchar unveiled: two-year comprehensive exploration of rare arsenic and thallium hyperaccumulation in North Macedonia's unique metalliferous site

Tomica Mišljenović[1], Ksenija Jakovljević[1*], Katerina Bačeva Andonovska[2], Guillaume Echevarria[3], Mirko Salinitro[4], Antony van der Ent[4]

1 University of Belgrade – Faculty of Biology, Belgrade, Serbia. 2 Research Center for Environment and Materials, Macedonian Academy of Sciences and Arts, Skopje, Macedonia. 3 Econick SAS, Lunéville, France. 4 Wageningen University and Research, Wageningen, The Netherlands.

The abandoned Allchar mine (North Macedonia) is a globally unique deposit with the highest known contents of thallium and arsenic mineralisation. During the two-year extensive study, plant and soil samples were collected, followed by elemental composition analyses. Our analyses confirmed the hyperaccumulation of Tl in three *Viola* taxa endemic to Allchar, with the highest concentration found in *V. arsenica* (58,900 mg kg^{-1}). In *V. allchariensis* and *V. tricolor* subsp. *macedonica*, these concentrations exceeded the hyperaccumulation threshold, with maximum concentrations of 23,100 and 11,800 mg kg^{-1}, respectively. Very variable concentrations were found for As, with the highest concentrations in *V. tricolor* subsp. *macedonica* (408 mg kg^{-1}) and *V. arsenica* (381 mg kg^{-1}), but below the hyperaccumulation threshold. Synchrotron µXRF analysis confirmed that Tl in all three *Viola* taxa is endogenous and not the result of surficial contamination with fine substrate particles. Hyperaccumulation of Tl was also detected in *Plantago lanceolata*, *Hesperis matronalis*, *Clinopodium alpinum*, *Dianthus carthusianorum*, *Thymus thracicus* var. *alsarensis* as well as in *Silene latifolia* with an extremely high Tl concentration (79,200 mg kg^{-1}). Concentrations of As above the hyperaccumulation threshold were found in *Silene vulgaris*, *Alyssum kavadarcensis* and *Myosotis nemorosa*. An extremely rare simultaneous hyperaccumulation of Tl and As was found in *M. verna*. For the first time, the novel Z-spec technology was applied to analyse a large number of plant and soil samples, which significantly reduced costs and processing time. The identified As and Tl hyperaccumulators could be used in the reclamation of former mining sites in the Allchar area and these rare phenomena should be further investigated, including dosing trials.

P.0882 Can the members of the coffee family accumulate heavy metals? - Hyperaccumulation on Philippine Rubiaceae spp.

Alyssa Marie Lola[1,2,3], Cecilia Moran[3,4], Noriaki Murakami[1,2]

1 Graduate School of Science, Tokyo Metropolitan University, Tokyo, Japan. 2 Makino Herbarium, Tokyo Metropolitan University, Tokyo, Japan. 3 Plant Sciences Laboratory, University of Santo Tomas, Manila, Philippines. 4 Department of Biological Sciences, Manila, Philippines.

The Philippines is one of the most megadiverse countries in the world and consists of many ultramafic areas. Ultramafic is a term used to describe igneous or metamorphic rocks with high concentrations of heavy metals. Ultramafic regions promote the differential selection of species and the evolution of hyperaccumulators. Hyperaccumulators are a group of plants with the rare ability to extract certain metals and metalloids and accumulate them in normally toxic shoot tissue concentrations without any evidence of physiological stress. In the Philippines, many Rubiaceae spp. were observed thriving in extreme ultramafic conditions such as mining sites, suggesting the possibility of heavy metals accumulation. The study aims to determine the heavy metals concentrations and to evaluate the evolution of heavy metals using the Bioconcentration Factor (BCF) of the collected plant samples. The specimens were obtained from selected Philippine ultramafic islands. Energy-dispersive X-ray (EDX) and X-ray fluorescence (XRF) analysis were used for the hyperaccumulation analysis. The notable detected elements were Iron (Fe), Copper (Cu), Strontium (Sr), Manganese (Mn), Nickel (Ni), Chromium (Cr), Silicon (Si), Aluminum (Al), Molybdenum (Mo), and Tin (Sn). There were also some traces of Titanium (Ti) and Vanadium (V) in some of the samples. Interestingly, based on their concentrations, several of them exceeded the threshold limits for heavy metals set by Reeves et al. 2018. To evaluate the content of heavy metals, BCF was also calculated from all the samples. Results showed that many of the Rubiaceae spp. accumulate the mentioned heavy metals significantly such as *Ixora, Timonius,* and *Wendlandia* spp. This study showed that the members of the coffee family are sources of heavy metals accumulation which can be of greater importance in the development of so-called 'green technologies' such as phytoextraction, phytostabilisation, and phytomining.

P.0883 Herbarium to field journey in the discovery of a novel zinc hyperaccumulator - Cardamine waldsteinii

Tomica Mišljenović[1*], Ksenija Jakovljević[1], Guillaume Echevarria[2], Alan Baker[2,3,4], Sandro Bogdanović[5], Gordana Tomović[1], Antony van der Ent[6]

*1 University of Belgrade – Faculty of Biology, Belgrade, Serbia. 2 Econick SAS, Lunéville, France. 3 Université de Lorraine, Nancy, France. 4 The University of Melbourne, Parkville, Australia. 5 University of Zagreb – Faculty of Agronomy, Zagreb, Croatia. 6 Wageningen University and Research, Wageningen, The Netherlands *tomica.m@bio.bg.ac.rs.*

Hyperaccumulation of Zn is an extremely rare plant phenomenon with to date, less than 30 known examples. The discovery of new hyperaccumulators could be a difficult and time-consuming task, but a novel, non-invasive method of elemental analysis of herbarium samples using portable XRF devices has proven extremely useful, and has contributed to the discovery of a number of new hyperaccumulators of various elements. Systematic XRF scanning of Brassicaceae collections in two herbaria in Belgrade, Serbia (BEOU and BEO) revealed unusually high concentrations of Zn in the specimens of *Cardamine waldsteinii*. The highest Zn concentration exceeding the notional hyperaccumulation threshold was detected in a specimen from Bosnia and Herzegovina near Tuzla (3050 mg kg^{-1}), with high Zn concentrations also detected in several specimens from Mt Jelova Gora in W Serbia. Subsequently, fresh material was collected from non-metalliferous soil on Mt Jelova Gora and 2210 mg kg^{-1} Zn was detected in the leaf dry matter by atomic absorption spectroscopy. Additionally, XRF scanning of *C. waldsteinii* specimens from the Paris herbarium (P) revealed one sample with 4000 mg kg^{-1} Zn from Croatia. Following these results, further fresh material was collected from three non-metalliferous locations in Croatia. The dried leaves of these plants analyzed by Z-spec spectroscopy showed the highest Zn concentration of 7000 mg kg^{-1}, with an average of 3100 mg kg^{-1}. These results obtained confirm *Cardamine waldsteinii* as a new Zn hyperaccumulator. Further studies with dosing experiments will provide additional insights into the Zn tolerance of different populations and contribute to a better understanding of the mechanisms of Zn hyperaccumulation. This study shows that XRF screening of herbarium collections can provide rapid and valuable data which will lead to the discovery of new hyperaccumulators that would probably remain hidden without extensive chemical analyses.

P.0884 Biomonitoring of heavy metals with Evernia prunastri (L.) Ach. in situ and transplants in the environment of a recycling company

Rubén Pérez González[1], Ana Belén Fernández Salegui[1]

1 Biodiversity and Environmental Management Department, Universidad de León, León, Spain.

The concentration of six heavy metals (Al, Cr, Cu, Fe, Pb y Zn) was analysed using the lichen *Evernia prunastri* (L.) Ach. as bioaccumulation in order to evaluate the environment quality in the surroundings of a recycled industry located in León, Spain. The methodology was based on two techniques: the use of the lichen in situ and the placement and subsequent collection of transplants after four months. Sampling was systematically divided into eight transects according to the cardinal points, being the industry the central point. Pollution maps and cluster and correlation analysis were made in order to evaluate element's dispersion and identified common sources, respectively. The results showed that the closest sampling points to the industry accumulated the higher concentration, decreasing with distance, with the elements pattern deposition in the direction of the prevailing winds. In situ samples showed higher concentrations than transplant ones. Among elements, Cu was significantly higher around the industrial zone, followed by Zn; while the other ones showed normal concentration. Elements with similar behaviour and common sources were detected. This study highlights the presence of anthropogenic atmospheric pollution, with the recycled industry as the main source which can be a risk to the nearby population if there is prolonged exposure.

P.0885 Screening of wild plants colonizing Sb mine tailings for the selection of suitable phytoextractors

Gaia Regini[1], Ilaria Colzi[1], Isabella Bettarini[1], Maria Beatrice Castellani[1], Elisabetta Bianchi[1], Pierluigi Cortis[2], Antonio De Agostini[2], Donatella Fibbi[3], Alexandra Antal[3], Gabriele Petracchi[3], Marco Dainelli[1], Cristina Gonnelli[1]

1 Department of Biology, University of Florence, Florence, Italy. 2 Department of Life and Environmental Sciences, University of Cagliari, Cagliari, Italy. 3 GIDA, Prato, Italy.

Metallophytes are plants surprisingly well adapted to metalliferous soils, due to the selective pressure that these unfavourable substrates exert. Based on different metal tolerance strategies, these plants can be mainly divided in "excluders", that limit metal uptake and/or its translocation to the shoot, and "accumulators/hyperaccumulators", able to accumulate metals in their shoots at extraordinarily high concentrations. Moreover, "indicator" plants accumulate metal concentrations that reflect the metal content in the environment. The features of metallophytes make of these plants an optimal choice for environmental technologies for soil remediation purposes, such as phytoextraction. The aim of this work was to investigate spontaneous plants colonizing mine wastes and to identify suitable accumulating species for antimony (Sb) phytoextraction of sewage sludge. Antimony is commonly used in various industrial activities, causing wastewaters and sewage sludge contamination, as observed at the wastewater treatment plant (WWTP) of Prato, managed by GIDA SpA. Although the sewage sludges are regularly disposed by incineration, phytoextraction may provide an alternative low-cost remediation approach. To this aim, Su Suergiu mine (Villasalto, Sardinia) was selected based on Sb contamination of the mine tailings. There, different spontaneous plant species and a representative substrate sample were collected and analyzed by ICP for determination of Sb concentrations. The analyses allowed to discover the "excluder" or "accumulator" behavior of each collected plant. Almost all the species showed to be Sb excluders, except for *Dittrichia viscosa*, whose Sb concentration in shoots suggested that it may be an indicator species. Therefore, further investigations in hydroponic culture are in progress to effectively test the Sb tolerance and accumulation capacity of *D. viscosa*. This preliminary kind of investigations are fundamental for selecting the most suitable species for Sb phytoextraction. In the next step, *D. viscosa* will be tested by cultivating it directly in the sewage sludges from GIDA WWTP.

P.0886 Integrated transcriptome and metabolome analysis reveals the mechanism of tolerance to manganese and cadmium toxicity in the Mn/Cd

Guo Yu[1], Habib Ullah[2], Asfandyar Shahab[1]

1 College of Environmental Science and Engineering, Guilin University of Technology, Guilin, China.
2 Department of Environmental Science, Zhejiang University, Hangzhou, Zhejiang, China.

Understanding the molecular mechanism of tolerance to heavy metals in hyperaccumulators is important for improving the efficiency of phytoremediation and is interesting for evolutionary studies on plant adaption to abiotic stress. Celosia argentea Linn. was recently discovered to hyperaccumulate both manganese (Mn) and cadmium (Cd). However, the molecular mechanisms underlying Mn and Cd detoxification in C. argentea are poorly understood. Laboratory studies were conducted using C. argentea seedlings exposed to 360 μM Mn and 8.9 μM Cd hydroponic solutions. Plant leaves were analyzed using transcriptional and metabolomic techniques. A total of 3960 differentially expressed genes (DEGs) in plants were identified under Cd stress, among which 17were associated with metal transport, and 10 belonged to the ATP transporter families. Exposures to Mn or Cd led to the differential expression of three metal transport genes (HMA3, ABCC15, and ATPase 4). In addition, 33 and 77 differentially expressed metabolites (DEMs) were identified under Mn and Cd stresses, respectively. Metabolic pathway analysis showed that the ABC transporter pathway was the most affected in Mn/Cd exposed seedlings. Conjoint transcriptome and metabolome analysis showed that the glutathione (GSH) metabolic pathway was over-represented in the KEGG pathway of both DEGs and DEMs. Our results confirm that the ABC transporter and GSH metabolic pathways play important roles in Mn and Cd detoxification. These findings provide new insight into the molecular mechanisms of tolerance to Mn and Cd toxicity in plants.

S.100. METHODS IN INTEGRATIVE TAXONOMY: BRIDGING THE PHYLOGENY TO CLASSIFICATION GAP

P.0887 Inga: Unfolding the chocoensis clade and the issue of cryptic diversity

Bocanegra-González K.T.[1]

1 The University of Edinburgh, Edinburgh, UK. 2 Royal Botanic Garden Edinburgh, Edinburgh, UK. 3 Research Group on Biodiversity and Dynamics of Tropical Ecosystems -University of Tolima, Ibagué, Colombia.

Crypticism refers to the presence of species that are morphologically similar or indistinguishable, but genetically different, or vice versa. Although common in highly radiated groups, it had not been evidenced in the tropical tree genus *Inga*, although there were some hints in the species *Inga chocoensis* Killip ex T.S. Elias, which shows subtle but considerable differences throughout its distribution. Even in the past, a separate species *Inga coprocarpa* N. Zamora & Poveda was proposed. In this study, 50 individuals classified as *I. chocoensis* were morphologically evaluated, and next-generation molecular analyses were conducted using target capture technique with 1320 loci, with which a phylogeny was subsequently constructed. Morphologically, characteristics that separate three species were distinguished, but these features are subtle and unless the identifier is an expert, they are imperceptible. On the other hand, phylogenetic analysis delimited 4 species within the clade, which include the 3 species delimited morphologically. In this way, the species *I. chocoensis*, *I. coprocarpa*, described in the past were delimited, and the new species *I. calimaensis* and *I. crassanectaria* were delimited and described. The results demonstrate the presence of crypticism in the genus Inga, especially in the so-called *chocoensis* clade, and highlight the importance of combining morphological and molecular approaches for accurate identification. Especially because underestimating real diversity leads to a lack of adequate species protection and limits their conservation and management.

P.0888 Anthoceros fusiformis Austin (Anthocerotophyta) in Japan consists of two undescribed species

Taichi Ikematsu[1], Masaki Shimamura[1]

1 Graduate School of Integrated Sciences for Life, Hiroshima University, Higashi-Hiroshima, Japan.

Anthoceros fusiformis, a species of hornwort, has a disjunct distribution from the West Coast of North America to northern parts of Japan. In Japan, this species has been distinguished from the other species of *Anthoceros* by the following characteristics: 1) the strap-shaped thalli with deeply dissected lobes, 2) lacking gemmae, 3) the sporophytes growing over 1 cm, 4) smooth stripes-like regions without protuberances along either side of the spore trilete mark. In the course of our study for a taxonomic revision of *Anthoceros* in Japan, it became clear that the plants previously thought to be *A. fusiformis* were distinguished into two undescribed species. DNA sequence data for a phylogenetic analysis were newly obtained from three plastid loci (*rbcL*, *trnL–matK*, and *rps4*) from specimens of *Anthoceros* species collected throughout Japan. Regarding the plants treated as *A. fusiformis* in Japan, the analysis strongly supported that they were divided into two clades that excluded the accession of authentic *A. fusiformis*. The one clade consisted of plants growing in mountainous areas, such as near streams, and the other clade consisted of plants growing in anthropic habitats, such as parks or abandoned agricultural fields. The mountain plants were nested in the clade of subg. *Sphaerosporoceros* and sister to *A. caucasicus* Steph. The anthropic plants were nested in the subg. *Indici*. Consequently, *A. fusiformis* should be excluded from the flora of Japan and two *sp. nov.* should be added. Each of the two newly recognized species and *A. fusiformis* can be easily distinguished by the ornamentations on their spores. The proximal facets of spores of the mountain plants have spines that coalesce to be cristate, those of the anthropic plants were covered with round papillae, and those of *A. fusiformis* were vermiculate and papillate.

P.0889 Unmasking the diversity of genus Ulota (Orthotrichaceae, Bryophyta) in Australasia

Nikolay Matanov[1], Isabel Draper[2,3], Juan A. Calleja[2,3], Francisco Lara[2,3] , Ricardo Garilleti[1]

1 Universidad de Valencia, Valencia, Spain. 2 Departamento de Biología, Universidad Autónoma de Madrid, Madrid, Spain. 3 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain.

Orthotrichoideae is a complex group of mosses, both taxonomically and biogeographically, which plays an important role in epiphytic communities in temperate regions and high tropical mountains worldwide. Four genera notably contribute to the subfamily's diversity: *Orthotrichum*, *Zygodon*, *Lewinskya* and *Ulota.* The current diversity of *Ulota* s.l. (including *Atlantichella*, *Rehubryum* and *Plenogemma*) encompasses 70 taxa mostly found in temperate and temperate-cold regions. In the southern hemisphere, the genus *Ulota* has two major centers of diversity with endemism rates of 100%: Patagonia (predominantly Chile) and Australasia (New Zealand and SE Australia). In the latter, 13 taxa have been reported. Indeed, although there have been several taxonomic revisions conducted on this group on these areas, its true diversity remains not fully understood. New taxa have been recently discovered, emphasizing the challenging nature of its understanding. The morphological complexity and high taxonomic diversity within *Ulota* and its close relatives make this group one of the most taxonomically intriguing. An integrative taxonomy approach is being employed. This approach combines morphological, ecological, and molecular analyses to ascertain the true biodiversity of the genus *Ulota* and its relationships with the ulotoid genera (morphologically cryptic genera). Additionally, we also aim to understand the genetic diversity, biogeographic patterns, and the adaptive and evolutionary history that have led to the current diversity in the southern hemisphere. The aim of this poster is to unveil the cryptic diversity of this group in Australasia through integrative taxonomy, taking into consideration morphology, ecology, and biogeography, along with phylogenetic reconstructions.

P.0890 The tribe Solandreae (Solanaceae) in Mesoamerica

Andrés Orejuela[1], Sandra Knapp[2]

1 Department of biology, University of Cartagena, Cartagena, Colombia. 2 Natural History Museum, London, UK.

The Solandreae tribe, part of the Solanaceae family, comprises approximately 80 species, mainly epiphytic or hemi-epiphytic lianas and shrubs. These species, currently undergoing taxonomic revision, are native to the Neotropics, ranging from Mexico and the Caribbean to Bolivia and southern Brazil. A significant portion, about 60%, is found in the Andean regions of Ecuador and Colombia. Distinct within the Solanaceae, Solandreae is notable for its diversity in floral forms, pollinators, and unique ant associations. In the Solanaceae, epiphytes, which include about 90 species across three tribes, are dominated by Solandreae, accounting for 90% of these species. Morphologically, Solandreae exhibits substantial variation in corolla features such as shape, size, and colour, ranging from large infundibuliform or campanulate to small campanulate forms in colours from pale or dull to bright. This suggests a complex coevolution with various pollinators including bats, hummingbirds, and bees, highlighting its ecological significance. This study presents a taxonomic revision of the Solandreae tribe as part of the ongoing revisionary studies for the Solanaceae within the Flora Mesoamericana project. This project is a pioneering effort in creating a large-scale regional flora written in Spanish. In Mesoamerica, Solandreae is represented by 3-5 genera, depending on the generic circumscriptions, and approximately 15 species, including a few taxonomic novelties and nomenclatural adjustments. This revision offers a comprehensive overview of Solandreae in Mesoamerica, featuring a distribution map, an identification key for all genera and species, live photographs, and preliminary conservation assessments.

P.0892 Old methods learn new tricks: applying traditional microscopy methods to lichens for the first time

Eva Troner[1]

1 Freie Universitaet Berlin, Berlin, Germany.

Lichens are chimeric organisms typically consisting of at least one fungal and one algal partner. However, only few studies are focused on how they interact with each other, and most were done in the last century. Here, we combined traditional microscopy and staining methods to compare four lichens with distinct morphology and ascertain the chemical nature of the lichen symbioses and interactions. Additionally, the specimens were examined for the presence of penetrative haustoria to confirm or deny the hypothesis that haustoria formation is mycobiont-driven, i.e., mycobiont relationships predict the presence / absence of haustoria.

P.0893 Diversification of the genus Eriosyce (Cactaceae) in relation to morphological disparification and climatic niche

Heidy M. Villalobos-Barrantes[1,2,3], Beatriz M. Meriño[1,4], Helmut E. Walter[6], Aron Cádiz-Véliz[1,4,5], Jorge Avaria[7], Pablo Guerrero[1,4,5]

1 Departamento de Botánica, Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción, Concepción, Chile. 2 Escuela de Química, Universidad de Costa Rica, San José, Costa Rica. 3 Centro de Investigación en Biología Celular y Molecular, Universidad de Costa Rica, San José, Costa Rica. 4 Institute of Ecology and Biodiversity, Concepción, Chile. 5 Millennium Institute Biodiversity of Antarctic and Sub-Antarctic Ecosystems, Concepción, Chile. 6 The EXSIS Project: Cactaceae ex-situ & in-situ Conservation, Emmerthal, Germany. 7 University of Reading, Reading, UK.

One of the most widely distributed biomes on the planet is the arid and semi-arid zones. Chile, with its particular geography and the set of orographic, paleoclimatic, and geomorphological processes, has a flora with high levels of biodiversity and endemism. Studying the processes involved in the origin of biodiversity can be a laborious task in groups with similar and often convergent morphologies such as the genus Eriosyce (Cactaceae). Few studies integrate the ecological and diversification mechanisms of arid zones, as well as the evolution of morphological characters and the niche that explains the diversity observed in plants adapted to this biome. Our study focused on: i) species delimitation using molecular data from the globose cactus "*E. curvispina*" with which we made Bayesian phylogenetic inferences on 87 individuals of Eriosyce, including nine populations of *E. curvispina*, and analyzing three plastidial non-coding introns, one plastidial gene and one nuclear gene. ii) relationship between morphological traits with environmental variables using the phylogenetic comparative method, to evaluate the evolution of traits such as length, volume, root type, and stem type of cacti of the genus Eriosyce and whether temperature and precipitation affect their evolution. iii) diversification was evaluated in terms of climatic and morphological niche. The results are: i) we developed 12 nuclear microsatellite pairs to evaluate the genetic structure. ii) we identified four groups that originated in independent cladogenetic events occurring at different temporal depths. iii) we observed that temperature has an impact on the length and volume of the cacti, and precipitation on the shape and type of stem, and iv) that these traits have evolved giving an adaptive advantage to these plants to colonize new places and survive over time and diversify.

P.0893bis DNA barcoding of the genus Parmelina (Parmeliaceae, Ascomycota)

Ruth Del-Prado[1], Zahira Rebollo[1], Guillermo Amo de Paz[1], David Pizarro[1], Pradeep K. Divakar[1]

1 Department of Pharmacology, Pharmacognosy and Botany, Faculty of Pharmacy, Universidad Complutense de Madrid, Madrid, Spain.

The species delimitation in lichen-forming fungi is currently in flux. A growing body of evidence based on the use of molecular data has demonstrated that the morphology-based species circumscription underestimate diversity in lichenized fungi, hiding distinct phylogenetic lineages under a single species name. In some species complexes, re-examination of characters has revealed previously overlooked morphological or chemical characters that support the recognition of these species-level lineages. However, there are also cases of cryptic species in which no characters could be identified to distinguish distinct lineages. In Parmeliaceae, the largest family of lichen-forming fungi, species boundaries have been intensively studied. As a result, species complexes and cryptic species have been reported from different genera. Additionally, the use of genetic distances using short, standardized gene regions (DNA barcodes) has provided complementary support for species identification, especially useful for detecting overlooked taxa in species complexes and cryptic species. In this regard, a threshold between intraspecific and interspecific genetic distances (barcode gap) was established in parmeliod lichens (Parmeliaceae) for internal transcribed spacer (ITS) sequences. The genus Parmelina, belonging to the parmelioid lichens, is an example that includes several species that remain taxonomically controversial. Previous studies have revealed the presence of species complexes and cryptic species within P. coleae - P. carphorrhizans, P. tiliacea - P. pastillifera, and P. carporrhizans - P. atricha. In this study, ITS sequences generated from specimens collected from Europe and North America have been analyzed applying molecular phylogeny and estimation of genetic distances approaches to explore species boundaries and cryptic lineages in the above mentioned complexes. Using a fast and accurate method we aimto identify candidate species within problematic groups and confirm the efficiency of the ITS region forthe identification of species in Parmelina. Complementarily we provide a DNA barcode reference library with well-identified specimens.

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S.101. MORPHOLOGICAL, ANATOMICAL, AND EVOLUTIONARY BASIS OF HABIT TRANSITIONS IN PLANTS

P.0894 Systematic wood micro-anatomical evaluation of Diospyros species in Southwestern Nigeria

Akinwumi J. Akinloye[1], Opeyemi P. Akinsulire[1], Chukwuma H. Illoh[1]

1 Department of Botany, Obafemi Aolowo University, Ile-Ife, Nigeria.

Wood micro-anatomy of 14 species of *Diospyros* in Southwestern Nigeria were investigated while diagnostic features of the genus identified. Transverse, tangential longitudinal as well as radial longitudinal sections of each matured *Diospyros* wood were obtained using Reichert sliding microtome and at 10 µm thickness. The woods were also macerated with Schulz's fluid. The cut sections and the macerates were stained with Phyto-dyes while the micro-anatomical differences in the tissue arrangements, shape, as well as cell inclusions were noted for delimitation purposes. The results showed that all the 14 *Diospyros* species studied had essentially similar generic micro-anatomical features. However, such wood micro-anatomical characteristics as tyloses, crystal types, fibre lengths and percentage of solitary vessels distinguished the taxa studied. Tylose was absent in *Diospyros. monbuttensis, D. nigerica* and *D. physocalicina,* separating the three taxa. However, the presence of crystal druses in *D. physocalycina,* and in *D. suaveolens,* druses and styloid in *D. tricolor* and crystal druses, styloid and prismatic crystal in *D. undabunda* is classificatory for the four taxa. Fibre length was significant (p= 0.478) in separating *D. iturensis* and *D. piscatoria* from the other taxa with the former having the longest fibre length while the latter had the shortest. It was concluded that wood micro-anatomical features are important parameters of characterization and classification and can be used in the identification of the studied taxa.

P.0895 Leaf anatomy of genus Glyphochloa

Maria A.A.R. Fonseca[1]

1 Department of Botany, St. Joseph Vaz College, Cortalim, Goa- India.

The genus *Glyphochloa* W.D.Clayton of the subtribe Rottboelliinae, tribe Andropogoneae and sub family Panicoideae (Watson & Dallwitz, 1994), is restricted to Peninsular India. All the species of this genus were earlier recognized under *Manisuris* L.Clayton (1981) reduced this to a single species and transferred others to the genus *Glyphochloa* W.D.Clayton. This paper brings out the anatomical studies of the genus *Glyphochloa* for the first time, relating to its taxonomy and ecology. This Genus is seen distributed along hard lateritic rocks in Peninsular and Central India, growing in the raining season. Free hand sections of leaf were taken, processed and observed under the light microscope. The genus *Glyphochloa* can be divided into two groups based on morphology: as single awned or two awned, growing at low and high altitude respectively. The anatomy of the leaf midrib shows prominent U or V shaped region in two awned species. The vascular bundles are well supported by sclerenchymatous patches on either side of the midrib. Epidermis in surface view is divided into longitudinal zones which distinguishes the intercostal zones from the costal zones, showing silica cells. Epidermal cells are barrel shaped, in few cases inflated. The mesophyll shows chlorenchymatous cells that radiate around all vascular bundles surrounded by bundle sheath cells. Single awned species, showed sclerenchyma for all vascular bundles, while in two awned species, sclerenchyma strands girders were seen at constrictions on either side of the leaf.

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P.0896 Life history sculpts the body plan of leaves in non-photosynthetic plants

Liming Cai[1], Saneeva George[1]

1 Department of Integrative Biology, The University of Texas at Austin, Austin, USA.

Plants' life is a constant battle for water and light, and their leaf architecture is a critical component of vegetative adaptation. However, more than four thousand parasitic plants have evolved unique mechanisms to exploit their hosts of photosynthesis products. How does the ground plan of their leaves respond to such a fundamental shift in selective regimes? In this study, we investigated the evolution of leaf architecture in parasitic plants using a combination of quantitative morphology, systematics, and collection-based science. Orobanchaceae provided a unique comparative framework spanning the entire spectrum of parasitism from photosynthetic free-living plants to three independent evolutions of full parasites. Using high-resolution images from digitized specimens, we mathematically analyzed leaf geometry from more than one thousand samples across Orobanchaceae. In addition, we also collected venation statistics from chemically cleared leaves using a deep learning-based technique. These high-resolution leaf morphology data were then combined with phylogeny and climate data to form an integrative understanding of the relative importance of life history and abiotic factors in shaping the vegetative body plant. Our study highlights the importance of leaf architecture in the adaptation of parasitic plants to different modes of lifestyle.

P.0897 Comparative anatomical and histochemistry study of Zephyranthes fosteri, Z. alba and Z. fosteri × Z. alba (Amaryllidaceae)

Lucía Y. Centeno-Betanzos[1*], Teresa Terrazas Salgado[2], Carlos E. Lozada-Becerra[1], Ricardo Reyes-Chilpa[3]

1 Faculty of Sciences, National Autonomous University of Mexico (UNAM), Mexico City, Mexico. 2 Institute of Biology, UNAM, Mexico City, Mexico. 3 Institute of Chemistry, UNAM, Mexico City, Mexico.

In this work, the anatomy and histochemistry of the species Zephyranthes fosteri, Zephyranthes alba and Z. fosteri × Z. alba (Amaryllidaceae) were studied in order to characterize these taxa and present elements that supported or refuted the hypothesis that Z. fosteri × Z alba is a hybrid of the first two and locates its alkaloids in tissues. These three taxa coexist in the Pedregal de San Ángel Ecological Reserve (REPSA) located in the University City of the National Autonomous University of Mexico (UNAM). The anatomical structure of the leaf, scape and bulb of these three taxa was described and compared. For histochemistry, fresh hand-cut tissues were used and the Warner, Dragendorff and Jeffrey reagent was applied to locate the alkaloids. The results showed that the main characters to distinguish Z. fosteri from Z. alba were: a) in the leaf, the differences in the size of the mesophyll and the diameter of the scape, b) the presence of veins and the striated shape of the cuticle in Z. fosteri, and c) the absence of palisade parenchyma in Z. alba. There was a positive reaction for the alkaloids in all the tissues studied in the three species, but in the bulb there was a greater reaction. In the aerial leaves the reaction was observed in the parenchyma close to the vascular bundles and in the palisade parenchyma. Z. alba presented more precipitates in its tissues compared to the other taxa. At a structural level, the results support the proposal that Z. fosteri × Z. alba could be a hybrid, due to the intermediate anatomical character it presents and the similarity in the internal structure with both parental species. The reaction of the alkaloids allowed us to visualize their location in the tissues and locate their highest concentration in the plant organs.

P.0898 Cell division patterns during early cork development in two Quercus spp.

Davide Botticelli[1,2,3,4], Carlos Vila-Viçosa[1,2,3,5], Ana Campilho[1,2,3]

1 CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Vairão -Universidade do Porto, Porto, Portugal. 2 Departamento de Biologia, Faculdade de Ciências, Portugal. 3 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal. 4 Department for Innovation in Biological, Agro-food and Forest system, University of Tuscia, Viterbo, Italy. 5 MHNC-UP - Museu de História Natural e da Ciência da UP, Porto, Portugal.

More than 350 hundred years have passed since Hooke's examination of a slice of cork under a microscope, and despite being the "first cells" to be called as such, little is known about the mechanisms regulating cork cells pattern formation. The main objective of this study is to address a distinct feature of the cork oak (*Quercus suber* L.) phellogen (the lateral meristem that produces phellem/cork). This tree's unique genetic program allows the same ring of meristematic cells to keep up with the inner trunk enlargement as long as the tree is alive. However, it is unknown how the same ring of phellogen cells is maintained and active for years. We hypothesize that cork oak's phellogen cells undergo frequent anticlinal divisions. As a strategy, early developmental stages of phellogen/cork tissue pattern are being compared between two oak tree species: the cork oak and the round-leaf oak (*Quercus rotundifolia* Lam.). Both species are iconic in Mediterranean landscapes, they are phylogenetically related (Eurasian Subgenus *Quercus*), but display contrasting periderms (triplet tissue composed from phelloderm- phellogen- phellem). The round-leaf oak produces a rhytidome (successive periderms) because the phellogen cell ring collapses periodically, as opposed to the single periderm of the cork oak. Young branches of cork oak and round-leaf oak were collected for light microscopy observation and analysis. Image analysis methods were optimized for a robust comparative analysis of tissue pattern features (orientation of cell division, cell types, cell numbers and cell size) between the two oak tree species. This poster communication will present our results so far.

P.0899 Genomic adaptation of mangrove sea-floating propagules in transition to intertidal zones

Jiayan Wang[1], Suhua Shi[1], Zixiao Guo*[1]

*1 School of Life Sciences, Sun Yat-sen University, Guangzhou, China *guozx8@mail.sysu.edu.cn*

Successful propagation is the prerequisite condition to maintain long-term population existence for plants that transit into extreme environments. Mangroves have invaded the intertidal zones, which are very narrow habitats linearly distributed along ocean coasts. Mangrove propagules must float in sea water and even disperse across seas before they can be fixed in the soil. How have the genomes of mangrove species evolved and adapted to develop sea-floating propagules? We used multi-omics methods to uncover the underlying molecular adaptations using *Heritiera* mangroves as the model. *Heritiera* mangroves have a strong ability for long-distance dispersal because their fruits have hard woody epicarp, fibrous mesocarp, and air spaces. We *de novo* sequenced and assembled high-quality genomes for *Heritiera littoralis* Aiton and *Heritiera fomes* Banks. Phylogenomic analysis indicates *H. littoralis* and *H. fomes* originated (at ~6.08 Mya) just before the start of Quaternary sea-level fluctuations. Whole genome duplication occurred earlier, permitting gene copy gains in the two species. Many of the expanded gene families are involved in lignin and flavonoid biosynthesis, likely contributing to buoyant fruit emergence. By examining *H. littoralis* fruits at three different developmental stages, we found that the upregulation of *WRKY12* and *E2Fc* likely constrains the production of p-Coumaroyl-CoA, the key internal substrate for lignin biosynthesis. Hence, to increase fruit impermeability, methylated lignins biosynthesis is shut down by downregulating the genes *CCoAOMT*, *F5H*, *COMT,* and *CSE,* while unmethylated lignins are preferentially produced by upregulating *CAD* and *CCR*. Similarly, cutin polymers and cuticular waxes accumulate with high levels before maturation in epicarps. In summary, our integrative multi-omics research elucidates the molecular mechanisms underlying mangrove propagation by sea-floating propagules. These new insights will be useful in mangrove restoration and protection.

P.0900 Unveiling liana wood anatomy: insights into convergence, wood configuration, and transcriptional modulation by physical support

André C. Lima[1,2], Sónia C. S. Andrade[1], Caian S. Gerolamo[1], Diego T. de Souza[1], Luiz L. Coutinho[3], Magdalena Rossi[1], Veronica Angyalossy[1]

1 Institute of Biosciences, University of Sao Paulo, Brazil. 2 School of Agriculture, Sao Paulo State University, Botucatu, Brazil. 3 Luiz de Queiroz College of Agriculture, University of Sao Paulo, Brazil.

Lianas display pronounced anatomical convergence within their vascular systems. In the xylem, this convergence manifests as a decrease in fiber content, an increase in vessel density, wider vessels linked with smaller diameter ones, and a heightened presence of parenchyma and phloem tissues interspersed throughout the xylem. We term this particular xylem configuration as lianescent xylem. Another lesser-explored characteristic is the initial developmental stage wherein the xylem is fibrous, and vessels are scarce and diminutive, present in most lianas and referred to here as non-lianescent xylem. Moreover, the transition between these phases is abrupt when examined in cross-section. The prevalence of these traits across lianas, regardless of family or order which they belong, strongly suggests the adaptive potential of such characteristics in habit evolution. Nonetheless, the factors governing the transition in xylem type formation and the regulation of xylem differentiation remain uncertain. In this study, we investigated the impact of physical support fixation on lianescent xylem production in *Bignonia magnifica* W. Bull (Bignoniaceae) liana by integrating detailed anatomical analyses of secondary xylem formation with the study of differential gene expression profiles in the cambium and differentiating xylem in the two phases. Our findings reveal that the initiation of lianescent xylem formation is triggered by physical support fixation, leading to a reduction in fiber content, the production of larger vessels, the inception of vessel production by the interfascicular cambium, and higher potential specific hydraulic conductivity. These changes are linked to a downregulation of genes associated with cell division and cell wall biosynthesis, alongside an upregulation of transcription factors, defense/programmed cell death genes, and hormone-responsive genes during the lianescent phase.

P.0901 Natural grasslands of Brazil: macroscopic wood anatomy of twenty-five small plants species

Tiago M. G. Pinto[1], Davi N. de Lemos[1], Maycon S. Teixeira[1], Giselda Durigan[2], Mario Tomaazello-Filho[1]

1 Universidade de São Paulo, Piracicaba, Brazil. 2 Instituto de Pesquisas Ambientais, São Paulo, Brazil.

In natural fields, small plants –herbs, subshrubs, and shrubs– consist of stems and roots with wood (secondary xylem) displaying a characteristic anatomical structure and applied in taxonomy and ecological studies. Botanical materials were collected from twenty-five species of small plants occurring in areas of three natural grassland physiognomies of the Cerrado and Atlantic Forest biomes in the states of São Paulo, Rio de Janeiro, Minas Gerais and Goiás**.** The wood of stem and root of small plants was cross-sectioned into 1 cm length segments, polished with sandpaper (increasing series: 80-1200 grains/mm²) for contrast and visualization of the anatomical structure. Similarly, sections of the tangential longitudinal plane of the wood were cut using a scalpel. The analysis of the anatomical structure was carried out with the naked eye and with a thread-counting magnifying glass (10x). The macroscopic anatomical description of the wood was adapted from the standard guidelines (Coradin and Muniz 1991), analyzing the growth rings and the anatomical constituents of the wood (secondary xylem), such as vessels, fibers, longitudinal and radial parenchyma (shape, dimensions, and distribution). The macroscopic anatomical characteristics of the transverse plane of the wood (secondary xylem) observed were: (i) radial parenchyma (visibility); (ii) pores/vessels (visibility; porosity; arrangement and grouping); (iii) growth rings (distinction and characterization of delimitation). The macroscopic characteristics of the tangential longitudinal plane of the wood observed were: (i) radial parenchyma (visibility and distribution). Small plants exhibit distinct anatomical wood structures characteristic of their species, with potential applications in taxonomy, distinct growth rings in some species with potential in herbchronology. The macroscopic dimensions of the anatomical wood elements indicate the importance of their microscopic analysis.

Reference: Coradin, V.T.R.; Muniz, G.I. *Procedure standards in wood anatomy studies: I.Angiospermae ; II. Gymnospermae.* Brasilia: IBAMA. DIRPED, LPF, 1991. 19p. (IBAMA. Technical Series , 15).

P.0902 Anatomical studies of floriferous zones in Cactoideae (Cactaceae)

Rafaella Munhoz[1], Natália Bonfante[2], Patricia Soffiatti[2], Mariana R. Fantinati[3]

1 Department of Biological Sciencies, Unesp, Assis, Brazil. 2 Department of Botany, UFPR, Curitiba, Brazil. 3 Botanical Museum "Frederico Carlos Hoehne", Unesp, Assis, Brazil.

Cephalium is a specialized reproductive portion (floriferous zone) exclusive to Cactaceae Juss. It is present in some groups of the subfamily Cactoideae Eaton. and can be defined as a continuous region with confluent areoles and dense production of spines, trichomes and flowers, in addition to periderm production. However, there is a lack of anatomical studies on this structure. The aim of the present work was to investigate the anatomical traits of the dermal system and part of the fundamental system of the cephalium of specimens of *Coleocephalocereus fluminensis* (Miq.) Backeb. to provide a better understanding of its anatomy. Anatomical traits of the apical, median, and basal regions of the vegetative and reproductive (cephalium) portions of the stem were studied in longitudinal and cross sections and it was possible to obtain partial anatomical results. The cephalium region showed, in comparison with the vegetative portion, intense development of the periderm, discontinuous hypodermis with undefined layers, absence of palisade cortex, increased number of mineral inclusions and cortical bundles and decreased mucilaginous cells in the spongy cortex. These traits are most evident at the base of the cephalium but are also observed at apical and median regions. Studies like this can help to elucidate the role of cephalium as a potential synapomorphy for subgroups of Cactaceae.

P.0903 Leaf epidermal micromorphology in Peucedanum and related genera (Apiaceae): diversity and taxonomic significance

Kyeonghee Kim[1], Min-Kyeong Oak[2], Sungyu Yang[1], Goya Choi[1], Jun-Ho Song[3]

1 Herbal Medicine Resources Research Center, Korea Institute of Oriental Medicine, Naju, Republic of Korea. 2 Garden Education Office, Sejong National Arboretum, Sejong, Republic of Korea. 3 Department of Biology, Chungbuk National University, Cheongju, Republic of Korea.

Peucedanum L. comprises 100–120 species, mostly in Eurasia and Africa. This study is the first to examine the leaf epidermal micromorphology of 14 *Peucedanum* taxa, including two new endemic species, the medicinally significant *P. praeruptorum*, and related genera. This study used a large-area and multiscale automated field-emission scanning electron microscopic data. The leaves of all *Peucedanum* taxa except *P. chujaense* were amphistomatic, whereas *P. chujaense*, *Sillaphyton podagraria*, and *Heracleum moellendorffi*i were hypostomatic. Anisocytic and staurocytic stomata complexes are the most frequent type; rarely actinocytic and anomocytic also occur. Convex periclinal cell wall was found in all *Peucedanum* taxa; however, *Sillaphyton podagraria* and *Heracleum moellendorffii* had epidermal cells of a central conical periclinal wall. Non-glandular trichomes on leaves were only found in *P. praeruptorum*. Two types of epicuticular waxes were observed: scales and granules. Although most *Peucedanum* species share a similar epidermal morphology, the stomatal complex, epidermal cell and trichome types, and epicuticular waxes provide essential information for systematic and taxonomic investigations in this genus.

P.0904 The role of far-red and blue wavelengths in negative shoot phototropism in a temperate liana Hedera helix

Tomasz P. Wyka[1]

[1] Faculty of Biology, Adam Mickiewicz University, Poznań, Poland.

For climbers, supporting structures are a key environmental resource because they are needed for proper display of leaves and flowers. Several climber species have been shown to detect supporting structures remotely. The common ivy (*Hedera helix* L.), a temperate shade tolerant liana, uses negative phototropism (i.e., growth away from light and into darker areas) to locate nearby support (Wyka 2023; *Tree Physiology* 43:1874–1885). Whereas positive phototropism is common in plants and is controlled by blue light absorbed by phototropins, negative shoot phototropism has rarely been reported, and little information is available on its action spectrum. The purpose of this study was to test the activity of representative wavelengths in controlling phototropic responses of *H. helix*. Seedlings of *H. helix* were exposed to lateral overhead white fluorescent light in a growth chamber and presented with a black surface on the opposite side. This arrangement created a spatial light gradient that stimulated growth towards the black surface in control plants. Monochromatic LEDs were mounted on the black surface and directed towards the plants. Green (520 nm) and red (630 nm) light did not affect the direction of shoot growth. UVA (365 nm) and blue (460 nm) light disrupted the directional growth and caused disorientation of the shoots. Far-red (730 nm) light caused reversal of growth direction – shoots grew away from the black surface on which the LEDs were mounted. These results are consistent with blue, UVA and the far-red radiation guiding the shoot growth direction in negative phototropism. However, while gradients of blue and UV may indicate the location of opaque objects, such as trees, with respect to the solar asimuth, far-red light is also scattered from neighboring vegetation. To permit tree detection in the native understory environments of *H. helix,* these signals must be interpreted by plants separately.

P.0905 Leave anatomy of the genus Gundelia

Golshan Zare[1], Metin Armağan[2], Aslı Doğru-Koca[3], Osman Tugay[4]

[1] Hacettepe University, Faculty of Pharmacy, Pharmaceutical Botany, Ankara, Turkey. [2] Necmettin Erbakan University, Ereğli Faculty of Agriculture, Department of Field Crops, Konya, Turkey. [3] Hacettepe University, Faculty of Science, Department of Biology, Ankara, Turkey. [4] Selçuk University, Faculty of Pharmacy, Pharmaceutical Botany, Konya, Turkey.

Gundelia tournefortii was described by Linnaeus and has long been known as a monospecific. This genus is a controversial genus whose number of taxa has increased to 16 in Turkey in the last decade. Morphological characters such as inflorescence characteristics, flowers and fruits have been widely used to introduce new taxa. But all these characters show a wide range of variation in inter- and intra-species level. In this study, we try to find more reliable characters for the identification of these taxa. The leaf anatomy of 16 species of *Gundelia* grown in Türkiye was studied in detail. All the plant materials collected from different parts of Türkiye were kept in 70% ethanol for anatomical studies. Cross section of leaf, leaf epidermis, stomatal density, size and index of the studied taxa were examined by safranin and astra blue. In this study, we report a detailed anatomical property of the leaf and epidermis, such as stoma index, guard cell size, crystal type and density. These characters provided valuable characters for the identification of taxa in *Gundelia*. Although the anatomical characters of these taxa are not sufficient as diagnostic characters, they can be used together with morphological characters.

P.0906 Leaf anatomy of Mexican species of the genus Iresine P.Browne (Amaranthaceae s.l.)

Silvia Zumaya-Mendoza[1], Alicia Rojas Leal[2], Teresa Terrazas Salgado[2]

[1] Facultad de Ciencias, Universidad Nacional Autónoma de México, Mexico. [2] Instituto de Biología, Universidad Nacional Autónoma de México, Mexico.

Iresine belongs to the Amaranthaceae s.l. family, its species are distributed in different environments, so the leaf anatomy is expected to be diverse. The aims of this study were to describe the leaf anatomy of 25 species of *Iresine* present in Mexico. Mature and healthy leaves were removed from the herbaria and processed with conventional paraffin embedding techniques to obtain transverse and paradermal sections. The results show leaves of variable shapes and sizes, tomentose to glabrous; with cuticle thin to thick and stomata anomocytic at the same level as the epidermal cells. The mesophyll is heterogeneous, the palisade parenchyma has one to four layers of cells and occupies 20 to 70% of the mesophyll and the spongy parenchyma is loose or compact as in *I. ajuscana*, *I. pringlei*, *I. latifolia*, the crystals, druses or sandstones, are predominantly found in the mesophyll. The vascular bundles may or may not have sheath extensions of parenchyma or sclerenchyma as in *I. pringlei.* The midvein contour is round to square; immediately below the epidermises there is collenchyma in some species such as I. *orientalis* and one to four central vascular bundles are present (*I. diffusa*, *I. flavescens*, *I. palmeri*) with or without sclerenchyma. The combination of leaf characters could have diagnostic value in some species and other characteristics as for cuticle thickness, presence of sheath extensions and abundance of palisade parenchyma could be related to the environment in which *Iresine* species grow.

S.103. MOUNTAIN BIODIVERSITY AND EVOLUTION.

P.0907 Studies of architectural models of Azerbaijan bellflowers of subgenus Campanula (Campanulaceae)

Asya E. Akbarova[1], Rashad A. Salimov[2]

1 Institute of Botany, Baku, Azerbaijan. 2 Department of Science, Sumgayit State University, Sumgayit, Azerbaijan.

The genus *Campanula* L. is the most species-rich genera of the *Campanulaceae* Juss., with about accepted names of 458 species including 110 species in Caucasus and 46 species in Azerbaijan flora. Representatives of this genus grows in various environmental conditions: forests, meadows, rocks and rarely in deserts and semi – deserts. Most of them are numerous and varied in high mountains, in the subalpine and alpine belts. Plant samples collected during expeditions from different regions of Azerbaijan in 2018-2022, and *Campanula* herbarium specimens stored in the BAK of the Institute of Botany were used in this study. The life forms, habitat and bioecology of species were analyzed in the context of available relevant literature references. The wide distribution of bellflowers species correlates with the diversity of their life forms. The structural basis of life forms is the architectural model that determines the basic growth strategy of a plant. *Campanula* species are characterized by various architectural models, which indicates the genus is polytypic for architecture. Our findings show various architectural models can be observed in one section of the genus and/or the same one can be shared by species belonging to several sections. The studied species are grouped based on the architectural models as follows: model Tomlinson – *C. latifolia* L., *C. bononiensis* L., *C. odontosepala* Boiss. (all are in sec. *Campanula*), C. glomerata L. (sec. *Involucratae* (Fomin) Charadze), *C. alliariifolia* Willd., and *C. sarmatica* Ker.-Gawl. (both of them in sec. *Cordifoliae* (Fomin) Charadze); model Holltum – *C. sibirica* L. (in sec. *Campanula*); model Mc. Clure – *C. rapunculoides* L. (in sec. *Campanula*); model Aubreville – *C. collina* Sims. (in sec. *Cordifoliae* (Fomin) Charadze); model Troll – *C. kolenatiana* C.A. Mey., and *C. bayerniana* Rupr. (both of them in sec. *Symphyandriformes* (Fomin) Charadze).

P.0908 Echoes from the heights: digitizing specimens from the 1955 Karakoram expedition

Ashley Bales[1], Craig Meyer[1], Ashlyn Weaver[2]

1 Botanical Research Institute of Texas, Fort Worth Botanic Garden, Fort Worth, USA. 2 Rock Hill High School, McKinney, USA.

The Himalayan-Hengduan (H-H) mountain range contains unparalleled biodiversity due to its unique topology and environmental conditions. The region's geology and prolific rate of speciation translates to biodiversity that rivals rainforests, even in harsh conditions and high elevations. Due to ongoing effects of climate change, however, the H-H flora is now some of the most threatened in the world. Between change in precipitation, retreating glaciers, and temperature increase, the clock is ticking on these unique plants. A Harvard University's Mountaineering Club (HMC) expedition originating in "good climbing, good company, and good adventure" collected a critical snapshot of the flora in the summer of 1955 in the Karakoram Range, the most heavily glaciated part of the world outside the polar regions. Rather than focus solely on ascending the highest peaks of the Karakoram, the HMC "committed the expedition to a scientific program." They were accompanied by botanists Dr Grady L. Webster of Harvard and Dr Eugene Nasir of Gordon College, who conducted a botanical study of the area. Webster and Nasir collected over 800 specimens of vascular plants and bryophytes between 7,000-16,000 feet of altitude, with duplicates distributed to herbaria around the world. These collections represent over 100 species with several later discovered as new to science. Students and volunteers have been a key part of the BRIT Philecology Herbarium's effort to digitize its holdings as part of the NSF-funded All Asia grant (Award No. 2101846). Our work reconstructs the Harvard Mountaineering Club's path and places the specimens in historical, social, and scientific context. This expedition-centered project can be a prototype of outreach and engagement with curious but otherwise inexperienced students and volunteers. We discuss the unique challenges of the project, including georeferencing and consulting institutional archives.

P.0909 Conservation Units play a vital role in plant conservation: a Myrtaceae family case study in the Mantiqueira Mountain Range (Southeastern Brazil)

Nina Caldeira[1], Kelly Antunes[1], Pamela Tavares da Silvia[1], Luiz Menini Neto[1], Fabrício Alvim Carvalho[1]

1 Federal University of Juiz de Fora, Juiz de Fora, Brazil.

In a megadiverse country such as Brazil, species knowledge and geographical distributions are vital to support biodiversity conservation and sustainable use decisions. Myrtaceae is the seventh biggest angiosperm family in the world (ca. 6000 species); in Brazil, there are ca. 1200 species, 83% endemic. The Atlantic Forest domain is considered one of the biggest centers of the Myrtaceae diversity. Given the widely distributed nature of Myrtaceae and its well-established taxonomic and phylogenetic understanding, in this study, we used Myrtaceae as a model to examine species distribution patterns within the Mantiqueira Mountain Range situated in Southeastern Brazil. In southeastern Brazil, the Mantiqueira Mountain Range is a highland area among Minas Gerais, São Paulo, Rio de Janeiro, and Espírito Santo states. We compile the database of Myrtaceae registers at SpeciesLink and Jabot for each municipality (398 in total) limited by the Mantiqueira Mountain Range. To compile the database, online registers were consulted and marked on a grid measuring 0.25° x 0.25°, overlapping with Conservation Unit boundaries. A total of 354 species were identified; 38 of them are threatened, and two are endemic to the Mantiqueira Mountain Range. Of the 398 municipalities in the Mantiqueira Mountain Range, 259 (65.08%) had records of Myrtaceae. The grid squares with the highest species richness were located in areas previously sampled by experts or within Conservation Units. Removing records from these locations would reduce the sample by half (6627 registers), indicating that the sample is not biased solely due to the "museum effect" but also due to the availability of structure and logistics facilitated by the Conservation Units. Both sets of records highlight the importance of comprehensive data collection during fieldwork and the role of Conservation Units in floristic research.

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P.0910 Highlights of the highest tree inventory stablished in Brazil: the cloud forest particularities and future concerns at 2,330 m altitude

Nina Caldeira[1], Kelly Antunes[1], Lucas D. Santana[1], José Hugo C. Ribeiro[2], Walef D. Vieira[1], Fabrício A. Carvalho[1]

1 Federal University of Juiz de Fora, Juiz de Fora, Brazil. 2 Southeastern Federal Institute - Rio Pomba Campus, Rio Pomba, Brazil.

Occurring above 1,000 m high in Brazil, tropical montane cloud forests (herein, cloud forests) are frequently immersed in fog. They are one of the most threatened ecosystems in the world due to their strict distribution allied to human disturbances. Cloud forests are deeply dependent on fog coverage, low temperatures, and rainfall patterns. These particular environmental conditions enable cloud forests to be home to unique and threatened plant lineages. Here, we characterized different aspects (floristic composition, structure, and carbon stock) of the highest forest ever sampled in Brazil (Serra do Papagaio State Park, southeastern Brazil). In total, 450 trees with circumference ≥ 15.5 cm in ten 20x10 m plots were measured and identified. The carbon stock was estimated using allometric equations. The sampled trees represented 18 families, 22 genera, and 37 species. The forest has high density (2250 ind.ha^{-1}) and high basal area (63 m^2.ha^{-1}); both values are higher than the literature values for Brazilian cloud forests. The families Myrtaceae, Melastomataceae, Solanaceae, and the genera *Myrceugenia*, *Miconia*, and *Solanum* were the richest and representative of high-montane forests. *Myrceugenia bracteosa* (O.Berg) D.Legrand & Kausel, an endangered species, was the most important species (highest basal area, density, and frequency) and is dominant in the community. The estimated carbon stock of the forest, 2992 Mg.ha^{-1}, is outstanding and higher than in forests across several biomes, including the Amazon. With the ongoing scenario of global warming and climate emergencies, climate modeling has already revealed that the Brazilian cloud forests might disappear until 2080, with already severe adequability lost in 2030. We highlight that the Brazilian high-montane biodiversity and core ecosystem services (as the massive potential of stocking carbon) are severely at risk. Such impressive findings reinforce the increasing concern for cloud forests worldwide.

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P.0911 Genome architecture and population genomic structure of a bromeliad species adapted to an elevation cline

Paulo Aecyo[1], Marilia M. Tavares[1], Jacqueline S. Mattos[1], Fernando Della-Rosa[2], Alessandro Varani[3], Fábio Pinheiro[1], Cleber J. N. Chaves[1], Aureliano Bombarely[4], Diego M. Riaño-Pachón[2], Clarisse Palma-Silva[1]

1 Laboratory of Evolutionary Ecology and Genomics of Plants, Instituto de Biologia, Universidade Estadual de Campinas, Campinas, Brazil. 2 Laboratory of Computational, Evolutionary and Systems Biology, Center for Nuclear Energy in Agriculture, University of São Paulo, Piracicaba, Brazil. 3 Laboratory of Genomics and Bioinformatics, School of Agricultural and Veterinarian Sciences, São Paulo State University, Jaboticabal, Brazil. 4 Laboratory of Crops, Instituto de Biologia Molecular y Celular de Plantas, Universidad Politécnica de Valencia, Valencia, Spain.

Local adaptation is a complex process led by natural divergent selection, and can culminate in an ecological speciation event. However, the pace of climate change may pose significant risks to highly specialized populations. Populations of the diploid bromeliad *Pitcairnia flammea* Lidl. exhibit distinct phenotypic traits associated with ecological strategies across the elevation gradient of the Brazilian Atlantic Forest. Despite this, the genomic basis of these adaptations remain unexplored. Our research aims to elucidate the genomic basis of adaptation in *P. flammea*, focusing on how Single Nucleotide Polymorphisms (SNPs) and Structural Variations (SVs) contribute to genetic divergence and adaptation across an elevation cline. To achieve this, we assembled highly contiguous genomes of two individuals from contrasting altitudes using PacBio HiFi and Omni-C sequences and resequenced 74 individuals (Illumina short-reads) from eight populations in an elevational cline (sea level to 2,200m). Macrosynteny analysis with other bromeliads uncovered several gaps in pericentromeric regions, potentially enriched with repetitive elements. In fact, transposable elements account for ~75% of the genome of *P. flammea*. The demographic history inferred for each diploid genome suggested a notable decline in the effective population size of both populations since the late Miocene, potentially linked to climatic variations and restricted gene flow. Principal Component Analysis (PCA) identified three distinct groups within our samples, distinguishing the highland and lowland populations, and isolating a single midland population. STRUCTURE analysis identified six clusters, indicating limited gene flow among populations. Moreover, 48.83 Gbp of the short-read sequences did not align with the reference genome and will be used to characterize the SVs among the individuals together with PacBio HiFi sequences from one individual from each population. With that, our study will contribute to a deeper understanding of the resilience of tropical mountain species to climate change, particularly in the world's most biodiverse region.

P.0912 Airborne pollen trends in Sierra de las Nieves National Park (southern Spain)

Enrique de Gálvez Montañez[1], Marina Muñoz García[1], Rocío Ruiz Mata[1], M. Mar Trigo[1], Marta Recio[1], Antonio Picornell[1]

1 Department of Botany and Plants Physiology. University of Málaga, Málaga, Spain.

Sierra de las Nieves (southern Spain) is a protected space recently declared National Park with emblematic high and mid-mountain species and relevant forest masses surrounded by unfavourable environmental conditions. In a global warming scenario, it is important to determine how climate change can affect these forest species to establish conservation guidelines. In this study, airborne pollen was sampled by means of a Hirst-type volumetric pollen trap installed in "Las Conejeras" recreational area, bordering the domains of the National Park. In this study, data from 2018 to 2023, both inclusive, were considered to calculate trends in the Main Pollen Season (MPS) parameters. The MPS was defined by fitting a logistic regression to the accumulated sum of pollen concentrations as well as the calculation of derivatives. Data were managed by means of the AeRobiology package, implemented in R software. Different responses to climate change were observed within the most abundant pollen types with forest interest. Pollen types such as *Pinus* and Cupressaceae did not show any significant trend while others, such as *Olea*, showed an incipient trend, and others, such as *Castanea* and *Quercus* presented clear significant trends to bring forward the start of their pollination period due to the increase in temperatures. According to these results, the responses to global warming showed diverse behaviours in this protected area, there being species whose conservation measures should be considered as a priority, given their greater sensitivity to temperature increases.

P.0913 Species composition and altitudinal distribution patterns of wild Allium L. relatives in the Kyrgyz Alatau mountain ridge

Nadezhda G. Gemejiyeva[1], Gulnara T. Sitpayeva[1], Liliya A. Dimeyeva[1]

1 Institute of Botany and Phytointroduction, Almaty, Kazakhstan.

The *Allium* species indigenous to Kazakhstan present substantial economic potential and a rich species diversity within the Tien Shan mountains. This investigation, utilizing data from the Herbarium (AA) and recent field studies, delineates 27 *Allium* species in the Kyrgyz Alatau region (*A. atrosanguineum* Kar. et Kir., *A. barsczewskii* Lipsky, *A. caesium* Schrenk, *A. carolinianum* DC., *A. decipiens* Fisch., *A. fetisowii* Regel, *A. filidens* Regel, *A. filifolium* Regel, *A. kokanicum* Regel, *A. hymenorhizum* Ledeb., *A. karataviense* Regel, *A. longiradiatum* (Regel) Vved., *A. obliquum* L., *A. oreophilum* C. A. Mey., *A. oreoprasum* Schrenk, *A. pallasii* Murr., *A. platyspathum* Schrenk, *A. sativum* L., *A. schoenoprasoides* Regel, *A. schoenoprasum* L., *A. semenovii* Regel, *A. suworowii* Regel, *A. turkestanicum* Regel), encompassing noteworthy endemic (*A. oreoprasoides* Vved.) and subendemic (*A. leptomorphum* Vved., *A. parvulum* Vved., *A. trachyscordum* Vved.) plants. *A. barsczewskii* exhibits an altitudinal range of 1030-2500 m a.s.l., spanning from savannoid steppes in the low-mountain belt (*Festuca valesiaca, Stipa capillata, Elytrigia trichophora, Bothriochloa ischaemum*) to subalpine grass-rich forb meadows (*Phlomoides oreophila, Bistorta elliptica, Dactylis glomerata*) and steppes (*Festuca valesiaca, Helictochloa hookeri*). Widespread at altitudes ranging from 1140 to 1839 m a.s.l., *A. caesium* thrives in rich forb floodplain meadows and intermountain valleys (*Phlomoides fetisowii, Betonica betoniciflora, Dactylis glomerata*). High-mountain species like *A. atrosanguineum* and *A. hymenorhizum* are found in alpine meadows (*Alchemilla retropilosa, Potentilla crantzii, Carex alatauensis*), including those at the Kumbel pass (3247 m a.s.l.). Certain species such as *A. oreophilum, A. platyspathum, A. semenovii,* and *A. carolinianum* are observed in proximity to snowfields. In steppes and steppe meadows of foothills and the low-mountain belt (800 – 1140 m a.s.l.), species like *A. parvulum, A. suworowii, A. oreoprasum, A. longiradiatum, A. leptomorphum,* and *A. karataviense* are distributed.

P.0914 Trees and shrubs of the Siberia and surroundings, Cochabamba- Santa Cruz, Bolivia

Erika Fernández[1], Jesus Jamachi[1], Mauricio Caballero[1, 2], Rosario Saravia[1], Vania Torrez[1], Leydi Flores[1], Adriana Llanque[1], Carmen A. Castillo[1], Nelly de la Barra[1]

1 Departament of Biology, Faculty of Science and Technology, Universidad Mayor de San Simón, Cochabamba, Bolivia. 2 National Forest Herbarium Martín Cardenas, Center of Biodiversity and Genetics, Universidad Mayor de San Simón, Cochabamba, Bolivia.

Siberia is a region with a large extension of cloud forests in the Yungas located between Yungas del Ichilo biogeographic sector and the first foothills of the Yungas del Piray-Río Grande sector in Bolivia. It is comprised of the southern limit of the Yungas biogeographic province in South America, where numerous biodiverse ecosystems rich in endemic species of plants, birds, reptiles, amphibians and insects develop. This paper presents an analysis of the richness, conservation status and endemism of the arboreal and shrub stratum. Collections were made from our own samplings, systematization of information and data from collections already recorded by other researchers, which gives us a total of 17 localities studied. The ecosystems sampled correspond to hillside forests, ravines, rocky walls and roadsides, located between 2,200-3,080 m altitude. Seventy-two families, 139 genera and 233 species were recorded. The families with the greatest richness of genera are the Asteraceae 18 (13%), Rubiaceae with 13 (9.4%) and Solanaceae with 8 (5.8%). The families with the highest species richness are Asteraceae with 32 (13.7%), Solanaceae with 20 (8.6%), Rubiaceae with 15 (6.4%), Rosaceae with 11 (4.7%), Fabaceae with 10 (4.3%) and Myrtaceae with 8 (3.4%). The data show that 206 (88%) are native species, 23 (10%) endemic, 2 (1%) naturalized and 2 (1%) cosmopolitan. Regarding conservation status, 18 (8%) species have some degree of threat, of which 9 (4%) are ENDANGERED and 9 (4%) are VULNERABLE. The high specific richness for trees and shrubs in the area is comparable to that reported for other areas of the Yungas in Bolivia, the percentage of endemisms and the estimation of the degree of threat show that the region deserves special attention to continue botanical research and promote the conservation of its ecosystems.

P.0915 Meeting the plants of the “Martín Cárdenas” Botanical Garden

Erika Fernández[1], Isabel Bellot[1], Mariana Zelada[1], Fernanda Bustos[1], Camilo Avalos[1], Martín Arteaga[1], Camila Sosa[1], Mauricio Caballero[1], Nelly de la Barra[1]

1 Department and Career of Biology, Faculty of Science and Technology, Universidad Mayor de San Simon, Cochabamba, Bolivia.

Botanic gardens are institutions serving a fundamental role in the conservation of a country’s regional flora, having an impact in the environmental education of its society. The Martín Cárdenas botanical garden was founded in 1962, being the first in Bolivia, currently sheltering a collection of native, introduced, and endemic plants; being an indispensable place to promote their conservation. The objective of the study was to strengthen the knowledge on the collected species in the botanical garden, considering its rich abundance and its state of conservation. As methods, an inventory was carried out between September 2021 and May 2022, recording a total of 346 species belonging to 87 families. According to the analysis of status, most species are introduced and in a smaller proportion native and endemic; in the latter, the cactis with important species such as *Neoraimondia herzogiana* and *Pereskia diazromeroana* are stand outs that form part of the first collection of Bolivian cacti. The species with the most abundance are *Jacaranda mimosifolia* and *Parajubaea torallyi*. We denominate emblematic native species plants which are representative inside the Bolivian context, for example, those which form part of the national symbols. The plants under the threatened category are *Parajubaea torallyi* (VU), *Cantua bicolor* (CR) and *Polylepis subtusalbida* (VU). In conclusion, highlighting the scientific, environmental, and social value of the botanical garden that represents a live collection of native and emblematic species holding value in relation to their conservation status. The species present in the garden have various geographical origins, emphasizing a varied and representative flora of the region and nation.

P.0916 Phylogenetics and character evolution in the diverse Neotropical genus Monnina (Polygalaceae)

Alina Freire-Fierro[1,6,7,*], Felix Forest[2], José Floriano Barea Pastore[3], James W. Horn[4], Xue-Jun Ge[5]

1 Herbario UTCEC and Grupo de Investigación "Diversidad Biológica y Conservación de Ecosistemas", Universidad Técnica de Cotopaxi, Latacunga, Ecuador. 2 Royal Botanic Gardens, Kew, Richmond, UK. 3 Universidade Federal de Santa Catarina, Curitibanos, Brazil. 4 Department of Biological Sciences, Florida Gulf Coast University, Myers, USA. 5 South China Botanical Garden, Guangzhou, China. 6 Natural History Museum, Smithsonian Institution, Washington, USA. 7 Missouri Botanical Garden, St. Louis, USA.

Monnina the second largest genus of Polygalaceae, is a Neotropical group widely distributed at a geographical and altitudinal ranges. Though the genus was described over 250 years ago, molecular phylogenetic hypothesis about its origin and the evolution of its morphological features had not been investigated in depth until recently. Following Bayesian and ML analyses of nuclear ITS and plastid *trnL–F* regions comprising ~ 40% of *Monnina* species we present here the main findings: Monnina is a *monophyletic* genus with the presence of indehiscent, 1-seeded fruit as a synapomorphy. Six clades were recovered. While Clades A, B, D and E include mostly herbaceous species, members from Clades C and F are primarily shrubby. While Clades A, B, D and E include few taxa each, Clade C and Clade F are the most diverse. Clade C is distributed in the Central Andes, and Clade F is primarily distributed in the mountainous regions from the Northern Andes and Central America. The same Clades C and F include species with fleshy fruits. These two character-states, shrubby growth form and fleshy fruits are phylogenetically correlated and probably contributed towards the increase in diversification rates in Clades C and F. The newly created niches result from the uplift of the Andes and the abundance of dispersal agents might have also contributed towards the diversification of *Monnina* in the Neotropical mountains.

P.0917 DNA barcoding, phylogenetic, and morphological analysis of selected Timonius Rumph. ex DC. spp. and its related allies

Alyssa Marie A. Lola[1,2,3], Noriaki Murakami[1,2]

1 Graduate School of Science, Tokyo Metropolitan University, Tokyo, Japan. 2 Makino Herbarium, Tokyo Metropolitan University, Tokyo, Japan. 3 Plant Sciences Laboratory, University of Santo Tomas, Manila, Philippines.

Guettardeae DC. remains one of the most problematic tribes of the Rubiaceae (coffee) family. Several taxonomists argued about the true positions of its members including the genus *Timonius* and its related genera namely, *Antirhea* and *Guettarda* (Rova et al. 2002 & 2009, Achille et al. 2006, Chavez et al. 2021). *Timonius* DC. is comprised of approximately 300 species worldwide, 30 of which are endemic in the Philippines, and many stay undescribed both locally and internationally. In the present studies about the genus and its close allies, a better representation of samples from Southeast Asia, especially in the Philippines is needed. This pushed the study on *Timonius*, specifically to identify the best barcode, update the existing phylogeny, and examine the morphological characters of the collected samples. DNA barcoding revealed that *atpB-rbcL* was an ideal barcode for *Timonius* based on the sequence characteristics of each locus. More importantly, phylogenetic analysis showed that all the collected samples belong to the Paleotropical dioecious clade as supported in the study of Achille et al. 2006 and Chavez et al. 2021. Moreover, the constructed tree revealed that *Timonius* can be divided into two subclades. This was backed up with morphological data wherein the defining characters were the plant's surface, stipule shape, floral and fruit arrangement, and pyrenes (number, orientation, and filling). Additionally, the species described as *Guettarda strigillosa* grouped under the *Timonius* clade instead of the *Guettarda* clade. This suggested that *Guettarda strigillosa* must be *Timonius strigollosus.* Morphological results corroborated with molecular data also revealed the possibility of divergent *Timonius* spp., which are proposed as new to science. Overall, this study provided a wider circumscription and an update on the systematics of *Timonius* spp. and its related genera.

P.0918 A snapshot of the endemic vascular flora of Andalusia (Southern Spain)

Gloria Martínez-Sagarra[1], Juan A. Devesa[1]

1 Department of Botany, Ecology and Plant Physiology, University of Cordoba, Spain

The Mediterranean region has long been recognized as one of the world'splant biodiversity hotspots, hosting around 25,000 species of vascular plants. The floristic diversity of the Iberian Peninsula (Spain and Portugal) comprises over 6,120 species of vascular plants (6,950 taxa), 26% of which are endemic.

Andalusia (southern Spain) stands out as the autonomous community with the highest plant diversity and number of endemic species in Spain. This is a result of geological and climatic factors, as well as the high diversity of ecological environments which have facilitated multiple speciation events. Devesa & Martínez-Sagarra (2023) conducted the most recent assessment of endemic plant richness in Andalusia, providing updated information for each taxon. Building upon this study, we provided an overview of the number, taxonomic composition, and geographic representation of vascular plant endemisms in Andalusia. Thus, the number of strict endemics (i.e., not exceeding the Andalusian autonomous community boundaries) amounts to 364 species (395 taxa). This territory also hosts at least 631 Ibero-Maghrebian endemic taxa and around 537 Iberian endemic taxa. Three endemic genera have been recognized: *Hymenostemma*, *Rothmaleria* (Asteraceae), and *Gadoria* (Plantaginaceae). Regarding taxonomic composition, *Linaria*, *Centaurea*, *Teucrium*, *Armeria*, *Arenaria*and *Narcissus*are the most representative genera (more than 10 species each). The distribution of the strict endemics is highly uneven across the major geographical units in the territory, including Sierra Morena, the Guadalquivir Depression, the Cádiz-Huelva coastline, and the Baetic mountain ranges. Notably, the latter, characterized by heterogeneous orography, lithology, and altitude ranges, harbors the vast majority of strict Andalusian endemisms (around 370 taxa; almost 94% of the total), which are distributed in varying proportions across its different mountains.

P.0919 Taxonomic species turnover along elevational gradients across the Andes

Alba Martínez-Castro, Jesús Muñoz, Luis Cayuela, Manuel J. Macía, Guillermo Bañares-de Dios, Íñigo Granzow-de la Cerda, Itziar Arnelas, Carlos Iván Espinosa, Esteban Álvarez-Dávila, Gabriel Arellano, Jürgen Homeier, Selene Baez, Jaime Peña, Marijn Bauters, Miro Demol, Hans Verbeeck, Cecilia Blundo, Agustina Malizia, Lucio Malizia, Rudi Cruz, William Farfán, Yadvinder Malhi, Alex Nina, Norma Salinas, Miles Silman

1 Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos, Móstoles, Madrid, Spain. 2 Departamento de Biología, Área de Botánica, Universidad Autónoma de Madrid, Madrid, Spain. 3 Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Universidad Autónoma de Madrid, Madrid, Spain. 4 Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, USA. 5 Real Jardín Botánico – CSIC, Madrid, Spain. 7 Herbario HUTPL, Departamento de Ciencias Biológicas, Universidad Técnica Particular de Loja, Loja, Ecuador. 8 Departamento de Ciencias Biológicas, Universidad Técnica Particular de Loja, Loja, Ecuador. 9 Sección Química, Pontificia Universidad Católica del Perú, Lima, Peru. 10 ECI, School of Geography and Environment, University of Oxford, Oxfordshire, United Kingdom.

Species turnover affects diversity at large scales. In mountain forests, rapid changes in abiotic conditions across short geographical distances contribute to significant species turnover. High species turnover in tropical forests may result from narrower environmental niches. Climatic niches result from cumulative physiological adaptability to climate changes. When species share a similar range of climatic conditions, their niches overlap, often resulting in competition for resources and the evolution of differences in resource used to avoid direct competition. Along elevational gradients, climatic conditions undergo significant changes, potentially constraining the climatic niche of certain species and thus playing a crucial role in species turnover. The tropical Andes exhibit remarkable environmental heterogeneity, characterized by significant variations in elevation and humidity, as well as a complex mosaic of geology and soils. These factors, coupled with historical climate variability in the Andes, have contributed to the formation of a region characterized by vast biological diversity. Our study focuses on examining species turnover along elevational gradients across a broad latitudinal range in the tropical Andes. Specifically, we provide numerical assessments of species turnover in tropical montane forests and examine how narrow environmental niches contribute to this turnover. We conducted a large-scale comparison of nine elevation gradients in tropical montane forests across the Andes, from central Colombia to northern Argentina. We observed that elevation shifts of approximately 500 m along the elevational gradient resulted in a high turnover of species composition, close to 80%, in the areas nearest to the equator, which decreases as we move away from the equator. This is a result of the reduced niche of tropical species, for which a change in altitude represents a change they do not tolerate in climatic conditions.

P.0920 Soil organic carbon in tropical Andean ecosystems study methods and approaches: a systematic review

Víctor Alfonso Mondragón Valencia[1], Apolinar Figueroa Casas[1]

1 Doctorado en ciencias ambientales UNICAUCA

Soil is the most important carbon (C) reservoir in the terrestrial biosphere, soil organic C (COS) is the result of the balance between organic matter inputs to soils and C loss through decomposition, leaching and erosion of organic matter. the main source of organic matter is dead plant material from both above and below ground tissues. The potential of soils as carbon sinks has attracted considerable scientific attention in recent years as an alternative to mitigate warming and as a key factor for soil health, there are areas that can be strategic to achieve this goal. Like tropical Andean ecosystems with soils mostly derived from volcanic ash and important carbon reservoirs and stabilisers, due to their high organic matter content, these ecosystems have high biological, cultural and agricultural diversity. These ecosystems are altered by the high concentration of human settlements and changes in land use; Given this situation, research questions were raised in the review, a gap in knowledge about the sequestration of COS in tropical Andean ecosystems was identified and the methods and approaches for its study should be clarified, understanding that there are various techniques for the determination of C, but little is addressed from the socio-ecological systems and there is diversity of information regarding the C models, this research suggests addressing the sequestration of COS within an interdisciplinary and systemic approach. This implies the development of methodological, sociological, ecological and technological processes that allow us to understand the problem from a holistic and integrative perspective, which allows us to understand the dynamics of the communities in the territories surrounding the conservation of ecosystem services.

Note: This abstract was translated with AI.

P.0921 Partitioning variation of leaf traits across biological scales in Cantabrian Mountains grasslands

Miguel A. Ortega Moreno[1], Rocío Peña García[1], María R. Pérez Vallejo[1], Ximena Baquero González[1], José R. Obeso Suárez[1], Paola Laiolo[1]

1 Biodiversity Research Institute, University of Oviedo-CSIC-Principality of Asturias, Mieres, Spain.

Trait variability can determine the potential of populations to respond to climatic changes and there is increasing evidence on its role in maintaining the stability of population, community and ecosystem dynamics. Most research on functional diversity addresses the variation at the specific and individual scale, but few studies include the lower levels of biological organization, such as the intraindividual scale. This study focuses on the relationship among leaf trait variation across hierarchical scales, including the intraindividual scale, examining how it relates to the elevation gradient. Our objectives were: (1) to determine which biological scale best explains the variability in leaf traits (community, population, individual, intraindividual); (2) to analyze changes along the elevational gradient (population, individual, intraindividual); and (3) investigate the relationship among trait variation (population, individual, intraindividual) and species richness (community). Samplings were carried out in 23 locations across a broad range of altitude, from 40 to 2178 meters, in the Cantabrian Mountains. A total of 22 128 leaves were collected from 2 855 individuals in 342 populations of 140 herbaceous plants species. Results reveal that interspecific and intraindividual variation are both high when compared with interindividual variation. Furthermore, this relationship varies with elevation: at lower ranges, intraindividual variation is more relevant, where the harsh climate likely constrains the range of trait values that individuals can exhibit. The partitioning of variation among biological scales also depends on local species richness, showing an interaction between community scale properties and variation at lower scales. This study underscores the importance of leaf variation at low biological scales in herbaceous plants. In a context in which climatic harshness in mountains potentially declines, we may anticipate a scenario where variation at the intraindividual scale increases in significance over to the species scale.

P.0922 Plant colonization after Aneto glacier retreat: Bottom up and Top down.

Palacio Sara[1], Alvarez Aina[1], Deschamps-Berger César[1], López Alba[1], López-Moreno José Ignacio[1], Vidaller Ixeia[1], Revuelto Jesús[1], René Pierre[2], Lavergne Sebastien[2], Tejero Pablo[1].

1 Instituto Pirenaico de Ecologia-CSIC, Jaca, Spain. 2 Laboratoire d’Ecologie Alpine-CNRS, Saint-Martin d’Hères, France.

Glacier retreat allows plants to colonize new areas. In the context of global warming, this phenomenon is becoming increasingly relevant, causing changes in high mountain landscapes and dynamics. This study investigates the relationship between the retreat of Aneto glacier (3400 m.a.s.l., central Pyrenees) over the last 150 years and vegetation colonization of previously ice-covered terrain. Five zones corresponding to different thawing periods have been identified based on the analysis of archive photos from the XIXth century and more recent aerial and satellite images. Vegetation sampling was carried out to determine the species present and the vegetation composition of each retreat belt. Additionally, basic functional traits of the species found were collected to perform a functional analysis of the colonization process. High-resolution drone images were also acquired to evaluate the representativeness of the sampling areas. There was a gradual reduction in plant diversity towards recently melted areas. However, looking at species composition, we observed evidence of bidirectional colonization in this terrain, from the ridges downwards (upper margin) and from the lower margins upwards in the alpine/subalpine belt. Additionally, we noticed that the floristic composition was more similar in the most advanced stages of succession than it is in the recently thawed areas. Finally, the study of functional traits helps to understand the colonization capacity of the species that have occupied this previously ice-covered area over the last 150 years. The results have two important implications, i) they prove the existence of nunataks in the central Pyrenees highlighting their role in postglacial colonization and ii) demonstrate the significant differences in the rate of colonization and origin of the species that have occupied the space released by the ice. Future work that integrates topographic, edaphic and genomic variables will contribute to a better understanding of the processes of periglacial colonization.

P.0923 Plant agro-biodiversity can be resource for the sustainable development of mountain areas: the case of “Copafam” landrace (Phaseolus coccineus L.)

Davide Pedrali [1], Luca Giupponi [1], Annamaria Giorgi [1]

1 Researcher Centre of Applied Studies for the Sustainable Management and Protection of Mountain Areas, University of Milan, Edolo, Italy.

Nowadays about 80% of global plant-biodiversity has been lost. Landraces are dynamic populations of plants that had not a crop improvement but rather they have adapted by evolving with the environment. Hilly and mountain areas of Italy are rich in plant biodiversity but many of these traditional cultivars are little or no characterized. The “Copafam” is a variety of runner bean *(Phaseolus coccineus* L.) that can be grown only in the mountains and it is now at risk of extinction. The main objective of this work was the characterization and enhancement of “Copafam” to evaluate its possible input as a raw material for the creation of innovative and functional products. The phytochemical and nutritional characteristics of “Copafam” was explored. Moreover, a sensory evaluation of model food formulation (biscuits) made by this landrace was assessed using a citizen science approach. The results show that the "Copafam" bean had a high dietary fiber and protein content (34.83 ± 2.48 g/100 and 21.93 ± 0.41 g/100 g dw) and it resulted in a great source of secondary metabolites as polyphenols (121.36 ± 5.31 mg GAE/g dw), flavonoids (6.51 ± 0.17 mg/kg dw), and anthocyanins (28.11 ± 0.16 mg Cy3 G/kg dw), having remarkable antioxidant activity too (76.42 ± 1.27 %). Biscuits made from "Copafam" flour were considered acceptable by consumers and were characterized by a darker colour, and crunchy texture. Considering the increasingly important impacts of climate change and the fast changes of the socio-economic contexts, landraces are becoming even more important. The high amount of functional molecules found in "Copafam" could represent innovative forms of consumption such as fortified foods to enhance products for human health. This research showed that the result of evolution can represent a valuable resource to preserve plant biodiversity and promote the sustainable development of mountain areas.

P.0924 Phylogenomics and biogeography of the arctic-alpine genus Androsace (Primulaceae)

Chuan Peng[1,2], Chihchieh Yu[1], Yaowu Xing[1,3], Sébastien Lavergne[4]

1 CAS Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Yunnan, China. 2 University of Chinese Academy of Sciences, Beijing, China. 3 Center of Plant Ecology, Core Botanical Gardens, Chinese Academy of Sciences, Mengla, Yunnan, China. 4 Laboratoire d'Ecologie Alpine, CNRS - Université Grenoble Alpes, Grenoble, France.

This work focuses on the *Androsace* genus (Primulaceae), which is largely distributed throughout the arctic and alpine regions of the Northern Hemisphere. Based on well-improved species sampling, especially for Asian species (103 species, ~160 globally), we constructed a highly supported maximum likelihood phylogenetic tree using chloroplast and nuclear genes. Our results confirm the inclusion of formerly known genera *Pomatosace Douglasia* and *Vitaliana* into *Androsace*. We show that the genome size of *Androsace* s. l. ranges from 0.5G to 7G, with high-elevation species having larger genomes and more repetitive sequences. More generally, our phylogeny provides novel insights into the biogeographic history of the genus, with repeated migrations between Asian, European, and North-American mountains. It also unravels important patterns of concerted life-history and habitat evolution.

P.0925 Exploring the last stand: Plant diversity, and conservation in Cagayan's Wangag watershed forest reserve, Philippines

Adriane B. Tobias[1,2,3], Arthur Glenn A. Umali[1,3*], Gerald T. Eduarte[3,4], Pastor L. Malabrigo, Jr. [1,3,5,6]

1 Department of Forest Biological Sciences, College of Forestry and Natural Resources, University of the Philippines, Los Baños, Philippines. 2 Graduate School, University of the Philippines, Los Baños, Philippines. 3 Pro-Seeds Development Association, Incorporated 4 Institute of Renewable Natural Resources, College of Forestry and Natural Resources, University of the Philippines, Los Baños, Philippines. 5 Museum of Natural History, University of the Philippines, Los Baños, Philippines. 6 Land Grant Management Office, Office of the Vice Chancellor for Planning and Development, University of the Philippines, Los Baños, Philippines.

This paper examines the transformative impact of a century of land use changes on the lowland primary forests of the Philippines, with a specific focus on the Wangag Watershed Forest Reserve (WWFR) in Cagayan. Spanning 6,992 hectares, the WWFR serves as a crucial refuge for lowland dipterocarp forests, facing imminent depletion. Our research employs a meticulous plant diversity assessment methodology, utilizing nine strategically placed quadrats along a 2-kilometer transect to document trees and understorey plants. Complementing this, a 2-hectare permanent biodiversity monitoring area (PBMA) facilitates ongoing research initiatives. Results underscore the rich biodiversity within the WWFR, with 122 morpho-species identified through systematic sampling and an additional 174 morpho-species through opportunistic sampling. The PBMA stands out for its prevalence of premium timber species, such as *Dipterocarpus gracilis* and *Shorea polysperma*, with Tanguile (*S. polysperma*) emerging as a dominant species. Notably, the PBMA records 7,067 trees per hectare, revealing a dense and diverse tree population, while also documenting five endemic species and 11 threatened plants, though large-sized threatened trees are notably scarce. A comparative analysis with a 2-kilometer transect highlights a mod-

erate level of plant diversity within the WWFR-PBMA. To bolster conservation efforts, we introduce a geodatabase and interactive map storing essential baseline data accessible through ArcGIS software. This research endeavors to contribute significantly to the understanding and preservation of Cagayan's critical lowland dipterocarp forests, providing valuable insights for sustainable management and conservation practices.

P.0926 The diversity of lichen flora at the National Park of Mount Merbabu, Central Java, Indonesia

Ludmilla Fitri Untari*[1], Kristina Dewi[2], Japareng Lulang[3], Ari S. Nugraha[4]

*1 The Plant Systematics Laboratory, Department of Tropical Biology, Faculty of Biology, Universitas Gadjah Mada, Yogyakarta, Indonesia. 2 The National Park of Mount Merbabu, Jawa Tengah, Indonesia. 3 School of Industrial Technology, Universiti Sains Malaysia, Pulau Pinang, Malaysia. 4 The Faculty of Pharmacy, University of Jember, Krajan Timur, Sumbersari, Jawa Timur, Indonesia. * ludmilla.untari@ugm.ac.id.*

Lichens are symbiotic organisms between algae (the phycobionts) and fungi (the mycobionts). Algae provide chlorophyll for photosynthesis, while fungi provide a supply of minerals and water from their environment, protection from desiccation, and reproduction. This symbiotic relationship tends to increase the ability of both organisms to adapt to different environmental conditions, due to the structure of the thallus, the physiology, and the specific chemical compounds. The objective of this research is to study the diversity of lichen species in Mt. Merbabu National Park (TNGMb). This study was conducted between December 2022 and December 2023 using a purposive sampling technique. Species identification was based on morphological, anatomical, and chemical characteristics. Several environmental parameters were also measured: pH, humidity, air temperature, rainfall, and altitude. A total of 36 species were identified from Mt. Merbabu National Park (TNGMb) and grouped into fifteen families, i.e. twenty species of foliose –squamulose lichens consisting of five families i.e. *Pannariaceae* (one species), *Parmeliaceae* (thirteen species), *Peltigeraceae* (one species), *Physciaceae* (three species), and *Verrucariaceae* (two species); ten species of crustose lichens consisting of eight families i.e. *Arthoniaceae* (one species), *Caliciaceae* (one species), *Fuscideaceae* (one species), *Graphidaceae* (one species), *Lecanoraceae* (one species), *Ochrolechiaceae* (two species), *Pertusariaceae* (two species), and *Phyctidaceae* (one species); and six species of fruticose lichens belonging to three families, namely *Parmeliaceae* (three species), *Ramalinaceae* (two species), and *Sphaerophoraceae* (one species). The measurement of the diversity index using the Shannon-Weiner is that the diversity index is 3.30 (high) with details of foliose lichens of 2,789 (moderate), crustose lichens of 2,064 (moderate) and fruticose lichens of 1,643 (moderate). Species descriptions and key species identification are presented in this article.

S.104. MTZ FLORAS, A WARNING LIGHT OF GLOBAL CONSERVATION FUTURE

P.0927 Bridging the gap: recent advances in extinction risk assessment and plant biodiversity conservation in Greece

Panayotis Dimopoulos[1], Georgia Fassou[1]*, Konstantinos Kougioumoutzis[1], Ioannis Bazos[2], Maria Panitsa[1], Panayiotis Trigas[3], Ioannis Tsiripidis[4]

*1 Laboratory of Botany, Department of Biology, Division of Plant Biology, University of Patras, Patras, Greece. 2 Department of Biology, National and Kapodistrian University of Athens, Athens, Greece, *gfassou@ac.upatras.gr. 3 Laboratory of Systematic Botany, Department of Crop Science, Agricultural University of Athens, Athens, Greece. 4 Department of Botany, School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece.*

Greece ranks among the most biodiverse countries in Europe, hosting ca. 6,900 vascular plant taxa, 21% of which are endemic. Despite this rich plant diversity, no attempt has been made until recently to assess the extinction risk of the total or major part of its vascular flora based on the IUCN criteria. The previously published

Greek Red List Books (1995 & 2009) cover assessments for only 466 plant taxa. However, these evaluations were either not conducted in accordance with the current IUCN criteria or are now considered outdated, as more than ten years have elapsed since the last red book was published. Recently, 54 experts from both Greece and abroad, under the coordination of the Hellenic Botanical Society and the support of IUCN, conducted an assessment of the extinction risk for the vast majority of vascular plant taxa in Greece, applying current IUCN criteria and methodology, as part of the project "Compilation of Red Lists of Threatened Species of Plants, Animals and Fungi of Greece", funded by Natural Environment & Climate Change Agency (N.E.C.C.A.). This comprehensive assessment has revealed that nearly 40% of the assessed endemic and 12% of the assessed non-endemic species fall under a threatened category. Consequently, we are now able to identify specific regions acting as biodiversity hotspots for threatened plant taxa and prioritize them accordingly. Furthermore, this work enables the assessment of the effectiveness of Greece's established network of protected areas in covering and safeguarding these critical regions through gap analysis. Our findings underscore these pivotal areas, and this expert-led, collaborative effort establishes a fundamental baseline for future conservation research. It also serves as a foundation for the preservation of ecosystem services and could prove instrumental in the timely, systematic, and effective prevention of plant extinctions in Greece.

P.0929 Conservation status of halophyte species in the Community of Madrid

Laura Tartilán García[1], Juan Manuel Martínez Labarga[2], José Araújo Díaz de Terán[3], Juan Carlos Moreno Saiz[1,4]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Universidad Politécnica de Madrid, Madrid, Spain. 3 Corps of Forestry Agents of the Community of Madrid, Spain. 4 Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Madrid, Spain.

Plant communities associated with endorheic wetlands and saline substrates in the interior of the Iberian Peninsula are of great biogeographical and conservation interest, as they harbor species with notable disjunctions and reduced populations. Many of these areas are part of the European network of protected areas Natura 2000. In the Community of Madrid, they are located to the south and southeast of the territory, in areas dedicated to extensive agriculture and livestock farming, but in recent years have seen the installation of industrial uses, landfills, etc. The plants of such salt marshes have not been thoroughly studied in Madrid, and there are hardly any examples of protected halophytic species in the region. With the aim of improving their knowledge, we set out to assess the conservation status of species that are very rare in the region, whose level of risk has not been evaluated at least recently, and which serve as indicators of both changes in land use and climate change. All of them are species with very narrow ranges in Madrid, with one or very few populations sometimes recently discovered: *Arthrocaulon macrostachyum* (Moric.) Piirainen & G. Kadereit (Amaranthaceae), *Cressa cretica* L. (Convolvulaceae), Frankenia laevis L. (Frankeniaceae), and Limonium latebracteatum Erben (Plumbaginaceae). During 2023 and 2024, we conducted field studies to census their populations, map their locations, and determine the pressures and threats looming over the plants and their habitats. With this information, we were able to classify the species according to the IUCN criteria and assign the most appropriate regional risk category. We also managed to propose the most suitable measures for in situ and ex situ conservation of these plants, as well as suggesting general management strategies for the halophytic communities in central Iberia, which have been experiencing habitat degradation while undergoing periods of increasing drought and desiccation.

P.0930 Forest management and conservation of Pinus sylvestris forests in Sierra de Guadarrama

Sandra Navas Sastre[1], Rut Sánchez de Dios[1], Felipe Domínguez Lozano[1], Laura Hernández Mateo[2], Fernando Montes Pita[2]

1 Faculty of Biological Sciences, Complutense University of Madrid, Madrid, Spain. 2 CSIC-INIA, Spain

Scots pine forests (*Pinus sylvestris*) constitute the most emblematic tree formation in the Sierra de Guadarrama. They also have high biogeographical value. These forests have been subject to various types of management since ancient times, and some of them have been included in the Sierra de Guadarrama National Park. In recent times, there has been a great interest in developing management approaches that simultaneously support biodiversity, production, and optimize the benefits of climate mitigation. However, the direct and indirect effects that forest management has on biodiversity are not yet fully understood. Thus, our objective is to assess the effects that forest management has had on understorey plant biodiversity of these pine forests between two locations with different silvicultural treatments. Taxonomic, functional and phylogenetic diversity have been compared using multivariate statistical techniques. Our results show significant differences between pine forests subjected to more intensive management versus those managed with techniques that generate homogeneous stands. The latter forests are more diverse and maintain a higher conservation value. In a global change context, where the southern populations of *Pinus sylvestris* hold significant biogeographical value, our findings underscore the importance of management strategies focused on the conservation of species and communities.

P.0928 Rewilding urban ecosystems with native seeds

Zuzana Ferencova[1], Clara Espinosa del Alba[2], Víctor González-García[2], Sara Gutiérrez-Cruz[3], Borja Jiménez-Alfaro[2], Eduardo Fernández-Pascual[2]

1 Atlantic Botanic Garden of Gijón, Spain. 2 IMIB Biodiversity Research Institute (University of Oviedo – CSIC – Principality of Asturias), University of Oviedo, Mieres, Spain. 3 City Council of Gijón, Spain.

In urban environments, spontaneous flora mainly occurs within human-designed green areas, in abandoned lots or as remnants of pre-urban vegetation. These ecosystems are highly disturbed by mowing, trampling or nutrient deposition, leading to reduced native biodiversity and limited ecosystem services. In recent years, there has been a growing emphasis on ecological restoration and urban rewilding within cities, intending to establish self-sustaining and resilient urban ecosystems. Native seed mixes can be used to restore the taxonomical, structural and functional diversity of urban green spaces, but their supply depends on previous knowledge of urban floras and their seed biology. Here we present a streamlined workflow to design a native seed mix for the city of Gijón/Xixón (Spain). We conducted a floristic survey of spontaneous vegetation in seven urban habitats with different levels of anthropogenic disturbance: forest remnants, meadows, city parks, abandoned residential lots, abandoned industrial lots, margins of traffic corridors and pavement cracks. The survey identified 240 species of vascular plants growing spontaneously in the city. Of these, we selected 60 native species that occurred with high frequency, assuming their adaptation to urban conditions. For these species, we measured functional traits (plant height, specific leaf area, seed mass, seed production, seed dispersal), phenological traits, germination requirements and ecosystem services/disservices (pollination and allergenic potential). We used these criteria to select 29 species with the highest potential for restoration of biodiversity and ecosystem services. We also conducted a public opinion survey to determine citizen perception of these plants and used this information to select a final mix of 15 species to produce and test in restored urban lots. This seed mix is being used for rewilding actions of the project “Gijón Ecoresiliente”, supported by the Biodiversity Foundation of MITECO within the framework of the Recovery, Transformation and Resilience Plan (PRTR) - European Union -NextGenerationEU.

P.0931 Iberian flora on the EDGE: prioritizing the conservation of Evolutionarily Distinct and Globally Endangered plants

Ana Otero[1], Antoni Buira[2], Ignacio Ramos[1, 3], Lisa Pokorny[2], Carmen Acedo[4], Llorenç Sáez[5], Santiago Martín Bravo[6], Irene Villa-Machío[7], Tamara Villaverde[8], Virginia Valcárcel[1], Félix Forest[9], Rafael Molina-Venegas[1, 3], Juan Carlos Moreno Saiz[1, 3], Pedro Jiménez-Mejías[6], Mario Fernández-Mazuecos[1, 3]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Real Jardín Botánico, CSIC, Madrid, Spain. 3 Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Madrid, Spain. 4 Universidad de León, León, Spain. 5 Universitat Autònoma de Barcelona, Bellaterra, Spain. 6 Universidad Pablo de Olavide, Sevilla, Spain. 7 Missouri Botanical Garden, St. Louis, USA. 8 Universidad Rey Juan Carlos, Madrid, Spain. 9 Royal Botanic Gardens, Kew, Richmond, UK.

Almost 20% of Iberian vascular plants are considered threatened under IUCN categories CR, EN or VU. Unfortunately, limited economic resources entail the need to prioritize conservation actions. Most regional Red Lists follow IUCN categories and criteria, mainly based on population size, area of occupancy and extent of occurrence. Although these parameters are appropriate to evaluate threat status, it is also crucial to explore the evolutionary legacy of taxa to prioritize their evolutionary singularity and thus, ensure its long-term preservation. This can also help adapt management actions to protect genomic and evolutionary peculiarities. The Evolutionarily Distinct and Globally Endangered (EDGE) metric integrates two components: evolutionary distinctiveness (ED), based on phylogenetic branch lengths, and global endangerment (GE), representing extinction risk derived from IUCN categories. Recently, the EDGE metric has been updated (EDGE2) to incorporate uncertainty in both components and consider the extinction risk of closely related taxa. Under this framework, we aim to calculate regional-level EDGE scores for all endemic and threatened vascular plants from mainland Spain and the Balearic Island. Our workflow is divided into three main steps involving the collaboration of main Spanish herbaria (MA, LEB, UPOS, among others) and academic institutions: (1) to elaborate the list of target species based on the *Atlas of the Vascular Flora of the Iberian Peninsula* (AFLIBER), the Red List of the Spanish Vascular Flora, and the latest taxonomic updates; (2) to reconstruct a large phylogenetic tree representing more than 70% of the ~6.5K taxa (species and subspecies) found in the Iberian vascular flora, including nearly all threatened taxa (~1K), using a combination of genomic Hyb-Seq data at the genus level (~1K genera), and Sanger sequencing data at species level (~5K taxa); and (3) to calculate EDGE scores, thus implementing the evolutionary history in the prioritization of conservation efforts for Iberian Spanish vascular plants.

P.0932 Biogeographical urban homogenization and the role of green spaces connectivity in the city

Roberto Zeferino Leandro[1], Felipe Dominguez Lozano[1], Aitor Gaston Gonzalez[2], Miguel Berdugo Vera[1]

1 Facultad de Ciencias Biológicas, Universidad Complutense de Madrid, Madrid, Spain. 2 Escuela Técnica Superior de Ingeniería de Montes, Forestal y del Medio Natural, Madrid, Spain.

Biotic homogenization is closely linked to non-native species, which are more likely to establish themselves in urban habitats. However, native species may also play a significant role in the homogenization of urban habitats. The high dynamism and anthropogenic disturbances of urban habitats contribute to the high turnover of both native and non-native species, favoring plants better adapted to these conditions. These “urban exploiters” gradually displace other types of flora, promoting greater urban homogenization. Little is known about how this homogenization could affect biogeographical patterns or the distribution of less common flora. Urban connectivity could be key in determining the potential effects of this homogenization. Traditionally, increased connectivity has been considered a positive factor for biodiversity, but considering homogenization, it could play a negative role. In urban environments, connectivity depends not only on natural factors but also on anthropogenic ones, which amplifies its effects. Madrid is a medium-sized European city located between two distinct biogeographical regions with a barrier separating two different soil floras. This city has an extensive system of parks and urban green areas, as well as a comprehensive inventory of urban flora. For these reasons, Madrid is the ideal study area to test several hypotheses related to homogenization, the origin of urban biotas, biogeographical barriers, and connectivity. Our main objective is to determine if biogeographical homogenization has been occurring in an urban environment, and if so, to what extent and for which group of flora. Another objective is to see if urban connectivity promotes the reduction of biogeographical barriers and the relationship between homogenization and connectivity in urban environments.

S.105. NATURAL HYBRIDIZATION AND SPECIES CONSERVATION.

P.0933 Hybridisation breaking the ploidy barrier: new insights into historically overlooked interploidy hybridisation

Elizabeth Davies[1,2], Peter Hollingsworth[2], Alex Twyford[1,2]

1 Institute of Ecology and Evolution, University of Edinburgh, Edinburgh, UK. 2 Royal Botanic Gardens Edinburgh, Edinburgh, UK.

Whole genome duplication, otherwise known as polyploidy, is a mutation underlying much of the biodiversity that spans the tree of life. Present in plants, animals, fungi, and prokaryotes, polyploidy increases the adaptive potential of organisms exposed to stressful conditions due to increased genetic variation. Whole genome duplication is also a major force of speciation, as a difference in chromosomal copies usually confers a strong and instantaneous barrier to reproduction. However, recent research has uncovered instances of hybridisation and introgression between species of different ploidies, despite this assumed reproductive barrier. This raises many questions as to the strength of ploidy differences in preventing hybridisation and to the role interploidy hybridisation may have played in the evolution of species diversity. As research increasingly shows interploidy hybridisation to be an underestimated evolutionary process, our research investigates the interaction between hybridisation and ploidy across a broad time scale. Using population sampling and whole genome sequencing in the species rich genus *Euphrasia* (eyebright), we investigate how hybridisation leads to the establishment of polyploid species, how new species arise through previously overlooked interploidy hybridisation, and how species of different ploidies hybridise in natural, cross-ploidy zones. Our research expands our understanding of this overlooked process by investigating how recurrent interploidy hybridisation affects plant evolution and diversity.

P.0934 Hybrid breakdown in natural interspecific hybrids in the Dimorphandra genus

Aldineia Buss[1]; André C. Muniz[2], Tiago Vilas-Boas[1]; Alexandre A Duarte[1], Maria B. Lovato[2]; José P. de Lemos Filho[1]

1 Departamento de Botânica, Universidade Federal de Minas Gerais, Minas Gerais, Brazil. 2 Departamento de Genética, Ecologia e Evolução, Universidade Federal de Minas Gerais, Minas Gerais, Brazil.

Estimates of hybrid fitness contribute to knowledge about the role of natural hybridization in the evolutionary trajectory of species, including reproductive isolation, adaptive trait introgression, and hybrid speciation. In the ecotonal area between the Brazilian savanna (Cerrado) and the Atlantic Forest three *Dimorphandra* tree species are found, *D. mollis*, *D. exaltata,* and *D. wilsonii*. This last taxon was recently identified as a population of inter-specific hybrids between *D. mollis* and *D. exaltata*. In this hybrid zone are found mainly F1 hybrids, with a few hybrids of later generations. To examine the occurrence of putative heterosis and hybrid breakdown in this hybrid zone, we evaluate the fitness of the parental species, and their F1 and backcross hybrids, by comparing biometric data of fruits and seed traits, and evaluating seed germination at different temperatures. We found the occurrence of heterosis, since the fruits of F_1 hybrids compared to their parents were almost a third larger, contained more seeds, and their seeds were heavier. The putative parental species showed different germination responses to temperatures. The F1 hybrid, in general, showed intermediate germination performance to *D. mollis* and *D. exaltata*, for both, the maximum percentage achieved and the amplitude of the germination range. Compared to parental species and F1, the backcrossed hybrids showed a loss of vigor in fruit traits, seed production, and germination fitness, consistent with hybrid breakdown. Our results suggest that heterosis for fruit traits may be a factor that promotes the establishment of F1 hybrid plants in the field. Introgression can be an important factor for the increase of genetic diversity in the parental species, mainly the threatened *D. exaltata,* although the hybrid breakdown represents an important barrier to gene flow.

P.0935 Development of male and female gametophytes of a neotropical orchid hybrid: permeability of postzygotic reproductive barriers

Mariana Ferreira Alves[1], Fábio Pinheiro[2], Karen Lúcia Gama De Toni[1], José Fernando Andrade Baumgratz[1]

1 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brzsil. 2. Universidade Estadual de Campinas, São Paulo, Brazil.

The study of hybrid zones presents a unique opportunity to obtain information about reproductive barriers and the mechanisms involved during plant speciation. In this study, we investigated the mechanisms of postzygotic reproductive isolation in the natural hybrid *Epidendrum* x *purpureum*, which occurs in sympatry with *Epidendrum denticulatum* and *Epidendrum orchidiflorum*, the parental species. To investigate the pollen viability of hybrid specimens, floral buds and flowers at anthesis were collected. To analyze the development of the megagametophyte, self-pollination was carried out on first day flowers. Fruits were collected10 to 40 days after pollination. Flowers and fruits were processed following the usual methodology for performing light anatomy and confocal microscopy. The results indicate that most microgametophytes develop regularly, but in the same pollinia, non-viable microgametophytes are also observed. Inviable microgametophytes are result of a symmetrical mitotic division, which produces a microgametophyte with two identical cells. Occasionally, microgametophytes have been observed with only the formation of cell walls without any cytoplasmic content. The development of the megagametophyte occurs about 15 days after the self-pollination process. The megagametophytes undergo regular meiosis and mitosis, forming a mature megagametophyte of the *Polygonum* type. Eventually, up to four megagametophytes may be observed developing in the same ovule. At the end of development, it is possible to see ovules with two mature megagametophytes presenting two egg cells. Our results show that the development of microgametophytes and megagametophytes can be abnormal, suggesting incomplete post-zygotic reproductive isolation, with *E.* x *purpureum* showing partial fertility.

P.0936 Genomic introgression, local adaptation, and climate-induced vulnerability of two closely related pine species in SEA

Jie Gao[1], Wei Zhao[2], Kyle W. Tomlinson[2], Jing-Fang Guo[4], Zheng-ren Zhang[1], Yao-wu Xing[1], Xiao-Ru Wang[3]

1 Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Menglun, Yunnan, China. 2 Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Menglun, Yunnan, China. 3 Department of Ecology and Environmental Science, Umeå University, Umeå, Sweden. 4 Beijing Forestry University, Beijing, China.

Understanding how adaptive introgression and local adaptation influence climate change resilience is vital for conserving forest trees. Here, we aim to infer the historical divergence and genomic introgression patterns of *Pinus kesiya*, a tropical pine species across Southeast Asia that has received limited attention thus far, and its closely related species, *P. yunnanensis*, in subtropical China. Moreover, we endeavor to identify specific genomic variations that potentially facilitate local adaptations, thereby enabling us to predict the extent of their adaptive vulnerability under impending climate changes. We conducted genotyping by sequencing, identifying 20,037 SNPs from 357 individuals across 42 sites. Our analysis unveiled a 15.5 Myr evolutionary history marked by continuous gene flow and a broad hybrid zone in southern Yunnan. Through Bayesian genomic cline analysis, we identified 1664 loci displaying exceptional patterns of introgression, indicating their potential roles in either adaptive introgression or reproductive isolation. Additionally, we detected 628 and 900 SNPs associated with climate variation in *P. kesiya* and *P. yunnanensis*, respectively. Subsequently, we employed nonlinear multivariate Gradient Forest modeling to map turnover in allele frequencies along environmental gradients and predict areas most sensitive to climate change. Our predictions highlighted areas where future populations of *P. kesiya* in the contact zone and marginal populations of *P. yunnanensis* might be at risk under climate change. Our study sheds light on the genomic differentiation, historical divergence, and asymmetric introgression between *P. kesiya* and

P. yunnanensis, contributing to our understanding of their evolutionary dynamics and adaptation processes. Furthermore, our study underscores the importance of integrating genomic, environmental data, and transplanting experiments, to predict the adaptive capacity of key forest species in the face of rapid climate change in the future.

P.0937 Plathymenia trees in the Cerrado and Atlantic Forest are threatened by the high risk of non-adaptedness and ecological vulnerability to climate change

André C. Muniz[1], José P. Lemos-Filho[2], Maria B. Lovato[1]

1 Departamento de Genética, Ecologia e Evolução, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil. 2 Departamento de Botânica, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

The response capacity of a species to climate change can be evaluated by the usage of the projection of ecological niche models and through the evaluation of the risk of non-adaptedness (RONA) using genomic data. The main goal of this work was to evaluate the ecological and genomic vulnerability of *Plathymenia reticulata*, a species from the Cerrado, a neotropical savanna, and *P. foliolosa*, from the Brazilian Atlantic Forest, to determine their ability to cope with climate change. The current and future habitat suitability and the genetic changes needed to adapt to climate changes were predicted for both species. The habitat suitability was predicted using species distribution model algorithms implemented in the BIOMOD2 package using records from the GBIF database and bioclimatic data from Worldclim as predictors. The RONA was evaluated using 45 individuals from nine populations of *P. reticulata* and 24 individuals from six populations of *P. foliolosa* using polymorphism of single nucleotide obtained with the ddRad sequence protocol. The distribution of both species will greatly decrease in the period 2080-2100 according to the future projections, even in the less pessimistic models. *P. reticulata* and *P. foliolosa* populations are adapted to different climates based on the redundancy analysis with genomic data. Based on the genomic offsets of the adaptive loci, a mismatch between local adaptations to the current and the future climate is predicted for both species. In addition, *P. reticulata* showed a higher RONA than *P. foliolosa*. We suggest the reevaluation of the two *Plathymenia* species in the IUCN red lists. This should consider the genomic and ecological vulnerability of the two species for the elaboration of conservation strategies and management.

P.0938 The hybrid hypothesis of the Santolina rosmarinifolia aggregate in the Iberian plateau revisited

Miguel Serrano[1], Lucía Pérez-Pardal[2,3,4], Roi Carballal[5], Santiago Ortiz[1], Celestino Quintela-Sabarís[6], Sofia Duarte-Coimbra[2,3,4], Albano Beja-Pereira[2,3,7]

1 Department of Botany. University of Santiago de Compostela, Santiago de Compostela, Spain. 2 Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Universidade do Porto, Porto, Portugal. 3 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, Campus de Vairão, Vairão, Portugal. 4 Faculdade de Ciências, Universidade do Porto, Porto, Portugal. 5 Consellería de Medio Ambiente, Xunta de Galicia, Santiago de Compostela, Spain. 6 Grupo de Ecoloxía Animal, Universidade de Vigo, Vigo, Spain. 7. DGAOT, Faculdade de Ciências, Universidade do Porto, Porto, Portugal.

Despite the propensity of plants to hybridise, the detection of well-defined hybrid zones has been proved a relatively elusive task. The present work addresses this aspect in the genus *Santolina* (Asteraceae), specifically within the so-called S. *rosmarinifolia* aggregate in NW and Central Iberia. A hybrid hypothesis has been explicitly proposed for this species aggregate, a process that would have taken place on the northern Iberian plateau. Thus, between two species, *Santolina semidentata* in the Northwest and *S. rosmarinifolia* in the Centre-East, there would be a presumably hybridogenetic taxon that would bring together a series of traits of both species. This phenotype has been described as *S. rosmarinifolia* subs. *castellana*, although its morphological heterogeneity in different populations could suggest that it is not fully stabilized. We used ddRADseq sequencing approach to characterize the population structure and to determine the presence of a hybrid zone, trying to detect either clines or genomic mosaics along the ranges of the taxa. Overall, the "*castellana*" phenotypes are recovered within the variability of *S. rosmarinifolia*, and there is no clear evidence of a cline pointing to a well-defined hybrid zone between the core ranges of *S. semidentata* or *S. rosmarinifolia*. We detect signatures of hybridisation, which would have been bidirectional, but which mainly affect populations at the edge of the area, even in territories without nearby populations of the other species. In fact, the tree structure inferred by Treemix analyses suggests that gene flow has occurred at different historical moments, so that the traces of introgression of *S. rosmarinifolia* into *S. semidentata* populations would respond to older events than vice versa. This is supported by introgression in areas without current proximity or overlap in distributions. Past historical biogeographical processes appear to have shaped the hybrid genomic variability in the group.

P.0939 The maintenance of ecological divergence in hybrid zones involving widely distributed and narrowly endemic species: the case of two petunias

Silva-Arias GA[1,2], Caballero-Villalobos L[3,4], Turchetto C[4,5], Giudicelli GC[4], Bombarely A.[6], Freitas LB[4]

1 Instituto de Ciencias Naturales, Facultad de Ciencias, Universidad Nacional de Colombia, Colombia. 2 Population Genetics, Department of Life Science Systems, School of Life Sciences, Technical University of Munich, Germany. 3 Subdirección Ecosistemas, Instituto de Hidrología, Meteorología y Estudios Ambientales, Bogotá, Colombia. 4 Laboratory of Molecular Evolution, Department of Genetics, Universidade Federal do Rio Grande do Sul, Brazil. 5 Department of Botany, Universidade Federal do Rio Grande do Sul, Brazil. 6 Instituto de Biología Molecular y Celular de Plantas, CSIC and Universitat Politécnica de Valencia, Spain.

Hybrid systems provide valuable insights into the evolutionary forces driving species divergence. An intriguing hybrid model in the Brazilian Pampa region involves two sympatric and recently diverged *Petunia* species with distinct ecological preferences, suggesting an ecological speciation scenario. This system has been a well-studied model of pollinator shift due to the evolution of tightly linked genes related to floral pigmentation, which led to the development of highly distinctive floral morphologies and a pronounced differential pollinator preference. Additional studies also indicate post-zygotic barriers linked to hybrid necrosis involving genes physically linked to the pigmentation genes. However, the permanent presence of hybrid individuals in nature leaves the question of how species integrity is upheld in this system unanswered. Adding to the intrigue is the persistent asymmetric gene flow toward the narrowly endemic species *P. exserta*, as consistently disclosed by numerous demographic reconstructions. We investigated the influence of demographic and selective factors in two contact zones between *P. exserta* and *P. axillaris* using GBS genomic scanning. Our results highlight the significant impact of selfing on shaping the genetic diversity of populations in the contact zones. Consequently, genetic drift likely plays a crucial role in maintaining species divergence despite ongoing gene flow. Furthermore, high differentiation patterns in auxin transport-related genes introduce an additional factor linked to habitat preference that may have initiated the divergence between these species.

P.0940 Understanding hybrid origins: integrative taxonomy of Stipa in Central Asian mountains

Patar Sinaga[1,2], Ewelina Klichowska[1], Arkadiusz Nowak[3,4], Marcin Nobis[1]

1 Institute of Botany, Faculty of Biology, Jagiellonian University, Kraków, Poland. 2 Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland. 3 Polish Academy of Sciences Botanical Garden – Center for Biological Diversity Conservation in Powsin, Warszawa, Poland. 4 Botanical Garden of the Wrocław University, Wrocław, Poland.

Plant families frequently undergo hybridization, which increases genetic diversity but can also result in genetic swamping and lower fitness. One of the genera that has over 30% of its species derived from hybridization is *Stipa* (Poaceae), which is found in warm temperate areas of Europe, Asia, and North Africa. We examined hybridization and introgression using an integrative taxonomy approach based on Central Asian *Stipa* samples. The results of this study contribute to a better knowledge of hybridization in the *Stipa* genus, particularly in the sect. *Smirnovia*. Based on SNP markers and morphological characters, we were able to identify two novel nothospecies: *S. lingua* × *S. caucasica* subsp. *nikolai* and *S. magnifica* × *S. caucasica* subsp. *nikolai*. The majority of *S. magnifica* × *S. caucasica* samples were backcross hybrids; however, all *S. lingua* × *S. caucasica* samples showed signs of being F1 hybrids according to

SNP markers. Ultimately, by illuminating the complex hybridization dynamics and bringing attention to the evolutionary processes that occur within this diverse genus, this work advances our knowledge of the taxonomy of *Stipa*.

P.0941 Genetic diversity of Pyrus pyraster and P. spinosa based on SSR markers: evidence of gene flow from cultivated to wild populations

Antonio Vidaković[1], Zlatko Šatović[2,3], Zlatko Liber[4], Igor Poljak[1]

1 Faculty of Forestry and Wood Technology, University of Zagreb, Zagreb, Croatia. 2 Faculty of Agriculture, University of Zagreb, Zagreb, Croatia. 3 Centre of Excellence for Biodiversity and Molecular Plant Breeding, Zagreb, Croatia. 4 Faculty of Science, University of Zagreb, Zagreb, Croatia.

Southern Europe is home to two naturally occurring pear species: the European wild pear (*Pyrus pyraster* (L.) Burgsd.) in the continental and the almond-leaved pear (*P. spinosa* Forssk.) in the Mediterranean region. In addition to these two species, the cultivated pear (*P. communis* L.) is also grown throughout Europe. Since wild pears grow in the vicinity of orchards, gene flow between the cultivated species and their wild relatives is to be expected. The aim of this study was to determine the genetic diversity of natural populations and whether gene flow from the cultivated pear can alter the genetic composition of wild pear populations in close proximity. We collected samples from 21 populations of European wild pear and 22 populations of almond-leaved pear as well as of cultivated pears from three orchards. DNA fingerprinting based on nine microsatellite markers (SSR) was used to analyze the genetic diversity and structure of the wild pear populations and to assess the relationship between wild and cultivated pears. In general, we found a higher genetic diversity of the European wild pear compared to the almond-leaved pear. In three Mediterranean European wild pear populations, significant introgression of the cultivated pear genome into wild populations was observed, whereas in the almond-leaved pear it was rare and only observed in a few individuals. Furthermore, in regions where the ecological niches of the two wild pear species studied overlap, hybrids between them were also found. This study provides valuable insights into the genetic variability of these species and can significantly advance their use in sustainable forest management, conservation, and breeding programs.

S.106. NEOTROPICAL BOTANICAL INVENTORIES: DOCUMENTING WHAT IS LEFT? PERSPECTIVES FROM ACROSS TROPICAL AMERICAS

P.0942 Flora of Patos de Minas (Minas Gerais, Brazil): a new important floristic hotspot in the Cerrado biome

Álvaro Pereira de Carvalho[1], Norma Aparecida Borges Bitar[1], Amanda Aparecida Vieira Dias[1], Lorrayne de Barros Bosquetti, Rafael Felipe de Almeida[2], Higor Antonio-Domingues[2]

1 Centro Universitario de Patos de Minas, Minas Gerais, Brazil. 2 Royal Botanic Gardens Kew, Richmond, UK.

South American savannas cover ca. 2.9 million km² representing 10% of savanna coverage worldwide. The Brazilian Cerrado biome is the largest savanna block in South America, representing almost two thirds of the savannas in South America with 14.000 plant species, 7.500 of them represented by endemics. Patos de Minas is a Brazilian municipality located in the heart of South American savannas, in the State of Minas Gerais, with most of its natural vegetation cover been already replaced by coffee and soy farming. Some floristic studies in this area have been carried out in the last decade, but mostly of them still unpublished and representing a gap on the knowledge of the Brazilian savannic flora. To continue the cataloguing of the flora of Patos de Minas, we performed a floristic survey in a riparian forest of a *Cerrado* fragment at the *Areado* District. All specimens' sheets were deposited in the UNIPAM herbarium from Centro Univesitario de Patos de Minas. A total of 108 species were catalogued distributed among ca. 70 genera and 37 families of flowering plants and lycophytes.

The most species rich families in the study area were: 1. Asteraceae (12 spp.), 2. Orchidaceae (7), 3. Leguminosae (5), 4. Undetermined sterile specimens (5), 5. Malpighiaceae (4), 6. Myrtaceae (4), 7. Rubiaceae (4), 8. Bignoniaceae (3), 9. Convolvulaceae (3), 10. Euphorbiaceae (3). A single species of the rare lycophyte family Selaginaceae was also recorded. Five woody sterile specimens remain unidentified and will be followed up the next flowering season.

P.0943 A savannic jewel: a checklist of the flowering plants from Quirinópolis and surroundings (State of Goiás, Brazil)

Rafael Felipe de Almeida[1,2], José Silonardo Pereira de Oliveira[1], Fernanda Rosa Moraes[1], Thais Alves-Silva[1], Isa L. de Morais[1]

1 Universidade Estadual de Goiás, Quirinópolis, Brazil. 2 Royal Botanic Gardens, Kew, United Kingdom.

South American savannas cover ca. 2.9 million km² representing 10% of savanna coverage worldwide. The Brazilian Cerrado biome is the largest savanna block in South America, representing almost two-thirds of the savannas in South America with 14.000 plant species, 7.500 of them represented by endemics. Quirinópolis is a Brazilian municipality located in the heart of South American savannas, in the State of Goiás, with most of its natural vegetation cover already replaced by sugar cane and soy farming. Few natural vegetation patches are still preserved within areas of the Serra da Confusão do Rio Preto and lowland wetland savannas (i.e., veredas) used for cattle grazing. Over the last 14 years, several field expeditions have been made monthly to the natural areas of Quirinópolis for flowering specimen collection, all of them currently deposited at the JAR herbarium at Universidade Estadual de Goiás. After the digitisation of all its specimen labels at the JAR herbarium in 2022, we were able to compile the first checklist of flowering plants for Quirinópolis and surroundings with 877 species, 435 genera, and 101 families collected. The most species-rich families were 1. Asteraceae (108 spp.), 2. Leguminosae (86), 3. Cyperaceae (72), 4. Melastomataceae (55), 5. Myrtaceae (41), 6. Poaceae (39), 7. Lamiaceae (34), 8. Malpighiaceae (34), 9. Bignoniaceae (29), 10. Apocynaceae (28). A total of 30 families (i.e. Balanophoraceae, Bixaceae, Caryocaraceae, Chloranthaceae, Connaraceae, Dioscoreaceae, Heliconiaceae, Asparagaceae, Icacinaceae, Krameriaceae, Lacistemataceae, Loganiaceae, Loranthaceae, Menispermaceae, Moringaceae, Myristicaceae, Olacaceae, Peraceae, Polemoniaceae, Portulacaceae, Rutaceae, Santalaceae, Sapotaceae, Smilacaceae, Solanaceae, Styracaceae, Triuridaceae, Turneraceae, Urticaceae, and Violaceae) were represented by a single species in the studied area. Even though more than half of the natural area of this municipality has already been replaced by human activities, its flora is still very rich and shows recently recorded endemic species.

P.0945 Herbarium records and the extreme habitat loss in the north of Espírito Santo, Brazil

Julia Meirelles[1]

1 Herbário MBML, Instituto Nacional da Mata Atlântica, Santa Teresa, Brazil. julliameirellesbot@gmail.com

Brazil, despite having one of the largest flora in the world, has huge habitat loss for soil usage. In the Atlantic Forest (MA), Espírito Santo state (ES) in the southeastern region is one of the most biodiverse with several taxa been described recently. It is also one of the most deforested, especially the northern region, where only one protected area is located. Vouchers of vascular plants from the herbaria CAP, CVRD, MBML, SAMES and VIES were analyzed on the Specieslink. Pinheiros municipality is the best sampled, specially Córrego do Veado Biological Reserve, reinforcing the importance of protected areas in the Atlantic Forest. It is a preserved and isolated fragment, managed by Chico Mendes Institute for Biodiversity Conservation (ICMBio). Montanha is the second largest municipality in area (>1 million km^2) and only 0.1 specimens/km^2 probably due to intense deforestation of this territory. Ponto Belo municipality with 359km^2, has the lowest collection density, with P.2 specimens/km^2. Despite being restricted to a few *tabuleiro* forest fragments and inselbergs, the vascular flora diversity in the North region is considered high, with 132 families (>50% of ES and MA total), 537 genera (ca. 25% of the MA) and 955 species (ca. 6% of the MA and ca. 15% of ES). At least 80 species are extinction threatened following IUCN criteria (> 8%). The results obtained highlight the importance of conservation units to document and save biodiversity from habitat loss and herbaria as a source of information for creating preservation policies and a basis for the recovery of degraded areas. Based on the georeferenced data, matrices for seeds of native species can be made available to the community in future restoration efforts. This work is the initial stage of a project that seeks to understand the distribution patterns of ES flora.

P.0946 Historical collections and fieldwork display rich angiosperm diversity in the previously overlooked Brazilian Semi-arid region

Ilana C. Oliveira[1], Grênivel M. Costa[2], Denis N. Carvalho[1], Reyjane P. Oliveira[1]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Universidade Federal do Recôncavo da Bahia, Cruz das Almas, Brazil.

Brazil is the country with the richest flora in the world, with many areas still poorly analyzed in floristic studies, as is the case of a region within the Semi-arid from Bahia state, known as the Sisal Territory (ST). It is totally included in the Caatinga Domain, the largest and most isolated area of seasonally dry tropical forest, which is part of the SDTF global biome. The native vegetation of ST has been historically replaced on a large scale by planting sisal (*Agave sisalana* Perrine ex Engelm), a naturalized xerophytic species in Northeastern Brazil. To better understand the flora of ST we made collections of Angiosperms in selected areas, and using databases from the virtual herbarium network, we searched for previous records in the 20 municipalities that composed this region. Historical collections have been made since the 19th century, often random, increasing in number after 2000. There are only two systematic and long-term floristic studies in this region, in Conceição do Coité, the municipality with the highest density of collections, and Tucano, showing highest number of records. ST currently includes 1,092 species, 514 genera and 114 families of Angiosperms, with the greatest richness of non-woody species; 56 spp. are naturalized and 18 cultivated. Among the native species, 134 are endemic to the Caatinga Domain and 14 are threatened with extinction. The richest family is Fabaceae (178 spp); the most representative genus is *Chamaecrista* (L.) Moench (20 spp,), and the most collected species was *Colicodendron yco* Mart. (Capparaceae). A new species of Apocynaceae was recently described based on collections made in that region. These data demonstrate the high richness of Angiosperms occurring in ST, with novelties for science and indication of areas within the Brazilian Semi-arid that have been little collected, with potential for floristic studies and conservation priorities.

P.0947 A sinetometric study of pseudofilamentous Desmids (Zygnematophyceae): The Brazilian case

Carlos W. do N. Moura[1], Geraldo J. P. Ramos[2], Kátia L. M. Brito[1], Maria A. dos Santos[1], Daniele M. da Silva[1], Ivania B. de Oliveira[3], Camila B. de Araújo[4], Thaís G. da Silva[5], Márcio F. dos Santos[6], Kleber R. de S. Santos[7], Paulo H. S. Vieira[1], Bruna F.de Souza[2], Larissa A. do O. Santos[2], Ariane F. dos Santos[1], Carlos E. de M. Bicudo[8]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Universidade Estadual de Santa Cruz, Ilhéus, Brazil. 3 Universidade do Estado da Bahia, Irecê, Brazil. 4 Universidade Federal de São Carlos, São Carlos, Brazil. 5 Aix-Marseille Université, France. 6 Instituto Gonçalo Moniz, Salvador, Bahia, Brazil. 7 Centro Universitário Leonardo da Vinci, Indial, Brazil. 8 Instituto de Pesquisas Ambientais, São Paulo, Brazil.

Desmids are a diverse and polyphyletic group of green algae that inhabit terrestrial (subaerial) and freshwater ecosystems. The family Desmidiaceae (Zygnematophyceae) is made up of unicellular or grouped individuals forming pseudofilaments and Brazil is recognized as one of the main centers of diversity for this microalgae group. A scientometric study of the literature on pseudofilamentous desmids was made with the review of 71 articles of taxonomic or floristic studies published over 150 years. We catalogued 82 taxa encompassing the genera *Bambusina*, *Desmidium*, *Groenbladia*, *Hyalotheca*, *Mateola*, *Onychonema*, *Phymatodocis*, *Sphaerozosma*, *Spondylosium* and *Teilingia*. The results show that approximately 14% of taxa are endemic to Brazil. The most representative genera are *Desmidium* (23 species), followed by *Spondylosium* (21), *Bambusina* and *Sphaerozosma,* both with 10 taxa. Most taxa are considered rare (60), with up to five citations, followed by taxa of occasional occurrence (24), with up to 10 citations. Only eight taxa are considered common: *Bambusina borreri*, *Desmidium baileyi*, *D. graciliceps*, *D. grevillei*, *Hyalotheca dissiliens*, *Spondylosium desmidiiforme*, *Spondylosium pulchrum*, and *Teilingia granulata*. Regarding the geographic distribution of pseudofilamentous desmids in Brazil, we identified gaps, mainly in the northeast region, where only Bahia State has 23 taxa citations. This disparity is also reflected in the different Brazilian biomes, highlighting the lack of collections in the Caatinga (seven taxa), Pampa and Pantanal (20), Atlantic Forest (49), Cerrado (60), and Amazon (65). Although these last two biomes have the great majority of records, nowadays they are facing serious challenges in conserving their sources and rivers. To overcome these gaps and challenges, a study integrating morph-molecular taxonomy (polyphasic approach) are required for a true understanding of Brazilian pseudofilamentous desmids, especially in underexplored areas. Acknowledgments: Financial support CNPq -Process 405654/2023-5.

P.0949 The family Lauraceae in the Atlantic rain forest of Espírito Santo, Brazil

Lilian S. Santos[1], Pedro L.R. de Moraes[2]

1 Programa de Pós-Graduação em Biologia Vegetal (Interunidades), Universidade Estadual Paulista "Júlio de Mesquita Filho" - UNESP, Rio Claro, Brazil. 2 Departamento de Biodiversidade, Instituto de Biociências de Rio Claro, Universidade Estadual Paulista "Júlio de Mesquita Filho" - UNESP, Rio Claro, Brazil.

Lauraceae are a pantropical family of economic importance with about 55 genera and 2500-3500 species. They are one of the richest angiosperm families in the Neotropics with ca. 470 species in Brazil. Espírito Santo is a state in southeastern Brazil within the Atlantic Rainforest domain. This region is a key, though much fragmented, biodiversity hotspot in which Lauraceae are an important structural and functional component. There are still taxonomic knowledge gaps in the state, including under-sampled sites, unidentified herbarium material, and the absence of a published flora. Therefore, a broader understanding of the family considering research and conservation is still necessary. This study aims to expand the knowledge of Lauraceae in that state through taxonomic treatment, including description of taxa, identification keys, illustrations, brief comments, and evaluation of the number of species and their geographical distribution through new floristic surveys and specimens deposited in herbaria. Until the moment, 16 genera (*Aiouea*, *Aniba*, *Beilschmiedia*, *Cassytha*, *Cryptocarya*, *Damburneya*, *Endlicheria*, *Licaria*, *Mezilaurus*, *Nectandra*, *Ocotea*, *Persea*, *Phyllostemonodaphne*, *Rhodostemonodaphne*, *Urbanodendron*, and *Williamodendron*) and ca. 130 species have been recorded for the state, of which 18 species are threatened and 15 are endemic. From over 6800 records in the *species*Link database, 57% are from two municipalities, Linhares and Santa Teresa, evincing a biased sampling. All Lauraceae collections from herbaria of the state (CVRD, MBML, SAMES, VIES) will be analyzed and field expeditions will be undertaken to collect new specimens in its least sampled regions. An interactive multiple-entry key will be created with the software Lucid v.4, in order to facilitate the recognition of the species, considered complex from a morphological and taxonomic point of view.

P.0950 Flora of Bahia: the tribes Capsiceae, Lycieae, Physaleae and Solandreae (Solanaceae)

Tânia R. S. Silva[1], Gabriel B. Silva[1]

1Department of Biology, Universidade of Feira de Santana, Feira de Santana, Brazil

Solanaceae Juss. comprises 100 genera and 2,500 species, many of which are of significance in terms of food, medicine, and ornamental use. In Brazil, there are 36 genera and 509 species. The objective of this study is to survey the species of four tribes (Capsiceae, Lyciae, Physaleae, and Solandreae) occurring in the state of Bahia. Field expeditions were conducted to collect plant material. Specimens from the ALCB, BHCB, CEPEC, HUEFS, HURB, and RB herbaria were analyzed, along with type specimens from other herbaria available in online databases. The occurrence of 24 species in these tribes was recorded as follows: Capsiceae, with 2 genera (*Capsicum* L. and *Lycianthes* (Dunal) Hassl) and 10 species; Lycieae, with Lycium L and 1 species; Physaleae, with 3 genera (*Athenaea* Sendtn., *Iochroma* Benth. and *Physalis* L.) and 10 species and Solandreae, with 2 genera (*Dyssochroma* Miers and *Solandra* Sw) and 4 species. Of these, 12 are endemic to Brazil, and two new species: *Dyssochroma caatinga* and *D. jardimii*. This work is part of the master's thesis, developed in the Postgraduate Program in Botany.

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P.0951 The impact of the Flora da Bahia project on science and education for crafting a comprehensive Flora of Brazil

Tânia R. S. Silva[1], Lucas C. Marinho[2], Reyjane P. Oliveira[1], Daniela S. Carneiro-Torres[1], Ligia S. Funch[1], Luciano P. de Queiroz[1], Alessandro Rapini[1], Ana M. Giulietti-Harley[1]

1 Department of Biology, Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Universidade Federal of Maranhão, São Luís, Brazil.

The Flora da Bahia (FBA) project was started in 1997 under the guidance of the Sociedade Botânica do Brasil to update the knowledge of Brazilian flora. Centred in Bahia state, in an area of about 560,000 km² in Northeastern Brazil, this project united a network of all state institutions, herbaria and taxonomists. Researchers have devoted themselves to collecting and identifying specimens along distinct environments in the Atlantic forests Caatinga and Cerrado for at least three decades. It increased herbaria, DNA and in-spirit collections, fostering the training of skilled taxonomists in postgraduate courses and producing comprehensive taxonomic treatments at various hierarchical levels. The synergy of the FBA with other flora programs in Brazil, such as PPBIO, PROTAX and REFLORA, culminated with the establishment of the Flora e Funga do Brasil project in 2015. The assessment and impact of FBA are grounded in a thorough bibliographic search from the inaugural treatment published in December 2003. All this investment subsidised the description of at least 927 new species of Angiosperms, whose types were collected in Bahia, including Bromeliaceae (114 species.), Melastomataceae (78), Orchidaceae (72), Myrtaceae (68), Leguminosae (58) and Euphorbiaceae (53), among many others. So far, 110 treatments have been published regarding FBA, mainly in the periodic Sitientibus Serie Ciências Biológicas. The prolific output of this project encompasses 1,265 descriptions (17 algae, 2 gymnosperms and 1246 angiosperms), representing c. 13% of the 9957 angiosperm species reported to Bahia. Several of them are rare, endangered or useful species. The increase of specimens housed at HUEFS herbarium – currently the largest plant collection in Northeastern Brazil – is highlighted as a significant impact of FBA. More than a hundred postgraduate students were associated with the FBA project, studying distinct plant groups.

Acknowledgment: CNPQ, CAPES, FAPESB and UEFS

S.107. NEW DIRECTIONS IN EARLY MODERN BOTANY COLLECTIONS AND ARCHIVES

P.0952 Herbariograph: A deep-learning tool for classifying images from specimen items

Fabio Andrés Ávila[1,2], John Park[1,3], Leanna Feder[1], Damon P. Little[1]

1 New York Botanical Garden, New York City, NY, 10458, USA. 2 The Graduate Center, City University of New York, New York City, NY, 10017, USA. 3 USDA Scientific Computing Initiative (SciNet) / Oak Ridge Institute for Science and Education (ORISE), Oak Ridge, TN 37830, USA.

Herbarium specimens are the physical evidence of plant diversity worldwide and a rich source of research data. With approximately 400 million items across 3,500 registered herbaria, in 185 countries, only an estimated 10% have associated digital images. Despite this low proportion, information in those images facilitates numerous avenues of research aimed at understanding the hidden complexity and variation of plants. The first step in harnessing this information is to sort images by the types of items represented in them. To address this challenge, we introduce *Herbariograph*, a new image dataset and deep-learning model designed to automatically recognize all of the image types commonly served by collection databases. The dataset consists of 18 image categories with 12,288 images each retrieved from publicly available repositories. The model is a small convolutional neural network (CNN) scaled to the dataset. Preliminary analyses produce an accuracy score of 0.9853 on the test dataset. The use of tools such as *Herbariograph* will help to automate specimen image processing to make targeted dataset creation faster, better, and more accessible.

P.0954 Representative Mutisiana plants from the department of Cauca in the Álvaro Fernández Pérez Herbarium (AFP) Popayán-Colombia

Luis Gerardo Chilito López[1], Iván Darío García[2], Anacristina Bayona[3], José Joaquín Varela[4]

1 Alvaro Fernández Pérez Herbarium. Popayan. Colombia. 1-4Popayán University Foundation, Popayan, Colombia. 2-3 Minuto de Dios University Corporation, Bogota, Colombia.

The Great Botanical Expedition of the New Kingdom of Granada chaired by José Celestino Mutis, as the beginning of explorations and knowledge of the national flora, is the most important legacy of the Country, hence its importance of preserving it. The Álvaro Fernández Pérez Herbarium (AFP), founded in 1994 in honor of the Colombian chemist, botanist and naturalist, houses nearly 8,000 exsicados, especially from the south-west of the national territory, including representative species allusive to the expedition. The objective was to identify the representative Mutisiana plants from the department of Cauca deposited in the AFP Herbarium. The review of the material in the collection and the database was carried out. Subsequently, the scientific names were updated in virtual botany databases and the composition, distribution and sampling localities were determined. Results showed 415 specimens, distributed in 18 families and 52 species. Among the families, Campanulaceae, Fagaceae, Moraceae, Orchidaceae, Passifloraceae, Rubiaceae and in genera Begonia, Centropogon, Cinchona, Passiflora, Ficus, Maxillaria and Psychotria stood out. The most representative species were Alnus acuminata, Cinchona pubescens, Ficus Americana, Lozania mutisiana, Persea mutisii, Quercus humboltdii, Passiflora magnolifolia, Trichantera gigantea. These species derive their importance from occupying different strategic ecosystems, conservation and urban areas in the territory of the department, in addition to their history, abundance, ornamental, medicinal, nutritional, ecological uses and threat status. The majority of specimens collected were made in the Botanical Garden of Popayán, Colombian Massif, Pacific Caucano, Gorgona Island, urban area of Popayán, Munchique and Puracé National Natural Park, in paramo ecosystems, tropical humid forest, tropical dry forest and Andean forests. of the Central and Western Cordilleras. The herbarium as a research center is a fundamental input for the development of research aimed at safeguarding the information that represents the Nation's heritage, especially the vegetation of the region.

P.0955 Bridging the past and future: Kew herbarium's innovations in collections management

Mariana H. Santana[1], Ellie Graves[1]

1 Royal Botanic Gardens Kew, London, UK.

Kew Herbarium holds a collection of approximately 7 million vascular plant specimens, with 330,000 designated as type specimens, covering about 95% of vascular plant genera. This comprehensive collection is a reference resource that reflects global plant diversity, and its richness continues to expand as we receive species new to our collections from researchers and institutions worldwide. Currently, Kew Herbarium is amid a four-year project to digitise its entire collection. The project aims to transform our science collections into a global online resource allowing researchers to tackle some of the biggest challenges facing our planet today. In addition to this digitisation effort, Kew is actively pursuing museum accreditation. This requires the review and development of current and new procedures to ensure best practice in the management of our collections. Each year the herbarium receives approximately 15-20,000 new acquisitions, comprising not only freshly collected Kew material but also loaned items from other institutions, as well as gifts and donations. To ensure the maintenance of digitised collections and to meet the criteria essential for accreditation it is crucial to develop workflows that capture and process new material before its incorporation into the collections. To achieve this goal, the New Acquisitions team has reviewed historical unstandardised workflows, developed, trialled, and implemented agreed-upon Collection Operation Procedures in collaboration with relevant stakeholders. These procedures specifically address the management and digitisation of new acquisitions, including those from the Millennium Seed Bank and DNA voucher specimens. Our next steps focus on the adoption and incorporation of digital data records captured from the field for incoming specimens. This initiative aims to create streamlined and effective workflows that leverage our new Integrated Collections Management System.

P.0956 Mobilizing international Australian historical and type collections - online activation!

Shelley A. James[1], Lauren Gardiner[2], Amber Horning[2]

1 Western Australian Herbarium, Department of Biodiversity, Conservation and Attractions, Kensington, Australia. 2 Cambridge University Herbarium, Cambridge, UK.

From the earliest days of Australian colonization and exploration, botanical collections have been sent to herbaria overseas for western scientific study. Where there is a duplicate set, collections have been repatriated back to Australia with time, but many specimens remain housed overseas. These specimens document the floral diversity of Australian ecoregions that have now been altered, and of species that have not yet been described and may now have been lost to our ecosystems. Many such collections are type specimens, and others have historical exploration and botanical significance, all of which are not readily available for taxonomic and cultural research. The Cambridge University Herbarium (CGE) is the fourth largest herbarium in the UK and contains an estimated 12,000 specimens of Australian origin. A collaborative project between the Western Australian Herbarium (PERTH) and CGE, supported by the The Winston Churchill Memorial Trust, Australia, will enable Australian collections to be located, updated, digitized, mobilized, and shared - decolonization and repatriation in digital form. Data and high-resolution images will be made available to the scientific community, historians, and the public via a citizen science platform for curation and annotation by taxonomists and the public alike. Access will be invaluable for botanical research in this age of accelerated biodiversity loss, and as travel to, or shipping of, physical specimens is increasingly fraught and costly.

P.0957 Pyotr Kostromitinov's wood collection from Fort Ross: An evidence of the early botanical exploration of northern California

Ksenia N. Kuznetsova[1,2], Anna V. Stepanova[1,3], Ekaterina L. Kotina[1,4], Alexei A. Oskolski[5]

1 Komarov Botanical Institute, St. Petersburg, Russia. 2 State museum of the history of St. Petersburg, St. Petersburg, Russia. 3 The State Hermitage museum, St. Petersburg, Russia. 4 Saint-Petersburg State Forest Technical University, St. Petersburg, Russia. 5 University of Johannesburg, Johannesburg, South Africa.

Systematic attribution of the wood samples collected in 1830 by Pyotr Kostromitinov, the Manager of Fort Ross, a Russian settlement on the Pacific coast of northern California, as been carried put. As some wood samples belong to the taxa which had not been described at the period of their collection, their labels provide interesting evidence for the first steps of botanical exploration of an exotic flora by the Russian colonists who were not professional naturalists. Particularly, Garrya has been recognized by them as Viburnum, Lyonothamnus as Arbutus, Torreya as Taxus, whereas different species of Ceanothus have been referred not only to this genus, but also to Rhamnus and Laurus. The meanings of some Russian vernacular plant names mentioned in the published historical documents have been clarified. For instance, the settlers of Port Ross used the name pal'ma (palm) not only to Arbutus menziesii (as it was evidenced by many documents) but also to Lyonothamnus floribundus. Douglas fir Pseudotsuga menziesii has been called by them as yel' (spruce) rather than as pikhta (fir). The Russian name lavr (laurel) was used not only for California laurel Umbellularia californica, but also for some Ceanothus species (probably C. velutinus). The reference of vernacular name chaga to Sequoia sempervirens has been confirmed. Unlike most early wood collections, Pyotr Kostromitinov's samples are made of thin stems and branches having no conspicuous surfaces showing their wood appearance. Such pieces are hardly suitable for demonstration of aesthetic or technical properties of timber. It's highly likely that Pyotr Kostromitinov's samples represent one of the earliest cases of collecting woods as the objects of particular interest for botany and, more generally, for natural history. It was an important novelty for 1830s, as the botanical exploration of woods did not have any sufficient conceptual background in those times.

P.0958 Colección Viva UAM - A living collection to teach Botany

Manuel Molina-Bustamante[1], Julia G. de Aledo[1,2], Darío Martínez-Atienza[1], Ignacio Ramos[1,2], Alejandro Alonso[1], Celina Ben-Saadi[1], Juan Antonio Calleja Alarcón[1,2], Alberto J. Coello[1], Raúl Díaz[1], Belén Estébanez Pérez[1], Mario Fernández-Mazuecos[1], Angélica Gallego-Narbón[1], Nagore García Medina[1,2], María Leo Montes[3], Laura Matas-Granados[1,2], Ana Otero[1], Jimena Mateo-Martín[1]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain. 3 Instituto de Ciencias Agrarias, CSIC, Madrid, Spain.

The *Colección Viva* Project (CV-UAM) is an initiative led by early career researchers that aims to create a living plant collection for educational purposes at the Biology building of the Universidad Autónoma de Madrid (UAM). This collection currently includes 78 species (spanning 68 genera and 48 families). They represent diverse features of educational interest, including evolutionary convergence, morphological adaptations, phylogenetic and taxonomic diversity, and cultural or ecological significance. Every plant is labelled with data on taxonomy, distribution and a QR code for additional information. Nowadays, the collection serves as teaching material in laboratory practices of various Biology and Environmental Sciences courses and is on permanent display at the Biology building of the Faculty of Science. The acquisition of specimens and infrastructure is financially covered by UAM through the laboratory practices budget, and complemented by personal donations.

Since its inception in March 2022, the CV-UAM has had the support of the Botany unit and the Department of Biology. However, its implementation and maintenance have been filled with challenges: the official approval to establish the collection within the Biology building, the provision of funding, the procurement of materials and infrastructure and its maintenance under harsh indoor conditions (fluctuating heating conditions and poor isolation), the acquisition of relevant specimens, the involvement of new members and their appropriate training. The collection has expanded significantly over time, and its objectives have evolved. This project provides opportunities to conduct cooperative and interdisciplinary work across all scholarly levels. We now intend to collaborate with other entities to enhance its performance, and exchange specimens and good practices. In the future, we wish to establish a network of educational living collections. In fact, CV-UAM has recently inspired similar initiatives in other academic institutions in Spain (UIB, URJC, UCM). Updates can be followed at @coleccionviva (Twitter/X).

P.0959 The botanical legacy of the scientific expeditions in the Portuguese Overseas Territories (1783-1808)

Pedro L.R. de Moraes[1,*]

*1 São Paulo State University (UNESP), Rio Claro, Brazil. *pedro.r.moraes@unesp.br.*

In 1783 four "Philosophical Expeditions" departure from Lisbon to Portuguese overseas territories, Brazil, Angola, Mozambique-Goa and Cape Verde Islands, in order to explore and catalogue the untapped natural resources. They were led by four young naturalists, students of Domingos Vandelli at the University of Coimbra. Numerous shipments of natural products of the flora and fauna were sent to the Royal Museum and Botanical Garden of Ajuda, including specimens, drawings, maps, and reports. In 1808 during the French occupation of Portugal, the best specimens and manuscripts from the Museum of Ajuda were expropriated by Étienne Geoffroy Saint-Hilaire for the Paris Muséum d'Histoire Naturelle. The official documents of the French requisition of specimens from the Portuguese collections informed a number of 2815 herbarium specimens: 1360 from Brazil (1114 – Alexandre Rodrigues Ferreira, 129 – Joaquim Vellozo de Miranda, 117 – José Mariano da Conceição Vellozo), 88 from Cochinchina (João de Loureiro), 216 from Angola (Joaquim José da Silva), 289 from Peru, 35 from Goa (Manuel Galvão da Silva), 562 from Cape Verde (João da Silva Feijó), 83 from Cape of Good Hope, and 182 from Uppsala. Up to the present, considering only the collections of the Philosophical Journeys, 1281 specimens of the so called Herbarium Lusitanicum in Paris have been located, belonging to 869 species attributable to Ferreira. From the other expeditions, 151 specimens from Angola, 345 from Cape Verde, and 15 from Goa have also been located. Among the disastrous consequences of that requisition, there was a gradual decline of the Royal Museum of Ajuda. The herbarium itself remained at Ajuda until 1874, when it was transferred to the Escola Polytechnica. The recovered specimens are currently at LISU, pertaining to the "Herbarium Brasiliense Dr. Alexandre Rodrigues Ferreira", which encompasses 1275 exsiccatae of 972 species (390 attributable to him).

P.0960 Multidisciplinary research on historical herbaria preserved in the Botanical Institute of Barcelona

Neus Nualart[1], Laura Gavioli[1,2], Alba Martín[1], Javier Martinez[1], Edgard Mestre[1], Iván Pérez-Lorenzo[1,2], David Pérez Prieto[1], Jordi López-Pujol[1,3]

1 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 2 Laboratori de Botànica, Facultat de Farmàcia i Ciències de l'Alimentació, Universitat de Barcelona, Barcelona, Spain. 3 Escuela de Ciencias Ambientales, Universidad Espíritu Santo, Samborondón, Ecuador.

The Botanical Institute of Barcelona (IBB) preserves a variety of herbaria dating from the 17th century to the early 20th century, of which four include plants collected prior to the year 1800. The oldest one is the herbarium of the Salvador family, which is considered the best-documented pre-Linnaean herbarium of Spain; it includes 4,960 specimens collected either by the brothers Joan (1683–1726) and Josep Salvador i Riera (1690–1760) and their father Jaume Salvador i Pedrol (1649–1740) or obtained by exchange with important contemporary botanists. The herbarium of Miquel Bernades Mainader (1708–1771) and his son Miquel Bernades i Clarís (1750–1801) comprises 817 specimens collected mainly in Spain that were used to prepare their unpublished manuscript entitled *Specimen Florae Hispanicae*, currently lost. The Ruiz & Pavón herbarium was produced thanks to the botanical expedition called "Expedición Botánica al Virreinato de Perú" (1777–1788) and includes 698 specimens from the current Ecuador, Perú and Chile. Finally, the herbarium of the Catalan pharmacist and naturalist Francesc Bolòs i Germà (1773–1844) contains information on medicinal uses and folk names in the labels, although many of them lack the collection locality. This contribution presents the research conducted with these four collections, encompassing the study of their plants and labels but also some associated documentation preserved in the IBB archive. This research spans various topics including taxonomy, nomenclature, history, floristics, ethnobotany, and linguistics, underscoring the significance of historical herbaria in advancing knowledge across diverse fields.

P.0961 PHYLOPYR: The genetic information of Pyrenean flowering plants accessible worldwide.

Tejero P[1,2], Viruel J[3], Hidalgo O[4], Pokorny L[5], Villaverde T[6], Martínez-Ortega[7], M Palacio S[1], Murienne J[8], Pladevall C[9], Nualart N.[4], Jiménez-Alfaro B[10], Calvo J[7], Ezquerra V, Ferrández JV, Illa E[11], Perez[11] A, Cambecèdes J[12], Catalán P[13], Etxeberria M[2], Mitxelena A[2], Otamendi M[2], Arrieta M.[2], García A[2].

1 Instituto Pirenaico de Ecología-CSIC. Jaca. Spain. 2 Botanika Saila. Sociedad de Ciencias Aranzadi Zientzia Elkartea. Donostia, Spain. 3 Royal Botanic Gardens, Kew. UK. 4 Institut Botanic de Barcelona (CSIC), Barcelona Spain. 5 Real Jardín Botánico (CSIC), Madrid. Spain. 6 Universidad Rey Juan Carlos, Móstoles, Spain. 7 Departamento de Botánica y Fisiología Vegetal, Facultad de Biología, Universidad de Salamanca, Salamanca, Spain. 8 Laboratoire Evolution et Diversité Biologique- IRD-UPS-CNRS, Université Toulouse III, Toulouse, France. 9 Andorra Recerca + Innovacio. Sant Julià de Lòria, Andorra. 10 Biodiversity Research Institute (Univ.Oviedo - CSIC - Princ. Asturias), Mieres, Spain. 11 Dept. de Biologia Evolutiva, Ecologia i Ciències Ambientals (secció Botànica). Universidad de Barcelona, Barcelona, Spain. 12 Conservatoire botanique national des Pyrénées et de Midi-Pyrénées, Bagnères de Bigorre, France. 13 Escuela Politécnica Superior de Huesca. Universidad de Zaragoza, Huesca, Spain.

Herbaria provide the witness and assurance of the existence of a plant in a place at a certain time, helping science being reproducible. Unfortunately, literature is full of examples where Voucher documentation of referred plants is missing. Moreover, most of genomic studies providing voucher support don't identify the concrete individual from where the DNA comes from. Particularly in the current "-omics" era, the need to identify and preserve the specimen from where molecules are obtained (i.e., DNA) is essential to enhance the potential future multidisciplinary work and even revise its classification. The PHYLOPYR project aims to reconstruct the Tree of Life of all flowering plants (circa 3,600) recorded in the Pyrenees using the Angiosperms353 probe set for target capture sequencing (TCS). With this universal prove set, sequence data can be generated for up to 353 nuclear low-copy orthologous genes, as well as complete organelles. All plant species will be freshly collected, except in the case of threatened and rare species for which herbarium specimens may be used. Initially, we intend to sample one population per species, vouchering three to five individuals. One individual per taxon will be designated as the molecular voucher and will be processed in the wet lab and sequenced. Sequenced will be accessible in open repositories in less than 2 years. The initial core team is formed by 23 researchers belonging to 13 institutions, including floristic and taxonomy experts (across the Pyrenees) and methodological and analytical experts (across Europe). Three herbaria (JACA [IPE-CSIC], ARANZADI, and BC [IBB, CSIC-CMCNB]) will safeguard the vouchers of the project. PHYLOPYR sequence database may contribute to cutting-edge research in many disciplines, such as plant systematic, biogeography, conservation, plant identification or phylogenomics. In this contribution we provide detailed information about the methodology willing to promote interactions and similar attempts worldwide.

P.0962 Correspondence of D.F.L. von Schlechtendal in the herbarium of Halle, Germany (HAL)

Natalia Tkach[1], Martin Röser[1]

1 Geobotany and Botanical Garden, Institute of Biology, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany.

D.F.L. von Schlechtendal (1794–1866) was a prominent 19th-century botanist. He held the position of Professor of botany at the University of Halle-Wittenberg from 1833 to 1866. His plant collection, which consists of approximately 70,000 specimens, is still preserved at the university. Schlechtendal is credited with describing over 1,600 new taxa, including 78 new genera, mostly from the New World, despite his limited travels. Schlechtendal's extensive scientific network is well-documented through his correspondence, which includes ca. 5,500 letters from about 500 individuals. Among these correspondents are numerous renowed botanists, natural scientists, travelers, and plant collectors, such as A. von Humboldt, A. von Chamisso (who is also known as a poet), A.H.G. Grisebach, A.L.P.P de Candolle, R.F. Hohenacker, and C.F.P. von Martius. The letters primary refer to publications and scientific questions concerning the journals 'Linnaea' and 'Botanische Zeitung' edited by Schlechtendal. The authors submit their manuscripts and, frequently, the specimens of new taxa as gifts, which are stored in our herbarium. The letters from scientists studying African, Central and South American plants serve as a valuable source of information. The texts are written in old German Kurrent script, the ink is fading and the paper is disintegrating. Therefore, we aim to transliterate all letters (63% are already finished), index them, digitize them and make them available online. Older ladies and gentlemen, who can still read the texts in Kurrent and transcribe them for us are a great help in our project. Some publications have already been released regarding these letters. This correspondence holds significant and supra-regional importance for current research and scientific study of the flora in their countries of origin.

P.0963 Specimens from Philip Miller's herbarium and where to find them

Wajer, J.[1]

1 Science Department, Division of Algae, Fungi and Plants, Natural History Museum, Cromwell Road, London, UK.

Philip Miller (1691-1771) was a famous British gardener and the director of the Chelsea Physic Garden from 1722 to 1770. Under his leadership, this small, three-acre plot of land in a quiet corner of West London was transformed from a suburban allotment into an internationally renowned hub through which thousands of new species of plants from around the world, particularly from South Africa and North America, were introduced into British and European horticulture. Miller's influence, however, stretched far beyond shaping the way our gardens look today. He was also a skilled botanist and during his long reign at Chelsea he discovered over a thousand new species of plants, all of which were diligently recorded in successive editions of *The Gardeners Dictionary* (1731-1771), his most famous work. The specimens upon which Miller based the descriptions of his new plant species were deposited in his own herbarium that included over ten thousand samples, according to a letter he sent to John Bartram in 1758. This invaluable collection was purchased by Sir Joseph Banks at an auction in 1774 and incorporated into his own herbarium, which later formed the basis of the Natural History Museum's General Herbarium, now one of the largest in the world with over five million sheets and counting. This poster will explore various idiosyncratic ways in which Banks and his assistants annotated Miller's specimens before they were mixed with the rest of his own collection. It will form a practical guide into finding and selecting the most appropriate material that correctly typifies the myriad of plants described by Miller in various editions of his *Gardeners Dictionary*. Additional elements of original material and the whereabouts of the specimens distributed by Miller to his scientific collaborators in the UK and throughout Europe will also be discussed.

S.108. NEW FRONTIERS IN PLANT PHYLOGENOMICS

P.0964 From Asparagales to Hyacinth: Phylogenomic insights in the evolutionary and biogeographic history of Scilloideae (Asparagaceae)

Tim Böhnert[1], Maria-Anna Vasile[1], Maximilian Weigend[1]

1 Bonn Institute of Organismic Biology, University of Bonn, Bonn, Germany.

Asparagales, comprises ca. 10% of all angiosperm species – roughly 36,000 spp. in 1,122 genera and 14 families, with Orchids accounting for nearly two-thirds of the species (ca. 25,000 spp.). The second largest family are Asparagaceae (ca. 2,900 spp.), currently subdivided into seven subfamilies, including Scilloideae (ca. 1,000 spp.). Scilloideae comprise iconic ornamentals such as hyacinths, star-of-Bethlehem, harebells and bluebells and are quite conserved in their basic morphology. Accordingly, genus concepts diverge dramatically between taxonomic treatments and are in a state of constant flux. Current concepts of the basic phylogeny and classification of Asparagales and Asparagaceae are widely, but not universally, accepted. Numerous individual relationships remain unresolved and, genus- and species level coverage remains unsatisfactory. Dating Asparagales has also been challenging, and published estimates of crown node ages range from 60 to 130 million years. Overall, although our understanding of this order has improved dramatically in recent decades, we are still far from a comprehensive systematic and biogeographic understanding of the group. The aims of this study are, (1) to construct a densely sampled (> 600 spp.), order-wide phylogeny of the Asparagales based on the Angio353 data of the PAFTOL project. (2) to use this expanded phylogeny to apply molecular clock dating for a time-calibrated, in-depth phylogeny of the entire order. (3) Based on a well-resolved, densely sampled and time-calibrated backbone, we plan to study the hyacinth subfamily Scilloideae in detail to resolve relationships, evolutionary patterns, and historical biogeography. Preliminary results confirm current family-level classifications, provide a highly supported backbone for Asparagaceae, and solve several long-debated inconsistencies between genera (e.g., *Scilla*) within Scilloideae. Finally, by adding a substantial number of newly sequenced species from the Geophyte Collection of Bonn Botanic Gardens, among others, we emphasize the importance of botanical living collections for large-scale phylogenetic studies.

P.0965 Dual use of Angiosperm353 data: from phylogenetics to species delimitation in the Acacia Microneurae group

Barbara Azevedo de Oliveira[1], Rod Fensham[1,2], Lyn Cook[1]

1 The University of Queensland, Australia. 2 Queensland Herbarium, Toowong, Australia.

Phylogenetics and population genetics have long used different types of data, but next-generation sequencing approaches provide the opportunity to capture data that can be used for multiple purposes based on extensive sequence coverage. These approaches have the potential to decrease time, effort and costs associated with addressing questions both above and below the species level. In this study, we utilise data from conserved exons and variable flanking regions to conduct phylogenetics and for species delimitation using tests of coalescence, including reciprocal monophyly followed by reducing the data to SNPs for population genetic approach comparisons. The study focuses on the Microneurae group of the genus *Acacia*, a dominant and widespread group in the semi-arid and arid zones in Australia. Firstly, we aim to elucidate the group's systematic relationships through the reconstruction of gene and species trees. Secondly, to test species delimitation of *Acacia georginae* and *A. cambagei* from individuals in allopatry and sympatry across their wide geographic range. We expect that species would be reciprocal monophyletic if alleles within each taxon share a closer common ancestor or coalesce more recently than with alleles from the other species. A lack of reciprocal monophyly would suggest potential recent divergence. To explore this, we assess reproductive isolation, especially in sympatry. Interbreeding might show low allele fixation, while distinct fixed alleles imply no interbreeding. This framework holds promise for more accurate systematic revisions by incorporating the underlying factors driving species divergence.

P.0966 Genetic diversity and distribution of Bunium and Elwendia (Apiaceae) in Iran: a phylogennomic perspective

Reza Haghi[1], Farkhondeh Rezanejad[2], Dörte Harpke[1], Frank R. Blattner[1,3]

1 Genebank Department, Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany. 2 Department of Biology, Shahid Bahonar University, Kerman, Iran. 3 German Centre of Integrative Biodiversity Research, Halle-Jena-Leipzig, Leipzig, Germany.

The genera *Elwendia* and *Bunium* encompass diverse species with aromatic properties distributed across Asia, Europe, and North Africa. This study focuses on elucidating the phylogenetic relationships within *Elwendia* and *Bunium*, which were previously considered as a single genus. Iran is ecologically and geographically important for these genera. A total of 195 populations representing eight different species of *Elwendia* (*E. afghanica, E. badghyzi, E. kuhitangi, E. caroides, E. cylindrica, E. intermedia, E. persica, E. wolffii*), and three species of *Bunium* (*B. paucifolium, B. cornigerum, B. rectangulum*) were collected from different provinces in Iran, with 15 additional samples from Afghanistan and Tajikistan. Genotyping-by-sequencing (GBS) was employed to analyze genome-wide single-nucleotide polymorphisms (SNPs). Phylogenetic analysis confirmed the division into two separate genera: *Bunium* (consisting of the western species) and *Elwendia* (eastern species). While most populations in Iran belonged to the *Elwendia* and were distributed in the eastern provinces, geographic overlap of *Bunium* and *Elwendia* was observed throughout the country. Although *E. persica*, a prominent species within *Elwendia* used for its secondary compounds, and its close relatives (*E. cylindrica*, *E. afghanica*, *E. badghyzi*, *E. kuhitangi*, *E. intermedia*) are morphologically similar and challenging to distinguish in some populations, the analysis clearly differentiated them. Additionally, population structure analysis revealed that some *Elwendia* species are hybrids of other species, indicating genetic mixing within the genus. Furthermore, sharing of subpopulations between *Elwendia* and *Bunium* genera was observed in certain populations, highlighting potential gene flow between the two genera. This study provides valuable insights into the evolutionary history and taxonomic relationships of Bunium and *Elwendia* species, particularly in clarifying the classification of *Elwendia persica* and its close relatives as medically and economically important species.

P.0967 Intracellular gene transfer (IGT) events from the mitogenome into the plastome of subtribe Ferulinae Drude (Apiaceae)

Sangjin Jo[1], Minsu Park[1], Komiljon Sh. Tojibaev[2], Ziyoviddin Yusupov[2], Sangho Choi[1], Jin-Hyub Paik[1*]

*1 Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon, South Korea. 2 Institute of Botany, Academy of Sciences, Tashkent, Uzbekistan. *corresponding author. jpaik@kribb.re.kr*

Intracellular gene transfer (IGT) is a phenomenon of genome evolution that occurs between plant nuclear and organelle genomes or between organelle genomes. The plastome is highly conserved, making it rare for foreign DNA to be introduced. The subtribe Ferulinae includes *Ferula*, which is one of the largest genera in Apiaceae. We discovered IGT occurrences in the *rps*12-*trn*V IGS region of the Ferulinae plastome's inverted repeat (IR) region. Partial mitogenome sequences with lengths ranging from 2.8 kb to 5.8 kb were imported. Furthermore, unlike other Scandiceae subtribes, Ferulinae plastomes were discovered to have two distinct mitogenome sequences. We named those sequences *Ferula* Mitochondrial Plastid (*Fe*MP). *Fe*MP1 lengths ranged from 336 to 1,100 bp, whereas *Fe*MP2 lengths ranged from 50 to 740 bp (no *Fe*MP2 in *F. conocaula* and *F. kingdon-wardii*). *Fe*MP2 contains the entire *rps*7 gene from the mitogenome. Ferulinae was monophyletic in the maximum likelihood (ML) tree generated using 79 protein-coding genes, however *Dorema* and *Fergania* were nested within the *Ferula* clade. *Ferula* plastome features are shared by *Dorema* and *Fergania*. Based on these findings, *Dorema* and *Fergania* must be reclassified. Overall, our findings can be used as a hypothesis to explain the plastome evolution of Scandiceae using the atypical plastome of Apiaceae. These findings will also aid in our understanding of plant organelle genome evolution.

P.0968 Phylogenetic relationships in the strawberry subtribe Fragariinae (Rosaceae, tribe Potentilleae) from whole genome sequences

Geraldine A. Allen[1],Aaron Liston[2], L. Torsten Eriksson[3]

1 University of Victoria, Victoria, Canada. 2 Oregon State University, Corvallis, USA. 3 University of Bergen, Bergen, Norway.

The subtribe Fragariinae consists of approximately 800 species and 12-14 genera, including the strawberries (*Fragaria*) and their relatives. We conducted whole genome shotgun sequencing of 28 species from all genera in the subtribe. Complete plastomes were recovered with GetOrganelle; nuclear genes were retrieved with HybPiper2 using 12353 *Fragaria vesca* genes as reference. Nuclear gene sequences were aligned with MAFFT and alignments that included genes for ≥ 90% of samples were retained for analysis. Maximum likelihood analyses of both plastome and nuclear trees revealed two main subclades within the Fragariinae: the *Drymocallis* subclade (including *Chamaecallis, Chamaerhodos, Dasiphora, Drymocallis* and *Potaninia*) and the *Sibbaldia* subclade (including *Comarum, Farin-*

opsis, Sibbaldia, Sibbaldiopsis and *Sibbaldianthe*). As shown by others, the highly diverse *Alchemilla* lineage (*Alchemilla, Aphanes* and *Lachemilla*) is included in the *Sibbaldia* subclade as sister to the central Asian genus *Farinopsis*. The placement of the two genera *Fragaria* and *Sibbaldianthe* was not clearly resolved. In the nuclear phylogenetic tree, *Fragaria* is weakly supported as sister to the *Sibbaldia* subclade, whereas in the plastome tree it is sister to the *Drymocallis* subclade with stronger support. Although *Fragaria* clearly diverged from the rest of the Fragariinae early in the history of the subtribe, the exact relationships are currently unclear. The Asian genus *Sibbaldianthe* is sister to *Sibbaldia*/*Sibbaldiopsis* in the nuclear tree, and sister to *Comarum*/*Farinopsis*/*Alchemilla* in the plastome tree. These conflicts and uncertainties suggest hybridization, in combination with polyploidy, has played an important role in the evolutionary history of the Fragariinae. Polyploid species or a mixture of diploids and polyploids occur in several genera, including *Fragaria, Sibbaldianthe*, and the *Alchemilla* group. *Sibbaldiopsis* is hypothesized to be an allopolyploid (and possibly polyphyletic) genus descended in part from *Sibbaldia*. Analyses are ongoing to identify the origins of these genera.

P.0969 Exploring phylogenetic backbone and deep reticulation of a non-model plant lineage using multi-source genomic data

Chao Xu[1,2], Ze-Tao Jin[1,2,3], Hui Wang[1,2,4], Si-Yu Xie[1,2,5], Xiao-Hua Lin[1,2,5], Richard G.J. Hodel[6], Yu Zhang[1,2,5], Dai-Kun Ma[1,2,7], Bing Liu[1,2], Guang-Ning Liu[2], Shui-Hu Jin[4], Liang Zhao[5], Jun Wu[3], Chen Ren[8], De-Yuan Hong[1,2], Bin-Bin Liu[1,2]

1 State Key Laboratory of Plant Diversity and Specialty Crops, Institute of Botany, Chinese Academy of Sciences, Beijing, China. 2 China National Botanical Garden, Beijing, China. 3 State Key Laboratory of Crop Genetics and Germplasm Enhancement, College of Horticulture, Nanjing Agricultural University, Nanjing, China. 4 College of Forestry and Biotechnology, Zhejiang Agriculture and Forestry University, Hangzhou, China. 5 College of Life Sciences & Herbarium of Northwest A&F University, Northwest A&F University, Yangling, China. 6 Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA. 7 University of Chinese Academy of Sciences, Beijing, China. 8 Key Laboratory of Plant Resources Conservation and Sustainable Utilization & Guangdong Provincial Key Laboratory of Applied Botany, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, China.

Phylogenetic networks, rather than purely bifurcating trees, more accurately depict the intricate evolutionary dynamics of most lineages, especially those characterized by extensive hybridization and allopolyploidization events. However, the challenges of achieving complete taxon sampling, and limited financial resources for studying non-model plant lineages, have hindered comprehensive and robust estimation of phylogenetic backbones with guidance from networks. The bellflower tribe, Campanuleae, characterized by a reticulate evolutionary history, serves as an ideal model to investigate how to diagnose nested ancient reticulation events. Here, by integrating multiple genomic data sources and a range of phylogenetic inference methods, we produced a robust phylogenetic backbone for the tribe Campanuleae. Our investigation of reticulate evolution indicates that hybridization and allopolyploidization were instrumental in shaping the diversity of the bellflower tribe, particularly during the initial diversification of the subtribe Phytematinae. Additionally, we ascertained that conflicting topologies resulting from distinct genomic datasets and inference methodologies significantly impact downstream estimates of divergence dating, ancestral area construction, and diversification rates. This study offers a universally relevant framework for deciphering how to use network-based phylogenetic structures using various genomic sources and inference methods.

P.0970 The Clusioid626 probe set: disentangling recalcitrant phylogenetic relationships in the clusioid clade (Malpighiales)

Irene Villa-Machío[1], Irene Masa-Iranzo[2,3], Lisa Pokorny[2], Andrea S. Meseguer[2]

1 Missouri Botanical Garden, St. Louis, USA. 2 Real Jardín Botánico, CSIC, Madrid, Spain. 3 Universidad Autónoma de Madrid, Madrid, Spain.

The clusioid clade (Malpighiales) includes five families, Bonnetiaceae, Calophyllaceae, Clusiaceae, Hypericaceae, and Podostemaceae, and comprises

94 genera with -2.2K mostly tropical species. From a phylogenetic perspective, Malpighiales is known as one of the most challenging angiosperm orders to resolve. Recent studies suggest that the clusioid clade may not be an exception (putatively paraphyletic). To resolve phylogenetic relationships in this clade, we have implemented a genomic approach, combining target capture and genome skimming (Hyb-Seq) to recover hundreds of low-copy nuclear orthologs and organellar DNA. We designed a custom probe set, the Clusioid626 kit, composed of 39.936 120-mer probes, for a total ~6.6M nucleotide data matrix, and mapping to 626 nuclear targets, including all targets in the Angiosperms353 probe set. Targets were selected based on size evenness and phylo-informativeness to prevent methodological biases in the phylogenomic inference. We tested our probe set on 49 samples from 24 clusioid genera representing all the tribes described in the clade, including data from 17 species downloaded from the NCBI SRA, and 32 newly generated accessions. Both nuclear and plastid datasets were analysed using the HybPiper pipeline. On average, 34.5% of reads mapped to our targets, recovering ~600 orthologs. Additionally, a new plastid target file was created to mine plastid coding regions from off-target reads. This plastid target file was based on the complete plastome sequence of 13 species from five Malpighiales families. Phylogenomic analyses of the nuclear dataset suggest that Podostemaceae may not belong to the clusioid clade. Relationships for the remaining families are fully resolved and strongly supported. Further, we infer Clusiaceae, rather than Bonnetiaceae, as sister to the remaining families. Similarly, we infer Calophyllaceae as sister to Hypericaceae, rather than Podostemaceae, which may point to both analytical artefacts and to biological processes.

P.0971 An assessment of a newly designed hybrid capture bait set for Urticaceae

Han-Chun Chien[1], Geng-Xi Zhu[1], Yu-Hsin Tseng[1]

1 Department of Life Sciences, National Chung Hsing University, Taichung, Taiwan.

Over the past decade, advancements in next-generation sequencing (NGS) and the continuous advancement of technology have made reduced-representation sequencing a highly efficient method for obtaining hundreds of nuclear loci. This method has become an important tool for plant systematics and evolution. Notably, Hyb-Seq technology, utilising a designed probe for DNA region capture, has been considered a cost-effective method and is widely applied in non-model organisms. This study aims to design a probe set to enrich nuclear loci for Urticaceae, a group of plants notorious for challenging DNA extraction due to polysaccharide abundance. Based on the published transcriptome of *Urtica dioica* and the newly assembled transcriptome of *Boehmeria nivea* and *Elatostema rivulare* in this study, we attempted to search for single-copy nuclear loci in Urticaceae by MarkerMiner. Meanwhile, we also identified Urticaceae homologs corresponding to Angiosperms353 loci as reference. Overall, 542 loci were retained, including 268 loci of Angiospems353. The representative Urticaceae taxa were collected from the field and herbarium, and, subsequently, we prepared the libraries for NGS and used these specific probes to capture the target loci. The reads obtained after sequencing will be assembled through different pipelines that are based on different assembly dependencies to evaluate the effect of different assembly pipelines, phylogenetic relationship and sequence analysis. This study systematically compares assembly and pipelines will lead to the understanding and identification of the potential factors affecting Hyb-Seq analysis that have been overlooked by researchers for a long time, to provide the strategies for future study of phylogenomics in the analysis and sampling.

P.0972 Effects of gene flow on inference of phylogeny, divergence times and historical biogeography in beeches

Ai-Ying Wang[1], Yu Liang[2], Mu-Qing Liu[2], Xiao-Xi Yang[2], Xiao-Yong Chen[3], Chien-Hsun Huang[4], Da-Yong Zhang[2], Wan-Jin Liao[2]

1 School of Ecology and Nature Conservation, Beijing Forestry University, Beijing, China. 2 College of Life Science, Beijing Normal University, Beijing, China. 3 School of Ecological and Environmental Sciences, East China Normal University, Shanghai, China. 4 School of Life Sciences, Fudan University, Shanghai, China.

Gene flow widely occurs among plant and animal taxa causing significant effects on phylogenetic analyses. Estimations of divergence time and historical biogeography patterns are strongly influenced by phylogenetic reticulation. However, existing approaches have not resolved such effects on evolutionary history. Here, a gene-partitioning-based backbone tree pipeline was used to reconstruct the phylogeny of beeches. Furthermore, the divergence time and ancestral area was estimated by considering the effects of gene flow based on 114 whole-genome sequences of the ten *Fagus* taxa worldwide. Beeches showed a reticular phylogeny with two main gene flow events. Two East Asian species (*F. longipetiolata* and *F. lucida*) formed the sister clade to other taxa in the subgenus *Fagus* after taking the effects of gene flow into account. The existing beech species are inferred to originate from East Asia in the early Oligocene, then spread to North America and Europe during the mid-Miocene. The estimated divergence time for the subgenus *Fagus* was 15.42 Mya under reticulated evolution, which is more ancient than previous estimates. Our findings highlighted the effects of gene flow on phylogeny, divergence times, and ancestral area reconstruction.

P.0973 Plastid genome evolution in the Polygalaceae family and its phylogenetic implications

Yin-Huan Wang[1]

1 School of Primary Education, Chongqing Normal University, Chongqing, China.

Polygalaceae is a nearly cosmopolitan plant family consisting of 30 named genera and over 1,200 species. Many species within this family are of economic importance, particularly in medicine and timber production. In recent years, the infra-family classification of Polygalaceae has undergone significant changes, primarily due to the redefinition of several genera, notably the polyphyletic *Polygala s.l.* Plastomes, the complete DNA sequences of plastids, exhibit variability in length and architecture within this family. To investigate the structural characteristics of plastomes and their potential for resolving phylogenetic relationships within Polygalaceae, this study assembled the plastome of *P. tatarinowii* and conducted comparative and phylogenetic analyses with 25 other plastomes of Polygalaceae and four plastomes from three other families within Fabales available in GenBank. In comparison with the typical angiosperm plastome, the plastomes of the majority of Polygalaceae species exhibited a quadripartite structure with lengths ranging from 143,284 bp (*Salomonia cantoniensis*) to 171,893 bp (*P. karensium*). However, the plastomes of the heterotrophic *Epirixanthes spp.* have lost the inverted repeat (IR) regions, resulting in significant reduction and rearrangement, with lengths varying from 33,131 bp (*E. elongata*) to 95,420 bp (*E. pallida*). All Polygalaceae species' plastomes showed varying degrees of IR expansion, gene loss, and rearrangement, except for those of the early-diverging genus *Xanthophyllum*. Plastome data proved effective in resolving the phylogenetic relationships among sampled species. Additionally, plastome features can serve as synapomorphies for certain clades. In summary, our study provides valuable insights into the structural diversification of plastomes and underscores the importance of plastome data in phylogenetic reconstruction within Polygalaceae.

P.0974 Reconstructing phylogenetic trees based on hierarchical and nested repetitive genetic structures

Zhuoxin Zhang[1], Jieyu Wang[2], Yu Liu[3]

1 South China Agricultural University, Guangzhou, China. 2 BGI Genomics, Shenzhen, China. 3 Beijing Normal University, Zhuhai, China.

In phylogenetic studies, popular mathematical frameworks such as Maximum Likelihood, Maximum Parsimony, and the Bayesian Method typically rely on states of single nucleotide, amino acid, or morphological character. However, these methods may not fully account for evolutionary events like sequence repetition, deletion, and chromosome regions exchange. Such events can lead to inaccuracies due to the overemphasis on individual state calculations in phylogenetics. In contrast, a recently proposed approach named "Ladderpath" (within the broader category of Algorithmic Information Theory), motivated by the concept of "evolutionary tinkering", offers an alternative mathematical framework. Similar methods have been successfully applied to the study of the evolution of compound structures (Liu et al., Sci. Adv. 2021) and structural symmetry (Johnston et al., PNAS 2022). Our study introduces a novel algorithm and accompanying online tool, the Ladderpath Calculator, designed for constructing phylogenetic trees from DNA sequences and genomic colinearity data. By iteratively extracting repetitive substructures and reconstructing them into a network structure with hierarchical relationships, Ladderpath can define and calculate the evolutionary distances between sequences. Testing revealed that

Ladderpath can process unaligned data by effectively identifying repetitive structures in sequences, yielding results comparable to those obtained from traditional algorithms. However, it shows ambiguity in cases of recent evolution due to the absence of distinct repetitive patterns. Notably, Ladderpath effectively utilizes syntenic blocks in genomic data, providing reliable results in colinearity scenarios. In summary, Ladderpath emerges as a novel approach in molecular phylogenetics, particularly advantageous for analyzing repeated data blocks. It also holds potential for future hybridization studies by facilitating the mapping of hierarchical and nested repetitive elements.

S.109. NEW INSIGHTS INTO PHYLOGENOMICS, SYSTEMATICS AND EVOLUTION OF SALICACEAE.

P.0976 The role of sex ratio bias for sex chromosome evolution

Xiaomeng Mao[1], Sophie Karrenberg[1]

1 Department of Ecology and Genetics, Uppsala University, Uppsala, Sweden.

Sex ratio selection is one of the important forces in the evolution of sex-determining systems. Strong female-sex ratio bias is common in natural populations of *Salix*, with no or only limited association with sexual dimorphism or environmental conditions. We investigated sex ratios in the arctic-alpine dwarf willow *Salix herbacea* L. and tested whether sex ratio was associated with germination, survival or flowering. We detected a strong and consistent overall female bias (proportion of females: 0.71-0.82) in both natural populations and under controlled conditions, but variable sex ratios in families (0.25-1). We did not find evidence for habitat segregation of the sexes or sexual dimorphism in survival or flowering. This suggests that sex ratio bias is already present in seeds. Candidate mechanisms that can lead to both overall female bias and variation in sex ratio among families are meiotic drive or cyto-nuclear interactions. To identify the mechanisms underlying sex ratio bias, we currently trace the transmission of maternal and paternal alleles to their offspring, using whole genome re-sequencing and a recently established draft genome of *S. herbacea* with putative ZW sex determination. We specifically focus on the transmission of sex-linked haplotypes to explore to which extent these regions are associated with the control of sex ratio. With this study, we will gain insights into mechanisms generating sex ratio bias and their association with sex chromosome evolution.

P.0977 Repeated evolution of arctic-alpine dwarfism

Vinciane Mossion[1], Xiaomeng Mao[1], Sophie Karrenberg[1]

1 Uppsala University, Uppsala, Sweden.

The repeated evolution of similar form and function in divergent lineages has long fascinated researchers because it might imply that evolution is predictable. Similar phenotypes can arise through new mutations or shared variation, either as shared ancestral variation or hybridization. A prominent example of repeated evolution is the dwarf stature of plants growing in arctic or alpine environments. In willows (*Salix*), such dwarfism has evolved multiple times in unrelated lineages. Here, we investigate the evolution of dwarfism in willows using whole genome re-sequencing (WGS) of four putative dwarf-shrub pairs and an outgroup (6 individuals per species) as well as published WGS data from about 40 additional Salicaceae species. First, we created a phylogenetic framework based on orthologous genes and confirmed multiple dwarf-shrub species pairs in distinct lineages. As a second step, we searched for signatures of repeated evolution along the genome using unsupervised recognition of local relationship patterns. We identified several genomic regions displaying tree topologies in which species are grouped by growth form rather than by species relatedness, which suggests a contribution of shared variation to the repeated evolution of dwarfism. We further tested orthologous genes for positive selection in branches leading to dwarf species by analyzing synonymous and nonsynonymous substitution rates. We found strong evidence for 60 candidate genes under positive selection. Further analyses are ongoing to test whether regions or genes controlling dwarfism are associated with lineage divergence. Moreover, we will explore the role of hybridization and ancestral standing variation for the repeated evolution of dwarfism using D and *f*-branch statistics and reticulate network analysis. Together, these analyses allow us to make inferences on the evolutionary processes underlying the common arctic-alpine dwarf forms in the genus *Salix*.

P.0978 Spontaneous hybridisation of Salix babylonica with native European willows (Salicaceae)—an overlooked risk for new alien hybrids?

Jana Geržová[1], Radim J. Vašut[1]

1 Department of Botany, Palacký University Olomouc, Olomouc, Czechia.

Hybridisation, an important evolutionary process in plants, also has a downside—the possibility of hybridisation between native and exotic species poses a potential threat to native populations or habitats. In Salicaceae, not only is *Populus ×canadensis* having a negative impact on European floodplain forests, but also exotic willow hybrids are a serious threat to alluvial habitats in South America and New Zealand. Some allochthonous willows are widely cultivated in Europe, particularly ornamentals of the *S. babylonica* group. However, despite their frequent contact with autochthonous European taxa, their spontaneous hybridisation has not yet been documented. Recently, we have repeatedly found suspect morphotypes in the field with morphological characteristics of such hybrids (*S. babylonica* × 'wind'). We therefore investigated whether such hybridisation occurs in Europe by comparing the genome size (GS) of the expected parental taxa and hybrids by flow cytometry, and by comparing genetic differences using genome-wide DArTseq genotyping. We have documented that all plants tested are tetraploids, slightly smaller GS of *S. babylonica* suggesting that some of the samples represent 'alien' hybrids. This was further confirmed by statistical analyses of SNPs generated by DArTseq, resulting in an intermediate position of putative hybrids between *S. babylonica* f. *tortuosa* and European willows. It confirmed the formation of novel hybrids between native and exotic willow species, with three types of hybrids between *S. babylonica* f. *tortuosa* and *S. alba*/*S. fragilis* being formed via different pathways. These hybrids are morphologically difficult to identify and may therefore be overlooked—their frequency in the field is still unknown. We have confirmed hybrids from Czechia and Italy, but apparently they occur in other European countries (e.g. Romania). This phenomenon was previously unknown in ornamental willows and is important to consider as it may represent a potential threat to the native willow gene pool in Europe.

P.0979 Allopolyploidization from two dioecious ancestors leads to recurrent evolution of sex chromosomes and reversion to autosomes

Li He[1,#,*], Yuàn Wang[1,#], Yi Wang[1,2], Ren-Gang Zhang[3], Yuán Wang[1], Elvira Hörandl[4], Judith E. Mank[5], Ray Ming[6]

*1 Eastern China Conservation Centre for Wild Endangered Plant Resources, Shanghai Chenshan Botanical Garden, Shanghai, China. 2 Laboratory of Systematic Evolution and Biogeography of Woody Plants, School of Ecology and Nature Conservation, Beijing Forestry University, Beijing, China. 3 Yunnan Key Laboratory for Integrative Conservation of Plant Species with Extremely Small Populations, Kunming Institute of Botany, Chinese Academy of Sciences, Yunnan, China. 4 Department of Systematics, Biodiversity and Evolution of Plants (with Herbarium), University of Goettingen, Göttingen, Germany. 5 Department of Zoology and Biodiversity Research Centre, University of British Columbia, Vancouver, Canada. 6 Centre for Genomics and Biotechnology, Fujian Provincial Key Laboratory of Haixia Applied Plant Systems Biology, Key Laboratory of Genetics, Breeding and Multiple Utilization of Crops, Ministry of Education, Fujian Agriculture and Forestry University, Fuzhou, China *lhe@cemps.ac.cn #Contributed equally to this study.*

Polyploidization presents an unusual challenge for species with sex chromosomes, as it can lead to complex combinations of sex chromosomes that disrupt reproductive development. This is particularly true for allopolyploidization between species with different sex chromosome systems. Here we assemble haplotype-resolved chromosome-level genomes of a female allotetraploid weeping willow (*Salix babylonica*) and a male diploid *Salix dunnii* using Hi-C and PacBio HiFi reads. We use phylogenomics of nuclear and plastid genomes to show that weeping willow arose from crosses between a female ancestor from the *Salix* clade, having XY sex chromosomes on chromosome 7, and a male ancestor from the *Vetrix* clade, having ancestral XY sex chromosomes on chromosome 15. Our analysis reveals that weeping willow has one pair sex chromosomes, ZW on chromosome 15, that derive from the ancestral XY sex chromosomes in the *Vetrix*-clade male ancestor. Moreover, the ancestral X chromosomes on chromosome 7 from the *Salix*-clade female ancestor have reverted to autosomal inheritance. Taken together, our results point to the rapid evolution and reversion of sex chromosomes following allopolyploidization in weeping willow.

S.110. NEW INSIGHTS ON BIG PLANT GENERA 1: DIVERSITY & DISTRIBUTION

P.0980 New circumscription of Tribe Cassieae in the higher-level classification of Caesalpinioideae (Leguminosae)

Juliana Gastaldello Rando[1], Matheus Martins Teixeira Cota[2], Alexandre Gibau de Lima[3], Roseli Lopes da Costa Bortoluzzi[4], Brigitte Marazzi[5], Adilva de Souza Conceição[6]

1 Universidade Federal do Oeste da Bahia, Bahia, Brazil. 2 Universidade Estadual de Feira de Santana, Bahia, Brazil. 3 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 4 Universidade do Estado de Santa Catarina, Santa Catarina, Brazil. 5 Natural History Museum of Canton Ticino, Lugano, Switzerland. 6 Universidade do Estado da Bahia, Bahia, Brazil.

Caesalpinioideae is the second largest subfamily of legumes with ca. 4,680 species and 163 genera. It is an ecologically and economically important group with global distribution. Following the recent re-circumscription of a new higher-level classification as presented in *Advances in Legume Systematics 14 (2)*, the subfamily now comprises 11 tribes. The tribe Cassieae was traditionally divided into five subtribes which included a total of 20 genera. However, ever since the first molecular phylogenies, the tribe has never been supported as monophyletic and all recent analyses support as monophyletic what was then considered subtribe Cassiinae (*Cassia*, *Chamaecrista* and *Senna*), but only with the inclusion of four other genera previously placed in the tribe Caesalpinieae (*Batesia*, *Melanoxylum*, *Recordoxylon* and *Vouacapoua*). The new classification is based on a phylogeny inferred using hundreds of nuclear genes. Cassieae is the richest non-mimosoid clade (702 spp.), *Cassia*, *Chamaecrista* and *Senna* are the largest genera. The recognition of *Cassia*, *Chamaecrista* and *Senna* is now well established and each of the three genera is supported as monophyletic. Although the three genera were traditionally considered closely related, phylogenetic analyses have shown that they do not form a clade. Taxonomic and nomenclatural information, morphological descriptions, Illustration, maps and notes are given for each genus. Cassieae is morphologically heterogeneous, with only a few features shared among all or nearly all. All Cassieae have once pinnate or bifoliolate leaves, most species have yellow petals, with only a few having other colors. Three genera have poricidal anthers (*Cassia*, *Chamaecrista* and *Senna*). *Batesia*, *Melanoxylum*, *Recordoxylon* and *Vouacapoua* are restricted to the New World, occurring in the Tropical Rain Forests of South America.*Cassia*, *Chamaecrista* and *Senna* are widely distributed, however with high diversity in the Neotropical region.

P.0981 Taxonomic revision of the mega diverse genus Begonia (Begoniaceae) in Northern Myanmar

Mya Bhone Maw[1], Tan Yun-Hong[2], Yu Wen-bin[3]

1 Biodiversity Research Group, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences. 2 Plant Diversity and Conservation Research Group, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences 3 Biodiversity Research Group, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, China.

Myanmar is one of the most biodiverse areas in Southeast Asia. However, biodiversity research in Myanmar has been hindered for many decades compared with other countries in East and Southeast Asia. Consequently, its flora and fauna are significantly underexplored. Northern Myanmar is a botanically important area with species richness and diversity, but little is known regarding the biodiversity of this region due to its high topography and political restrictions. The Begonia flora in Northern Myanmar is expected to be very rich but still poorly known compared to the other regional areas such as Northeast India and Southwest China. Moreover, it has never been systematically explored and still lacks awareness by the local community. In a combination of botanical explorations in Northern Myanmar – above all northern parts, Putao District, Kachin State, and Hkamti District, Sagaing Region – literature and herbarium specimen's examination, a total of 36 species of *Begonia*, belong to 3 sections (sect. *Platycentrum*, sect. *Dysmorphia*, and sect. *Petermannia*) has been recorded, with 14 being endemic and seven new to science. Habitat degradation must be a concern for the *Begonia* species in northern Myanmar. The field survey is a fundamental task in any biodiversity research considering Myanmar urgently needs to conduct field exploration as its many flora and fauna are still awaiting to be discovered and described. However, the ongoing crisis in Myanmar, following the military takeover, has further hampered research efforts and led to an increase in illegal mining and logging, resulting in forest fragmentation and threatening habitats. International projects are being reevaluated due to the crisis, potentially impacting biodiversity research in the country. Urgent field surveys are needed to discover and protect the unique flora and fauna of Myanmar, and promoting citizen science initiatives could help engage local communities in conservation efforts.

P.0982 How many Philippine Begonia section Petermannia species are there and where to find them?

Mark Arcebal K. Naive[1,2], Mark Hughes[3], Daniel C. Thomas[4], Wen-Bin Yu[1]

1 Center for Integrative Conservation and Yunnan Key Laboratory for Conservation of Tropical Rainforests and Asian Elephants, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Mengla, Yunnan, China. 2 University of Chinese Academy of Sciences, Beijing, China. 3 Royal Botanic Garden Edinburgh, Edinburgh, UK. 4 Research and Conservation, Singapore Botanic Gardens, National Parks Board, Singapore.

A taxonomic synopsis of Philippine Begonia section Petermannia (Begoniaceae) is presented. Following a study of 88 published names and their types, we accept 69 Begonia section Petermannia species for the Philippine flora. Except for B. dimorpha and B. rieckei, all are endemic to the archipelago. Lectotypes or neotypes will be designated for all names for which this is necessary. In addition, we propose the synonymy of several species under this section and report for the occurence of B. aptera as a new record for the country. A list of additional specimen examined to facilitate correct referencing and a map showing the distribution of the species will be provided. Furthermore, a preliminary phylogenetic relationship of endemic Philippine Begonia section Petermannia species based on plastome will be presented.

P.0983 Conservation Assessment of Philippine Begonia

Rosario R. Rubite[1], Mark Hughes[2], Kuo-Fang Chung[3], Danilo N. Tandang[3,4,5,6], Mark Angelo C. Bucay[3,5,6]

1 Department of Biology, College of Arts and Sciences, University of the Philippines Manila, Manila, Philippines. 2 Royal Botanic Garden Edinburgh, Edinburgh, Scotland, UK. 3 Biodiversity Research Center, Academia Sinica, Taipei, Taiwan. 4 Philippine National Herbarium, Botany and National Herbarium Division, National Museum of Natural History, National Museum of the Philippines, Manila, Philippines. 5 Biodiversity Program, Taiwan International Graduate Program, Academia Sinica and National Taiwan Normal University, Taipei, Taiwan. 6 Department of Life Science, National Taiwan Normal University, Taipei, Taiwan.

After almost 20 years of extensive fieldwork, we now have sufficient data to assess the conservation status of the Philippine *Begonia*. Out of 166 taxa, 163 species are endemic to the Philippines. Ninety-two (92) species are known only from the type locality, 54 taxa are known from fewer than five localities. The conservation assessment of each taxon was made following the IUCN Red List Categories and Criteria v15.1 (2022). Each species was assigned to one of the seven categories namely, Extinct (EX), Critically Endangered (CR), Endangered (EN), Vulnerable (VU), Near Threatened (NT), Least Concern (LC) and Data Deficient (DD). Preliminary assessments were carried to calculate the area of occupancy and extent of occurrence of each species. These were expanded by using information gathered from field observations, herbarium specimens and literatures. A large 105 species are threatened including 24 Critically Endangered taxa, 34 are Endangered while 47 are Vulnerable. The remaining 59 species include 4 Near Threatened, 21 Least Concern and 34 Data Deficient.

S.111. NEW INSIGHTS ON BIG PLANT GENERA 2: GENOMICS & TRAIT EVOLUTION

P.0984 Genomic insight of the ratooning ability of sugarcane

Md. S. Islam1*, Keo Corak2, Per McCord1,3, Amanda M. Hulse-Kemp2,4, Alexander E. Lipka5

*1 Sugarcane Field Station, USDA-ARS, Canal Point, USA. 2 Genomics and Bioinformatics Research Unit, USDA-ARS, Raleigh, USA. 3 Irrigated Agriculture Research and Extension Center, Washington State University, Prosser, USA. 4 Department of Crop and Soil Sciences, North Carolina State University, Raleigh, USA. 5 Department of Crop Sciences, University of Illinois, Urbana-Champaign, USA. *md.islam@usda.gov.*

Ratooning ability (RA) has a significant impact on the productivity and profitability of commercial sugarcane. The genetics underlying RA can be better understood to facilitate genomics-assisted breeding. Using 432 sugarcane clones throughout three crop cycles (plant cane, first ratoon, and second ratoon), a genome-wide association and genomic prediction study of five sugar and yield parameters of RA from a repeated field trial was carried out. The yield and sugar data were used to estimate the RA characteristics for the economic index (EI), stalk population (SP), stalk weight (SW), tons of cane per hectare (TCH), and tons of sucrose per hectare (TSH). Six potential quantitative trait loci (QTL) and seven nonredundant single nucleotide polymorphism (SNP) markers were found to be connected to five examined RA samples for the first time. Significant SNPs linked to the five RA characteristics were co-located with seven potential candidate genes. For those evaluated traits, the genomic prediction accuracies varied from 0.21 to 0.36, which is considered moderate. Prediction models with fixed effects did not outperform conventional models without fixed effects. With the help of this work, we may begin to comprehend the intricate genetic and genomic foundation of RA in sugarcane.

P.0985 Complete plastome sequences of seven Juniperus species from Kazakhstan

Shyryn Almerekova[1], Moldir Yermagambetova[1], Saule Abugalieva[1], Yerlan Turuspekov[1].

1 Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan.

Juniperus L. species are mainly distributed from sea level to above the timberline in the Northern Hemisphere and play an important role in forest ecosystems. There are approximately 75 species all over the world, which belong to three sections: *Sabina*, *Juniperus,* and *Caryocedrus*. In Kazakhstan, genus is represented by eight species *J. communis* L., *J. sibirica* Burgsd., *J.* x *media* Dmitr., *J. pseudosabina* Fisch. et C.A. Mey., *J. sabina* L., *J. semiglobosa* Regel., *J. seravschanica* Kom. and *J. davurica* Pall. In this study, we report the comparative plastome sequences of seven *Juniperus* species collected in Kazakhstan (*J. communis*, *J. sibirica*, *J. pseudosabina*, *J. sabina*, *J. semiglobosa*, *J. seravschanica*, *J. davurica*). The length of the sequenced *Juniperus* species plastomes ranged from 127,469 bp (*J. semiglobosa*) to 128,097 bp (*J. communis*). Each *Juniperus* plastome contained 119 genes, including 82 protein-coding genes, 33 transfer RNA, and 4 ribosomal RNA genes (16 genes contained one or two introns, 2 tRNA genes were duplicated). Comparative analysis of *Juniperus* species plastome sequences revealed 1145 simple sequence repeat markers. Phylogenetic tree for *Juniperus* samples was reconstructed based on 82 protein-coding genes and resulted in the segregation of *Juniperus* samples into two major clades, corresponding to the *Juniperus* and *Sabina* sections. The analysis of plastome sequences indicated that *accD* and *ycf2* were the two most polymorphic genes. Utilizing these two genes for phylogenetic assessment of *Juniperus* species confirmed their efficiency as DNA barcodes for this genus. The sequenced plastomes of *Juniperus* species have provided substantial genetic data, promising significant value for future genomic studies within this genus.

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S.112. NEXT GENERATION ZINGIBERALES: FROM TAXONOMY TO EVOLUTION

P.0986 Comparative leaf lamina micromorphology and anatomy of Goeppertia Nees species (Marantaceae) from the Atlantic Forest, Brazil

Julia R. da Costa[1], Giselle B. de Araújo[1], Mariana N. Saka[2], Alessandra I. Coan[3]

1 Programa de Pós-Graduação em Biologia Vegetal (Interunidades), Universidade Estadual Paulista - UNESP, Rio Claro, São Paulo, Brazil. 2 Departamento de Ciências Exatas e Biológicas, Universidade Federal de São João del-Rei - UFSJ, Sete Lagoas, Minas Gerais, Brazil. 3 Departamento de Biodiversidade, Instituto de Biociências de Rio Claro, Universidade Estadual Paulista - UNESP, Rio Claro, São Paulo, Brazil.

Goeppertia is the most diverse genus of Marantaceae with ca. 250 species distributed throughout the Neotropics. *Goeppertia* presents six informal groups, of which the "Breviscapus" clade is the most morphologically heterogeneous. This clade comprises ca. 90 species with high representation in the Atlantic Forest. The objective of the present study was to describe the leaf lamina micromorphology and anatomy of *Goeppertia* species occurring in the Atlantic Forest, in order to characterize them and discuss possible taxonomic applications. Standard scanning electron and light microscopy techniques were used. Nineteen species were sampled, seventeen of which are endemic to the Atlantic Forest – around 35% of the species diversity of this formation – and two that also occur in the Cerrado. All sampled species share the following set of micromorphological and anatomical characters regardless of whether they are exclusive to the Atlantic Forest or occur in the Cerrado: uniseriate epidermis, covered by a thin cuticle, and formed by cells with slightly thickened walls; sinuous anticlinal epidermal cell walls ("s" type) in cross section; paracytic stomata; presence of hypodermis; dorsiventral mesophyll; collateral vascular bundles; presence of aquiferous parenchyma formed by oblique cells in the midrib; presence of phenolic idioblasts, and crystalliferous cells. The other characters varied, such as: the presence of malpighiaceous trichomes on the abaxial leaf surface of *G. fatimae*; papillose cells on the adaxial leaf surface of *G. zebrina*; obtuse leaf margin in cross section of *G. bachemiana*; convex-convex outline of the midrib of *G. applicata* in cross section. These results add information to the knowledge of anatomical characterization of *Goeppertia* in the Atlantic Forest and indicate that anatomical data can be used as a tool to distinguish sympatric or morphologically related species of the genus.

P.0987 What is the correct scientific name for the red ginger?

Rudolph Valentino A. Docot[1,2], Thomas Haevermans[1], Axel D. Poulsen[3]

1 Institut de Systématique Évolution Biodiversité, Muséum National d'Histoire Naturelle, Centre National de La Recherche Scientifique, Paris, France. 2 Institute of Art and Sciences, Far Eastern University, Manila, Philippines. 3 Royal Botanic Garden, Edinburgh, Scotland, UK.

The justification for conserving names is often open to discussion. The red ginger, *Alpinia purpurata*, is probably the most widely cultivated ornamental member of the family in the world because of its eye-catching inflorescence bracts and easy propagation. It was first described by Eugène Vieillard as *Guillainia purpurata* based on a specimen from New Caledonia. Subsequently, *Hellenia bracteata* (now *Alpinia ludwigiana*) from Java, Indonesia, has been consistently associated with *A. purpurata* in various taxonomic revisions but was never considered conspecific. *Alpinia ludwigiana* is mainly distinguished by its single flower per bract (vs several in *A. purpurata*). A closer examination revealed that the type of *A. ludwigiana* represents a cultivated form that rarely has flowers and instead multiplies asexually viviparously by plantlets in the inflorescence.

With no other difference observed, *A. ludwigiana* and *A. purpurata* are no doubt conspecific and the former has priority and is the correct name for the red ginger. Additional four taxa, *Guillainia novo-ebudica*, *Alpinia grandis*, *Alpinia purpurata* var. *albo-bracteata*, and *Alpinia purpurata* var. *anomala* have been considered synonyms but should be reevaluated. Using a targeted enrichment NGS approach, the red ginger should be placed in another genus. Since *A. purpurata* has been used for a long period of time especially in the horticulture industry, the question is if the epithet should be conserved even if placed in a different genus. This study has yet to decide on this matter and is also focusing on determining its natural distribution and differentiating wild and cultivated forms.

P.0988 Phylogenomics, a new classification, and a conservation assessment of the tropical genus Heliconia (Zingiberales: Heliconiaceae)

Gary Krupnick1, Monica Carlsen-Krause[2], Tomáš Fér[3], W. John Kress[1]

1 Department of Botany, Smithsonian Institution, Washington, USA. 2 Latin American Department, Missouri Botanical Garden, St. Louis, USA. 3 Department of Botany, Charles University, Prague, Czech Republic.

Heliconia, a charismatic genus in the monotypic plant family Heliconiaceae, is a primarily neotropical taxon with ~187 species distributed in the Caribbean islands, Mexico, Central America, and South America, with six paleotropical species in Malesia, Melanesia, and Polynesia. Many species are widely cultivated as ornamentals. Using tissue sampled from field and herbarium collections for genomic sequencing, we have determined phylogenetic patterns of relationships within *Heliconia*, which have served to erect a new evolutionary classification of the genus and a phylogenetic-based conservation assessment of all species. To conduct the conservation assessments, specimen data were accumulated from herbarium collections world-wide and supplemented with information from the Global Biodiversity Information Facility (GBIF) for all 187 species. Species distributions were mapped, and the extent of occurrence (EOO) was calculated using GeoCAT. The i-Terra layer in GeoCAT was utilized to visualize land-cover vegetation loss resulting from human activities. In addition, species of *Heliconia* were mapped across 147 ecoregions with individual species distributed in 1 to 61 regions. Using data on distribution, habitat loss, and protected habitat status, we conducted global IUCN conservation assessments following IUCN Red List categories and criteria (IUCN 2012). We also calculated using the PlantSearch tool the number of botanical gardens and living plant collections holding *ex situ* specimens of each species. We found that 49% of *Heliconia* (91 species) are threatened with extinction and that most species maintained in *ex situ* living collections are of "least concern" with respect to conservation. A phylogenetic signal appears to be present in the conservation status with some clades containing more threatened species than expected by chance. We will continue to explore the impact of evolutionary history and habitat degradation on current day conservation status and the future of *Heliconia*.

P.0989 The Phylogeny of the Carolinensis Clade of Alpinia Roxb. (Zingiberaceae)

Seni K. Senjaya[1,2], Marlina Ardiyani[2], Axel D. Poulsen[3], Tomáš Fér[4], Quentin Cronk[1]

1 Department of Botany, University of British Columbia, Vancouver, Canada. 2 Research Center for Biosystematics and Evolution, National Research and Innovation Agency Bogor, Indonesia. 3 Royal Botanic Garden Edinburgh, Edinburgh, UK. 4 Department of Botany, Charles University, Prague, Czech Republic.

Recent molecular-based studies of the ginger genus, *Alpinia*, have established that it is polyphyletic with six clades, one of which is the Carolinensis clade. Despite recent progress, a comprehensive understanding of this clade, its constituent species, and their relationships is hindered by limitations in taxonomic sampling. Our hypothesis posits that the clade comprises species distributed east of Huxley's biogeographical line, classified by Smith as the subgenus *Dieramalpinia* (*pro parte*) sensu Smith. This taxon is morphologically distinctive in having densely packed flowers along zigzag monochasial cyme branches (cincinni), tubular bracteoles, and an inconspicuous labellum. To better understand the clade, our study employs a combination of Sanger and high-throughput sequencing, coupled with an expanded taxonomic sampling approach. We include 96 accessions, representing approximately 45 species, with a selected subset of 52 accessions used for Hyb-Seq analysis. These accessions were sourced from various Botanic Gardens and collections across diverse regions, including Sulawesi, Maluku, West Papua, Papua New Guinea, and the Bismarck Archipelago (primarily by A.D. Poulsen and teams). An initial phylogenetic tree, utilizing ITS data, robustly supports the monophyletic nature of the Carolinensis group, backed by strong bootstrap support. The finding also supports our hypothesis that the clade members morphologically largely belong to subgenus Dieramalpinia. Further morphological analysis groups the species members based on floral traits, particularly inflorescence branching patterns and the presence of the flower-subtending bract, into three distinct groups. However, the resolution of the evolutionary history within this clade remains unclear, posing a challenge to further tree interpretation and correlation analysis. Ongoing Hyb-Seq analysis is anticipated to provide additional resolution within the clade, and the comprehensive results are set to be presented at the upcoming conference.

P.0990 Fruit morphology of the genus Amomum Roxb. s.l. (Zingiberaceae) in India

Valukattil P. Thomas[1], Mamiyil Sabu[2]

1 Catholicate College, Pathanamthitta, India. 2 Malabar Botanical Garden & Institute for Plant Sciences, Kozhikkode, India.

Zingiberaceae are the largest of the order Zingiberales with about 56 genera and over 1,377 species. *Amomum s.l.*, the second largest genus after *Alpinia* in the ginger family, is widely distributed in South and Southeast Asia. In India, the members occur mainly in North-East India, Peninsular India and Andaman and Nicobar Islands. The genus *Amomum* has always posed challenges for classification based on morphological characters. De Boer *et al.* (2018) investigated *Amomum* in a multi-marker phylogenetic framework using matK and nrITS including multiple accessions of the type and recognized seven genera, of which three are represented in India viz. *Amomum*, *Meistera* and *Wurfbainia.* Thomas and Sabu (2023) reported 31taxa of Amomum s.l. in India. Fruit is a fleshy capsule showing variations. The capsule is dehisced by 3 valves in M. cannicarpa but is usually indehiscent in other species. The fruit wall is smooth (e.g., *M. koenigii*), echinate (e.g., *M. fulviceps*), ridged (e.g., *A. hypoleucum*), winged (e.g., *A. maximum*) or tubercled (*W. aromatica*). The shape and colour of the capsule are important in the classification of *A. Subulatum* cultivars. The shape of the fruit is generally globose. A smooth capsule with an apical depression is found in *A. sabuanum*. The fruit wall is usually pubescent or puberulous. The calyx may be persistent or deciduous. The seeds are aromatic, arillate and closely packed in the fruit. The seeds are brown to black. The aril is white, sweet and is regarded as the aid for seed dispersal.

S.113. ORCHID PHYLOGENOMICS: DIVERSIFICATION, TRAIT EVOLUTION AND BIOGEOGRAPHY

P.0991 Factors determining orchid species richness in the central Balkans

Vladan Djordjević[1], Spyros Tsiftsis[2], Vladimir Stevanović[3], Dmitar Lakušić[1]

1 University of Belgrade, Faculty of Biology, Institute of Botany and Botanical Garden, Belgrade, Serbia. 2 Department of Forest and Natural Environment Sciences, International Hellenic University, Drama, Greece. 3 Serbian Academy of Sciences and Arts, Kneza Mihaila, Belgrade, Serbia.

The Balkan Peninsula is one of the most important centres of orchid diversity. However, the effects of environmental factors on the spatial distribution and richness of orchids in the Central Balkan region have not been studied so far. The main aim of this study is to determine the factors influencing the spatial variation of the richness of 56 orchid species and subspecies in the Central Balkans. A regression analysis was used to analyse the effect of altitude and 19 bioclimatic factors (minimum value, maximum value, mean value) on taxa richness in the Central Balkans using the UTM grid at a 10 × 10 km spatial resolution. In addition to the total number of taxa, orchids with specific underground strategies (rhizomatous orchids, orchids with palmately lobed and fusiform tubers ("intermediate orchids") and orchids with spherical tubers ("tuberous orchids")) were analysed separately. This study demonstrated that altitude, including its minimum value, maximum value, mean values, and altitudinal range significantly affects orchid taxa richness. The effects of altitude and climate factors are most pronounced in the “intermediate orchids”, where the maximum values of the altitude and the minimum values of the temperature variables have the strongest influence on orchid richness. The results confirm the hypothesis about the evolutionary development of orchids and prove that orchids with palmately lobed and fusiform tubers are best adapted to cold conditions. This research provides a good basis for better orchid conservation planning and emphasises the importance of underground strategies as a feature of orchid life history that should not be ignored when studying patterns of terrestrial orchid diversity.

P.0992 Diversification rates and key innovations explain rich diversity of Arethuseae (Orchidaceae)

Chongbo Ma[1,2], Jian-Wu Li[3], Himmah Rustiami[4], Arief Hidayat[4], Xiao-Hua Jin[1,2]

1 State Key Laboratory of Plant Diversity and Specialty Crops, Institute of Botany, Chinese Academy of Sciences, Beijing, China. 2 China National Botanical Garden, Beijing, China. 3 Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Yunnan, China. 4 Research Center for Biosystematics and Evolution, National Research and Innovation Agency, Cibinong, Indonesia.

Asian tropical and subtropical mountain ecosystems (ATSME) cover a diverse suite of complex ecosystems, ranging from tropical rainforests to alpine meadows, with well-developed evergreen broadleaf forests and monsoonal climates. Although the complexity of mountain ecosystems is closely related to rich biodiversity, the mechanisms underlying such associations remain poorly understood. Here, species diversification in orchid tribe Arethuseae with approximately 700 species mainly endemic in ATSME was investigated. Our results indicated that dramatic increases in situ diversification rates of Arethuseae were accompanied by a gradual decrease in the extinction rate at the Oligocene–Miocene boundary and mid-Miocene. The innovation of pseudobulbs and epiphytic habit may have provided evolutionary opportunities for adaptive radiation of Arethuseae. The intensification of the Asian monsoon and expansion of montane rainforests as well as their interactions were important for the formation and maintenance of mountain biodiversity in Asia. ATSME serve as both cradles and museums for diversification in Arethuseae. This study provides new insights into how biotic and abiotic factors drive the evolutionary radiation of tropical and subtropical mountain plants in Asia, and is important for the development of conservation strategies in Asian mountains.

P.0993 Studies on morphological and anatomical variations among the Bulbophyllum fimbriatum from Western Ghats of India

Shivram Khadke[1], Pooja Nikade[1]

1 Department of Botany, Smt. Kasturbai Walchand College, Sangli M.S. India.

The plants of the genus *Bulbophyllum* have thread-like, fibrous roots that creep over the surface of trees, rocks or hang from branches. The stem is divided into rhizomes and pseudobulbs. There are usually only one or two leaves present at the top of the pseudobulb. The thin sections of root, pseudobulb and leaf were stained and observed under the compound microscope and cell dimensions measured with the help of a scanning electron microscope. Internal features such as cuticles, epidermal layers, cortex, endodermis and thickening levels of water storage cells in roots of *B. fimbriatum* were examined. Cuticle was developed from 2 to 3 layers of cells provides smooth pattern. Epidermis is uniseriate and developed from elongated/polygonal cells. The progressive correlation was found between root area and cortex thickness (16 to 21 layers of mesophyll cells). The arrangement of vascular bundles is radial in shape with 9 to 11 arch surrounded by bundle sheath cells. Size of the vascular bundles was found to be expanded towards pith of *B. fimbriatum*. The pholems are found to be covered by sclerenchymatous cells, while the xylem is covered by parenchymatous cells. The velamen tissues are developed from elongated cells. The variation in epidermal layers, endodermis, thickening level of storage cells and developmental pattern of vascular bundles observed in the present study showed wide range of xerophytic adaptaion in *B. fimbriatu.* These anatomical features will be helpful for taxonomic identification of *Bulbophyllum* species.

P.0994 Advances in the understanding of the phylogenetic relationships and diversification patterns of the genus Epidendrum

Liza M. Linares Rosales[1], Gerardo A. Salazar Chávez[2], Eric Hágsater Gartenberg[3], Eder Chilquillo Torres[1], Lidia I. Cabrera Martínez[2], José D. Édquen Oblitas[4], Jessy P. Arista Bustamante[4]

1 Museo de Historia Natural, Universidad Nacional Mayor de San Marcos, Lima, Perú. 2 Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, México. 3 Herbario AMO, Instituto Chinoin, A.C., Ciudad de México, México. 4 Universidad Nacional Toribio Rodríguez de Mendoza de Amazonas, Chachapoyas, Perú.

Epidendrum is the largest genus of orchids in the Neotropics, comprising approximately 2,400 species with remarkable morphological diversity and wide distribution (from North Carolina in the United States to Argentina), thriving in a variety of habitats from sea level to high Andean environments at 4,200 meters above sea level. It represents a significant biological model for investigating evolutionary diversification in species-rich lineages. The intrageneric classification and elucidation of its evolutionary history are still ongoing tasks. In this study, for the first time, an exploration of the phylogenetic relationships of 105 *Epidendrum* species was conducted, with an emphasis on Andean taxa, analyzing DNA sequences of the Internal transcribed spacers of the ribosomal DNA (ITS) using Maximum Likelihood and Bayesian Inference criteria with the GTR+I+G nucleotide substitution model, obtaining terminal supports greater than 0.92 in 91% of cases. The resulting phylogenetic relationships recover species associations (clades) that coincide with several groups recognized based on morphology *sensu* Hágsater, including Schistochilum, Anceps, Geminiflorum, Spathiger, Oerstedella, Aquaticum, and Difforme, as well as others ungrouped due to taxonomic sampling biases. An analysis of distribution areas using a Bayesian Binary MCMC method for ancestral states (BMM) infers that the ancestral distribution would be located in the northern Andes, from where centripetal dispersion originated, with a derived South American diversification and a significant diversification event towards Central America. These hypotheses generated from a nuclear marker can be contrasted with ongoing studies analyzing markers of the plastid genome.

P.0995 Orchidaceae in Ipanema National Forest, Iperó, São Paulo, Brazil

Fiorella F. Mazine[1], Alexandre S. Medeiros[1], Lina P. Cinosi[1], Carlos H. C. Martins[1], André Guilherme[1]

1 Herbário SORO, Universidade Federal de São Carlos, Sorocaba, Brazil.

The Ipanema National Forest (FLONA Ipanema) is a Federal Protect Area (PA) for Sustainable Use, with 5,179.93 ha, located in the Brazilian state of São Paulo, especially in the municipality of Iperó. Designed for the preservation and conservation of archaeological and historical heritage, the PA has rich biodiversity, with important areas of Seasonal Forest and Cerrado. Naturalists in the 19th century visited Ipanema region, including Auguste Saint-Hilaire, Carl von Martius, Friedrich Sellow and Ludwig Riedel. The main objective of this study was to survey the Orchidaceae species of FLONA Ipanema, offering data that will contribute to the management and conservation of the species. The work aimed to produce a list of species, as well as a species identification key and plates with photos of plants in the field. The species survey involved: 1) bibliographic survey, 2) consultation of the main herbaria with species collected in the area and 3) collection of material in the field. The collected materials were identified based on taxonomic keys, consultations with herbaria, specialized literature and consultation with specialists. To illustrate the species, plates of photographs taken in the field and of herbaria specimens were prepared. Orchidaceae is represented in Brazil by 2,666 species, of which 1,493 are endemic. In FLONA Ipanema the family is represented by 15 species, circumscribed in 12 genera: *Aspidogyne* (1 species), *Bulbophyllum* (1), *Capanemia* (1), *Cyclopogon* (2), *Cyrtopodium* (1), *Epidendrum* (2), *Maxillaria* (1), *Oeceoclades* (1), *Phymatidium* (1), *Prescottia* (2), *Trichocentrum* (1) and *Vanilla* (1). Among these species, nine are epiphytes, five terrestrial, one rupicolous and one hemiepiphyte. It is worth noting that nine species have not yet been evaluated for their conservation status and *Aspidogyne kuczynskii* (Porsch) Garay had its last collection in the area in 1905, with Ipanema being the type locality of the species.

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P.0996 Floral card specimens for the study of Australian terrestrial orchids

Andrew E. McDougall[1]

1 The Faculty of Sciences, Engineering, And Technology, The University of Adelaide. Australia.

Australia boasts a rich orchid flora, with close to 2,000 species, predominantly terrestrial. During a significant period of taxonomic activity in Australian terrestrial orchids (1985—2006), the focus for diagnostic features became increasingly minute. For the *Caladenia R.Br.* genus, the character states of tepaline osmophore cell configuration and number require microscope aid for determination. Unfortunately, sub-optimal collection and preservation practices prevailed during this time, including inadequate pressing methods. As a result, many specimens were poorly presented on sheets, even affecting some type specimens intended for naming purposes. Consequently, numerous diagnostic characters are not visible on these sheets. I adopted of a method involving dissection and preservation of orchid flowers on cards, initially proposed during the aforementioned taxonomic period. In this approach, the collection process starts by documenting the plant's location and capturing digital photographs of it in its natural habitat. The flower stem is then tagged with an identification marker before being cut and placed in a cool container. In the laboratory, detailed drawings and micrographs are produced, and the flower is dissected. The dissected segments are then affixed to sections of transparent acid-free archival tape, which are in turn attached to A5-sized acid-free rag-linen cards for preservation. Utilizing this method in our review of *Caladenia patersonii* R.Br. species complex in South Australia, along with digital photography, ensured preservation and measurement of diagnostic characters. I extended this method to other selected monocotyledonous geophytes, including *Arthropodium* R.Br., *Thysanotus* R.Br., and *Calostemma* R.Br., spp. The adopted method successfully preserves floral segments, with colours and diagnostic characters well-maintained and visible on the cards, facilitating easy microscopic examination. This technique ensures accurate and comprehensive documentation of orchid species and other unrelated monocotyledonous geophytes.

P.0997 The Orchid Flora of Bahia, Brazil: an outstanding diversity in a habitat-rich state

Denis Nunes de Carvalho[1], Thiago E. C. Meneguzzo[2, 3, 4], Cássio van den Berg[1]

1 Universidade Estadual de Feira de Santana, Departamento de Biologia, Bahia, Brazil. 2 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 3 Museu Nacional, Rio de Janeiro, Departamento de Botânica, Rio de Janeiro, Brazil. 4 Universidade de Brasília, Departamento de Botânica, Brasilia, Brazil.

In our updated checklist of *Orchidaceae* of the state Bahia, Brazil, we enumerate 518 species (spp.), 4 subspecies, 2 varieties. Of those, 62 new occurrences at specific and nothospecific level are new occurrences. A total of 66 (~13%) out of the 518 specific, infraspecific, and nothospecific taxa are endemic to Bahia, which includes the monotypic *Adamantinia* and *Thelyschista*. The most diverse genera are *Habenaria* (~50 spp.), *Epidendrum* (~40 spp.), and *Gomesa* (23 spp.). The genera with more endemics are *Cattleya* (10 spp.), *Encyclia* (5 spp.), and *Gomesa* (4 spp.). In the latest checklist by the Brazil Flora Group (2020; doi: 10.1002/tax.12640) 540 orchid species were listed for Bahia, but herein we accept about 100 less species names due to synonymizations, misidentifications, and names without voucher specimens. A study of the Bahian orchid specimens shows that most of the collections coincide with areas that are the most species-rich ones, being the Atlantic Rainforest followed by Caatinga, the ecotone Caatinga-Atlantic Rain Forest, and the Cerrado. This can also be explained by the niche and habitat variation as a consequence of different kinds of soils, terrains, and altitudinal range. The most diverse and collected areas of the phytogeographic domain Atlantic Rainforest are along the coast, in the areas surrounding the state capital of Salvador (northern) and the Ilhéus (southern). For the Caatinga domain they are mostly concentrated in the Chapada Diamantina mountain range, a montane elevated area among the drylands. The third most collected and species-rich area is ecotone in the Serra da Jiboia (northeastern). The western region of the Cerrado is marginal to this domain has very few collections and diversity, which is explained by being an under collected area that has been deforested for agriculture, despite the fact that the central areas of the Cerrados are considered a global hotspot.

P.0997 The orchid flora of Brazil: a challenging ongoing taxonomic monograph in a megadiverse country

Thiago E. C. Meneguzzo[1, 2, 3], Cássio van den Berg[4]

1 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Museu Nacional, Rio de Janeiro, Departamento de Botânica, Rio de Janeiro, Brazil. 3 Universidade de Brasília, Departamento de Botânica, Brasilia, Brazil. 4 Universidade Estadual de Feira de Santana, Departamento de Biologia, Bahia, Brazil.

Orchidaceae is one of the three most species-rich plant families of the world. In Brazil it is the second more rich (Flora e Funga do Brasil, reflora.jbrj.gov.br, 14 February 2024) after Fabaceae (212 genera, 2,877 species, 681 infraspecies) and followed by Poaceae (176 genera, 1,300 species, 93 infraspecies). Orchidaceae is represented in Brazil by 204 genera, 2,342 species, and 36 infraspecies when accounted only to native taxa. The endemic orchid taxa are 23 genera (~11% of total), 1,493 species (~64%), and 32 infraspecies (~89%). Nearly all the occurring genera are restricted to the Neotropics or adjacent regions, except by the pantropical *Bulbophyllum*, *Corymborkis*, *Eulophia*, *Liparis*, *Malaxis*, *Tropidia*, and *Vanilla*. The most species-rich area is the Atlantic Rainforest with 145 genera (~71% of the Brazilian taxa; 13 endemic), 1378 species (~36%; 851), and 16 infraspecies (50%; 6), with the of the Southeast region considered a biodiversity hotspot (5 genera, 410 species, 2 infraspecies endemic). The richness in absolute numbers is followed by the phytogeographic domains Amazon Rainforest (133 genera, 779 species, 8 infraspecies), Cerrado (109 genera, 636 species, 20 infraspecies), Caatinga (49 genera, 144 species, 3 infraspecies), Pampa (31 genera, 78 species), and Pantanal (3 genera, 4 species). We speculate that the Caatinga and Pantanal are underrepresented in collections which is likely caused by undercollection, difficulties on finding specimens in field in strongly seasonally marked areas, and proper study of the already collected specimens. Many challenges are faced on monographing such a rich family, e.g., names only known from the type specimen, access to type specimens, access to specimens deposited at small collections, undercollected areas, proper knowledge of some species morphological variation along its distribution range, increasing number of newly found heterotypic synonyms, workable long-length keys plus short descriptions that encompasses morphological diagnosable features

P.0999 The evolutionary origins of Orchidaceae in the Caribbean Islands hotspot

Charlotte Phillips[1, 2], Natalia A. S. Przelomska[1, 2], Betsaida Cabrera[3], Olivia Fitzpatrick[2], Frank Schubert[1], Steven Dodsworth[1], Oscar A. Pérez-Escobar[2]

1 School of Biological Sciences, University of Portsmouth, Portsmouth, UK. 2 Herbarium, Royal Botanic Gardens, Kew, London, UK. 3 Jardín Botánico Rafael Maria Moscoso, Santo Domingo, Dominican Republic.

The Caribbean Islands hotspot hosts 4.3% of all vascular plant biodiversity on Earth yet covers only 0.2% of the land area. The region is also highly threatened with biodiversity loss as less than 10% of the primary vegetation remains in a pristine state, and together with high species diversity this is why the area is considered a hotspot. Despite the known high levels of biodiversity, the origin and evolution of this diversity still remains poorly understood. This unique study system hosts around 700 species of orchid, making them one of the most diverse plant groups in the region, both in terms of species richness and endemism. Yet roughly 93% of all Orchidaceae species still require DNA sequencing in order to be placed within the phylogenetic framework of the family. We use the Angiosperms-353 target enrichment approach to obtain novel DNA sequences from both field-collected and herbarium tissue. Maximum likelihood gene trees were reconstructed and then used to infer a species tree using ASTRAL. Here, we place over 160 species, 25 of which have never been sequenced before, and 90 genera, representing a fifth of the Hotspot's orchid diversity. We present an updated framework with particular focus on the Caribbean Islands Hotspot, with insights into the origins and diversification times of Caribbean Orchidaceae. Wider sampling of unplaced taxa, especially monotypic clades is needed for better representation of the orchid tree of life. Understanding migration and dispersal patterns of these taxa will give further insight into the source of Caribbean orchid diversity, and the drivers of high levels of endemism and species richness. Furthermore, the framework produced here can now be used to address wider issues such as taxonomic inflation, accelerating the identification of species through barcoding, and understanding natural extinction patterns in a time of human-driven mass extinction.

S.114. MICROMORPHOLOGY AND PALYNOLOGY OF MAJOR INDIAN POLYGONACEAE: IDENTITY AND INTERRELATIONSHIP

P.1000 Micro-morphology and palynology of major Indian Polygonaceae: identity and interrelationship

Monoranjan Chowdhury[1], PayelPaul[2]

1 Professor, Plant Taxonomy and Biosystematics Lab. Department of Botany, University of North Bengal, Darjeeling, India. mchowdhury@nbu.ac.in. 2 Assistant Professor, North Bengal St. Xavier's College, Rajganj, Jalpaiguri, India. payelbot@nbu.ac.in.

The family Polygonaceae comprises a group of flowering plants integrated in the order Polygonales in the Magnoliophyta of the kingdom Plantae and is prevalent in temperate regions of the world. They have an extensive array of distribution in India stretching from the coastal plains to the subtropical, temperate to sub alpine regions of Himalaya. Present study aims to study 34 taxa of seven genera, Antigonon Endl., Bistorta Adans., Fagopyrum Mill., Fallopia Adans., Persicaria Mill., Polygonum L., Rheum L. and Rumex L. of Indian origin. Accurate species level identification and to understand their interrelationship comprehensive qualitative and quantitative investigation of Leaf architecture, stomata, trichomes and detailed pollen morphology using both light microscope (LM) and scanning electron microscope (SEM). The variable epidermal cells, six different stomatal patterns, among the trichomes variation especially peltate, capitate spheroidal and stellate types of glandular trichomes were observed. Pollen morphological attributes including aperture number, pollen shape, size in polar and equatorial view, colpi length, exine thickness have been observed. Based on aperture type and exine sculpturing pattern in SEM, 3 main pollen types and 12 subtypes have been identified. Pollen grains were recorded monad, isopolar and radiosymmetric type. Pantoporate, tricolpate, tricolporate aperture type and exine ornamentation appears to be valuable and unique characters were found useful tool for the delimitation and differentiation of closely related taxa. The studied characters under LM and SEM were further statistically analyzed through ANOVA, PCA, Pearson Correlation Matrix to understand the interrelationship among the taxa. The analyzed characteristics attributes have systematic value, as they are constant at specific and generic level therefore much helpful in species level identification and understanding of their interrelationship.

P.1001 Comparative study of the leaf epidermis characteristics and micromorphology in species of Sorbus L. (Rosaceae) from Bulgaria

Tsveta Ganeva[1], Krassimira Uzunova[1]

1 Faculty of Biology, Sofia University "St. Kliment Ohridski", Sofia, Bulgaria.

The structure and micromorphology of the leaf epidermis of *Sorbus aria* (L.) Crantz, *S. chamaemespilus* (L.) Crantz, *S. domestica* L., *S. aucuparia* L. and *S. torminalis* (L.) Crantz from Bulgaria were studied by light and scanning electron microscopy. The leaves of *S. aria* had smooth cuticle of the upper epidermis unlike striated one on the lower surface. Also high stomatal and trichomes densities were counted. *S. chamaemespilus* had the largest epidermal cells of the lower epidermis and the lowest stomatal and trichomes densities of all studied species. Cyclocytic stomatal type was observed only in *S. domestica*. The lower epidermis only of *S. aucuparia* had distinctive papillae, covered by tubular waxes. *S. torminalis* had the smallest size of the stomata and high stomatal density. The observed cuticular ornamentation and crystalloid epicuticular waxes on the leaf surface, combined with the results of the morphometric analyses of the epidermal cells, stomata and trichomes allow a clear distinction of the species.

S.115. PARADIGM SHIFTS IN FLOWER COLOR

P.1002 Phylogeny and evolution of flower color polymorphism in the subfamily Linoideae (Linaceae)

Mireya Burgos Hernández[1], Alejandra Villalvazo-Hernández[1]

1 Department of Botany, Colegio de Postgraduados, Texcoco, Mexico.

Linoideae is one of the two known subfamilies in Linaceae and the larger of the two. The taxonomy of the subfamily at the intergeneric and sectional levels has been questioned over the years. Furthermore, knowledge of the evolution of floral characters is still incipient. In particular, the evolution of flower color is still uncertain, despite its ecological importance and being a conspicuous and variable trait in angiosperms. We evaluated the phylogenetic relationships of genera and sections using a Parsimony Analysis and Bayesian Inference, and the ancestral states of flower colors were reconstructed based on S-DIVA model on a phylogenetic tree with branch lengths proportional to time. Four of the five currently accepted sections were monophyletic (*Cathartolinum*, *Dasylinum*, *Linum*, and *Syllinum*). The results suggest reassessing the taxonomic status of the segregated genera and re-incorporating them into *Linum*. We propose to accept the *Stellerolinon* section and re-evaluate *Linopsis*, whose representatives were recovered in three separate clades. Our results show a close relationship between *Linum bienne* and *L. villarianum* with the cultivated flax, *L. usitatissimum*, with strong support. Knowing the phylogenetic relationships of this species is essential to explore the potential use of available resources from its sister species. The ancestral flower color of Linoideae was yellow-white. Purple and yellow-white colors were recovered in the deep nodes. Meanwhile, the colors pink, blue, and red were the most recent to appear. These results seem to be related to diversification events, biogeographic history, and ecological aspects of the subfamily. Our reconstruction constitutes the first scenario to explore the evolution of flower color, leading to new hypotheses for future research on flax.

P.1003 Red flowers differ in shades between pollination systems and across continents

Zhe Chen[1], Yang Niu[1], Chang-Qiu Liu[2], Hang Sun[1]

1 CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Kunming, Yunnan, China. 2 Center for Gardens and Horticultural Studies, Guangxi Institute of Botany, Guilin, Guangxi, China.

Floral colour serves as a pivotal signal in plant–pollinator interactions. The well-known association between red flowers and bird pollination has been explained by the 'bee avoidance' and 'bird attraction' hypotheses. We reevaluated the two hypotheses from the perspective of colour perception. We conducted a comprehensive analysis by collecting reflectance spectra for 130 red flower species across different continents, categorizing them based on their pollination systems. Using colour vision models tailored to bees and birds, we estimated how these pollinators perceive the floral colours. Additionally, we examined differences in colour conspicuousness and spectral properties within and across continents. To delve deeper into the features of bee-pollinated red flowers, manipulation experiments were meticulously conducted. Red flowers tend to be pollinated by birds, but rarely by bees. Red flowers exhibit high conspicuousness to birds and significantly lower conspicuousness to bees when compared to other floral colours. Notably, red flowers pollinated by either bees or birds are more conspicuous to their respective pollinators. Furthermore, New World bird flowers are less conspicuous to bees than their Old World counterparts, attributed to differences in the secondary reflectance peak (SP) intensity. Transitioning from high to low SP in red flowers induces chromatic contrast changes, more pronounced in reducing bee attraction than enhancing bird attraction. Manipulation experiments confirm that ultraviolet SP enhances the visual attractiveness of red flowers to bumblebees. Our study underscores the nuanced differences in shades of red flowers associated with distinct pollination systems. Remarkably, red bird flowers are more specialized in the New World than in the Old World. The evolution towards colour specialization is more likely to result in higher efficiency of bee avoidance than bird attraction.

P.1004 Reinventing colour: the evolution of transcriptional regulation across origins of betalain pigmentation

Jasmina Dzurlic[1], Samuel F. Brockington[1]

1 University of Cambridge, Cambridge, UK.

In the flowering plant lineage of the Caryophyllales, betalain pigments are specialized metabolites that replace the otherwise ubiquitous anthocyanins that occur in all other land plants. It has recently been shown that the betalain biosynthesis pathway has evolved multiple times. Convergent origins of betalain biosynthesis provides a natural experiment to study repeated evolution of a metabolic pathway. While the betalain pathway is well studied, further investigation into and characterization of the transcriptional network of genes that regulate betalain biosynthesis is needed to fully understand the production of betalain pigmentation. Members of the myeloblastosis (MYB), basic helix-loop-helix (bHLH), WD40 repeat transcription factor complex (MBW) have been linked to both the regulation of anthocyanin and betalain biosynthesis genes. However, it remains unclear whether all partners of the MBW complex and/or additional or different regulators activate genes in the betalain pathway. Here we have investigated how specialized metabolism has evolved by studying transcriptional regulation between origins of betalain biosynthesis. It is known that BvPAP1 independently regulates betalain biosynthesis genes in *Beta vulgaris* in the Amaranthaceae origin. But our results suggest different origins of betalain biosynthesis have different regulatory mechanism across origins of betalain biosynthesis. Further research is needed to characterize the transcriptional regulators of betalain biosynthesis across all origins of betalain biosynthesis to fully understand evolution of novel metabolites through transcriptional networks and regulatory mechanisms that influence evolution of metabolic pathways.

P.1005 Decoding the colours of Caryophyllales

G.J.L. Garnett[1], M.A. Guerrero Rubio[1], N. Walker-Hale[1], H. Sheehan[2], S.F. Brockington[1]

1 Department of Plant Sciences, University of Cambridge, UK. 2 Institute of Chemical, Environmental and Bioscience Engineering, Vienna University of Technology, Austria.

Specialised metabolites are common in plants, with many of these compounds conferring some fitness benefit to the individuals that produce them. My work focusses on two plant specialised metabolites: anthocyanins and betalains. Together, these pigments are responsible for much of the red colouration visible in plants. Despite their similar appearance, there are important differences between these two pigments. Anthocyanins are ubiquitous in plants; contrastingly, betalains are rare, being found only in the order Caryophyllales where they have evolved convergently up to four times. Curiously, betalains and anthocyanins are mutually exclusive, having never been found to co-occur. Some have attributed this to functional redundancy; however, the role of betalains in plants is poorly understood. The replacement of anthocyanins with betalains in some members of the Caryophyllales could suggest that betalains possess novel adaptive advantages over anthocyanins that favoured their repeated recruitment. My research seeks to better understand the functional significance of betalains, using several interdisciplinary approaches. This knowledge should reveal the extent to which natural selection played a role in the convergent evolution of betalains. It is hoped this will improve our understanding of the evolutionary forces that drive convergence more generally; in turn helping to answer a fundamental biological question – how repeatable is evolution?

P.1006 The Evolution of camouflage in plants

Yang Niu[1], Hang Sun[1], Martin Stevens[2]

1 CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan, China. 2 Centre for Ecology and Conservation, College of Life and Environmental Sciences, University of Exeter, Penryn, UK.

Like animals, plants also use camouflage as a defensive strategy. In the last decade, several cases of camouflaged alpine plants were found in the Hengduan Mountains, SW China. Using Corydalis benecincta with leaf color dimorphism, we found that cryptic individuals have higher survivorship than green ones but show similar photosynthetic performance. With Corydalis hemidicentra, we found that leaf color diverged among populations, showing local-adapted camouflage. The efficacy of camouflage correlates with the damage rate by caterpillars or Parnassius butterflies. With Fritillaria delavayi, a traditional medicinal herb, we found that leaf color divergence and the efficacy of camouflage are associated with the harvest strength by local people. Camouflaged flowers in F. delavayi are hard to visually locate by bumblebees, which are pollinated by flies instead. We revealed that there are at least four common camouflage strategies shared by both plants and animals: crypsis, disruptive coloration, masquerade, and decoration. Plant camouflage exhibits many commonalities with animals, and this understudied parallel phenomenon can inform key questions in ecology and evolution.

P.1007 Carotenoids and anthocyanins: effect on Petunia flower colour and cell shape

Martina Cerri[1], Eleonore Cinti[1], Francesca Quattrocchio[2], Ronald Koes[2], Tijs Bliek[2], Lara Reale[1]

1 Department of Agricultural, Food and Environmental Sciences, University of Perugia, Perugia, Italy. 2 Department of Plant Development and Genetic, SILS, University of Amsterdam, Amsterdam, The Netherlands.

Petunia flower colour is useful to understand the protein trafficking pathway in petal epidermal cells. Cells in the epidermis of flower petals have also the important role of attracting animal pollinators by visual and/or chemical hints and by providing a landing site. These cells contain a central vacuole (CV) filled with anthocyanins, and numerous small vacuolar compartments, called vacuolinos, which lack anthocyanins but are involved in determining cell shape. Proton pumping P- ATPases acidify vacuolar lumen resulting in reddish colour because of the high protonation of anthocianins. The inactivation of this pump results in blue petals due to higher vacuolar pH and consequent lower protonation of anthocyanins. While anthocyanins are responsible for reddish/blue colours, other pigments can contribute to produce a further range of shade from yellow to orange, as carotenoids. The aim of our research is to understand, in *Petunia*, whether the acquisition of carotenoid accumulation in petals affects the genesis of organelles devoted to their storage (chromoplasts) and results in new colours due to the coexistence of chromoplasts and vacuolinos in the same cell. Flowers at anthesis were collected from lines accumulating anthocyanins, carotenoids, or none of the two. Small portions of petals were embedded in epoxy resin. Semithin and thin sections of these samples were observed in light and electron microscopy, respectively, to identify the presence of vacuolinos and chromoplasts and to compare cell shape. First observations revealed the presence of numerous plastids only in yellow (carotenoid rich) flowers; no plastids were observed in white flowers. Vacuolinos are instead present only in purple flower. We are currently analysing some genotypes with brown flowers, which accumulate both pigments, to find out whether these have both plastids and vacuolinos, and to elucidate how and if they affect each other by, for instance, determining the localisation in the cell.

P.1008 Anigozanthos: Kangaroo paw of a different color

Cameron A. Stern1

1 Macquarie University, Sydney, Australia.

Anigozanthos (kangaroo paw) is a genus of flowering plants native to Western Australia (WA). The genus consists of 11 species and 19 subspecies. Like many species native to the area, kangaroo paw plants are well adapted to the arid and fire prone climate. Understanding their evolutionary history, as well as their functionally adaptive traits, will help provide insight into their ability for future adaptation to a changing climate and how they can best be conserved. Flower color is a key phenotype shown to be an adaptive trait in many species and is considered relatively simple for genetic and biochemical analysis. Color is also a very important trait for the horticulture industry. The recent development of a blue-flowered kangaroo paw by Kings Park and Botanic Gardens has led to increased interest in understanding the genetic architecture of these uniquely colored flowers while providing the necessary plant populations to further the goals of both the public and private sector. To understand the biochemical variability of floral pigments in *Anigozanthos*, we collected over 200 flower samples representing each of the species and subspecies from across WA. Additionally, an F2 mapping population from the same genetic background as the original blue kangaroo paw was sampled. Both wild and cultivated samples are undergoing quantitative phenotypic and biochemical analysis (HPLC-MS) to get a clear picture of the floral pigments present in the genus and whether phenotypically similar colors are determined by the same pigments. HPLC-MS is also being done to characterize the pigments responsible for blue flowers. The genes contributing to this novel blue color will be mapped using reduced-representation genome sequencing of the F2 population. The results of this project will aid future breeding and conservation efforts of kangaroo paw and may provide a road map to conserving other native WA species.

P.1009 Coloring the California Flora

Justen B. Whittall[1], Victor Rossi[1], Katie Conrad[1], Joey Hernandez-Mena[1], Melissa Ospero Leon[2], Eduardo Narbona[2]

1 Department of Biology, Santa Clara University, California, USA. 2 Department of Molecular Biology and Biochemical Engineering, Pablo Olavide University, Seville, Spain.

Flower color variation is a hallmark of angiosperm diversity. However, the majority of our understanding of flower color ecology and evolution comes from a few, select species. Evaluating the roles of pollinators and non-pollinator agents of selection on flower color requires sampling on a much broader, floristic scale. Herein, we report the flower colors of over 500 species of California native plants. Color was quantified by combining UV & Vis digital images, reflectance spectra, and biochemical analyses. We have quantified the frequency of UV patterning across the California flora. In addition, we reveal the relative contributions of anthocyanins, carotenoids, and other rarer pigments to the coloring of the California flora. We compare the distribution of flower colors in light of their habitat, background coloration, light environment, elevation, conspicuousness to pollinators, and other factors. Preliminary results reveal the near absence of yellow flowers in forest shade, an excess of UV absorbing flowers in sand dune backgrounds, widespread floral blushing, the biochemistry of hummingbird red flowers, and many more exciting patterns. Overall, examining flower color on a floristic scale from multiple perspectives has led to several discoveries in flower color ecology and evolution.

S.116. PATTERNS AND PROCESSES DRIVING CLIFF PLANT COMMUNITIES: APPROACHES FOR THE CONSERVATION OF ENDEMIC CLIFF FLORA

P.1010 Reticulate evolution in Western Mediterranean populations of Pinguicula species (Lentibulariaceae) based on genomic analyses

Guillaume Besnard[1], Mario Martínez Azorín[2], Evgeny Mavrodiev[3], María Ángeles Alonso Vargas[2], Manuel B. Crespo[2], José Manuel Segura[4], Leonardo Gutiérrez[5]

1 CNRS, Université Paul Sabatier, Toulouse, France. 2 University of Alicante, Alicante, Spain. 3 Florida Museum of Natural History, University of Florida, Gainesville, USA. 4 Urbanización Jardines del Edén, Ogíjares, Granada, Spain. 5 Junta de Andalucía, Sevilla, Spain.

Pinguicula (Lentibulariaceae) comprises ca. 100 species, mostly with Holarctic and Neotropical distributions. The genus includes many narrow endemics, mostly in the Northern Hemisphere. Today, thirteen species (eight being narrow endemics) occur in the Iberian Peninsula, and one is endemic to the moroccan Rif mountains. Genomic analyses of organellar DNA sequences based on genome skims (low coverage sequencing data) were generated on 15 Iberian and North African accessions of taxa of *Pinguicula*. On each sample, we reconstructed a plastome and a nearly complete nuclear ribosomal cluster. The phylogenetic analyses show some incongruences between data sets. A population growing with *P. grandiflora* in western Sierra Nevada (provisionally named '*P. pallidescens*') shows intermediate morphology between the former and the narrow endemic *P. nevadensis*, which points out to a recent hybrid origin and is congruent with nrDNA analyses. However, plastome results relate '*P. pallidescens*' to *P. grandiflora* plus the central Iberian *P. casperiana*, being the relationships to *P. nevadensis* weaker. Regarding *P. submediterranea* from Sierra de Cazorla, nrDNA analyses show two ribotypes, one approaching the southern Iberian *P. tejedensis* and the other to the riffean endemic *P. fontiqueriana*, this again supporting ancestral hybridization origin. Conversely, plastome analyses recover *P. submediterranea* closer to the clade *P. tejedensis*-*P. mundii*, with distant connections to *P. fontiqueriana*. Considering *P. casperiana*, plastome analyses show two populations included in a clade merging *P. dertosensis* and *P. vulgaris*, all restricted to the Iberian Mountains. Whereas, nrDNA analyses recover one sample related to *P. fontiqueriana*, *P. vulgaris* and *P. dertosensis* and the other as sister to *P. grandiflora* plus *P. pallidescens*. Our results evidence a reticulate evolutionary pattern of the Western Mediterranean species of *Pinguicula,* with possible explanations on allopolyploidy and lineage exchange.

P.1011 Conservation status and threats of the Atlantic willow formations of the Asperillo cliff (Doñana, Huelva)

Juan M. Chaparro1*, Pablo J. Hidalgo[2], José Antonio Adame[1], Cristina Pérez-Carral[3], Nuria Montiel[2], Irene Herrera[2]

1 National Institute for Aerospace Technology, Huelva, Spain. 2 University of Huelva, Dpt. Ciencias Integradas, Huelva, Spain. 3 University of Huelva, Dpt. Ciencias Agroforestales. Huelva, Spain.

The Atlantic willow formations are coastal habitats of community interest in Andalusia (Spain). This type of community is present in the Asperillo cliff, from Mazagón to Matalascañas (Huelva), where we can find some Atlantic ravines and seepage from the phreatic layer that harbour a rich and interesting riparian flora in an environment where it is not usual. Climate change and the overexploitation of the aquifer in the Doñana Natural Area, could lead to the disappearance of these unique endangered formations within a few decades. The diagnostic species was the grey willow (*Salix atrocinerea*), which grew abundantly along the Atlantic Ocean coast until it began its decline. In this study, the residual presence of this unique species on the cliff front has been assessed in order to obtain a detailed mapping for its evaluation. Furthermore, other species of interest and invasive alien species have also been recorded. For this purpose, during a period of one month (September 2022) weekly samplings were carried out along the 24 km of coastline of the study area. The analysis was conducted with the most recent false-colour infrared orthophotography. Drone flies (DJI P4 Multispectral) were used to update the digital cartography or the most difficult areas to access. During the field work, polygons of each species were carried out. In order to get more accurate results, the polygons were reviewed with ArcGIS Pro. The results obtained were 421 polygons with an area of 9.46 hectares and showing an alarming decline. The current decline in grey willow cover is 42 % of the area compared to the expected potential area, and the sum of invasive alien species dominates 34.5 % of the sampled area. This study aims to highlight the importance of this community and to take measures to protect or restore it.

P.1012 Phenomorphology and growth patterns of Petrocoptis crassifolia Rouy growing at the edges of an altitudinal gradient in Ordesa and Monte Perdido National Park, Northeast Spain.

Maite Gonzalez[1], Sara Palacio[1], Pablo Tejero[2,3]

1 Biodiversity and Conservation Department, Pyrenean Institute of Ecology-CSIC, Zaragoza & Jaca, Spain. 2 Herbarium of Jaca, Pyrenean Institute of Ecology-CSIC, Zaragoza & Jaca, Spain. 3 Botany Department, Aranzadi Science Society, San Sebastián, Spain.

In the current context of global change, it is essential to understand the adaptive capacity and plasticity of alpine rock plants to develop appropriate conservation strategies. *Petrocoptis crassifolia* Rouy is a rupicolous endemism of the central Pyrenees. The phenotypic plasticity of the species seems to determine the capacity of populations to adjust to varying conditions in water availability and temperature of the environment in which they are established. It is possible that phenological events in the populations are determining growth rates and longevity, as well as various morphological adaptations related to reproductive success and survival. Our phenomorphological study of *P. crassifolia* populations combined the analysis of plant phenology with the assessment of morphological changes over time, thus characterizing the phenological cycle, morphology, growth and longevity for two populations separated from more than 1000 m in height within the Ordesa and Monte Perdido National Park, Spain. The work is part of the PRIOCONEX project for the development of strategies and criteria for the conservation of endemic, rare or vulnerable plants. We contributed to this task documenting differences in the development and phenology of populations under very contrasting environmental conditions, which show marked differences in growth rates, longevity, reproduction and phenological activity in response to the environment. Our results support the idea that rock plants benefit from high plasticity to compensate for niche limitation.

P.1013 Rupicolous communities of the southeastern end of Sierra de Gádor (Almería, Spain): analysis of an unusual richness

Francisco J. Pérez García[1], Encarna Merlo[1], Fabián Martínez Hernández[1], Antonio J. Mendoza Fernández[1], Esteban Salmerón Sánchez[1], Juan F. Mota Poveda[1]

1 University of Almeria, Almeria, Spain.

Sierra de Gádor has been recognized as one of the most important areas for the conservation of Spanish flora. Contributing to this is the presence of several endemic and/or rare plant species that live in rocky habitats. To evaluate the diversity of flora and vegetation, 69 relevés was carried out in all rocky environments. The surveys were located at the SE end of Sierra de Gádor, close to the city of Almería, under a semi-arid Mediterranean climate. Six rupicolous plant communities could be differentiated: a) com. of *Hypericum hispanicum* (calcarenites rocky outcrops, "lastras"); b) com. of *Sonchus pustulatus* (rocks near the sea in shade but sheltered from sea-breezes); c) com. of *Teucrium intricatum* and *T. rotundifolium* (calcareous walls, more rarely dolomitic); d) com. of *Pallenis marítima*, *Crithmum maritimum* and halophile taxa (sea cliffs and saline calcareous schists); e) com. of *Sarcocapnos enearphylla* (little caves and calcareous overhangs, more rarely dolomitic); f) com. of *Launaea lanifera* and thyme-scrubland species colonizing rocky outcrops. The first two are the most dissimilar to the rest, precisely those that are not described in the phytosociological bibliography. There is an important floristic value: 126 taxa were recorded. Among those that stand out are nine that have been classified in some risk category. Highlighting *Hypericum hispanicum* (EN) and *Sonchus pustulatus* (CR). These results show an unusual richness for a small area. This richness is attributable to environmental heterogeneity, which is due to a great environmental diversity, from three points of view: geological (limestone - with and without caliche crust -, calcarenites, dolomites, calcareous schists and phyllites); geomorphological (walls, little caves, overhangs and "lastras") and microclimatic (sunny/shady positioning and exposed/protected from sea-breezes). Although rock environments are considered less affected by human activities, the presence of a large city next to these communities poses a great risk.

S.117. PERSPECTIVES ON PLANT BIOME TURNOVER IN AN ERA OF MASSIVE DATA AND NEW METHODOLOGICAL DEVELOPMENTS

P.1014 Development of efficient breeding methods for fruit trees using genomics and image analysis: application in apple and citrus

Mai Minamikawa[1], Miyuki Kunihisa[2], Shigeki Moriya[3], Keisuke Nonaka[4], Tokurou Shimizu[4], Minoru Inamori[5], Hiroyoshi Iwata[5]

1 Institute for Advanced Academic Research, Chiba University, Chiba, Japan. 2 Institute of Fruit Tree and Tea Science, National Agriculture and Food Research Organization, Ibaraki, Japan. 3 Institute of Fruit Tree and Tea Science, National Agriculture and Food Research Organization, Iwate, Japan. 4 Institute of Fruit Tree and Tea Science, National Agriculture and Food Research Organization, Shizuoka, Japan. 5 Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan.

Genomics-based approaches, such as genomic selection (GS) and genome-wide association studies (GWAS), have paved the way for the efficient breeding of plants, especially perennial fruit trees. As new genotyping platforms are developed, genotyping data from different genotyping platforms need to be combined for GS and GWAS. We assessed the potential of GS and GWAS for fruit traits using the combined apple datasets from the different genotyping systems. The accuracy of genomic prediction (GP) and the detection power of GWAS were increased for most fruit-quality traits of apples when using the combined data. To further improve the accuracy of GP and GWAS for practical breeding, we need to increase the number and quality of phenotypic data. We developed a method to automatically measure the morphological features of citrus fruits by the image analysis of citrus fruits. Then, we evaluated the accuracy of GP and the detection power of GWAS using the fruit morphological features. The high GP accuracies and the significant associations were detected in several morphological features. These results suggest that marker genotype integration and fruit morphological features obtained from image analysis are useful for GS and GWAS.

P.1015 Patterns and drivers of beta diversity in the forests and savannas of Africa.

Mathew Rees[1,2], John L. Godlee[1], David J. Harris[2], Casey M. Ryan[1], Kyle G. Dexter[1,2]

1 University of Edinburgh, Edinburgh, UK. 2 Royal Botanic Garden Edinburgh, UK.

Understanding what drives the differences within and between biomes is crucial to predict how plant communities will react to disturbance and climate change. In Africa, savannas remain understudied relative to forests, despite their important roles for storing carbon and sustaining livelihoods. Here, using biome information for over 3200 species, we divide patterns of taxonomic and phylogenetic beta diversity between forests and savannas for continental Africa, using a combination of herbarium specimens and plot data. We find that savannas have on average higher taxonomic and phylogenetic dispersion than forests. Floristic ordinations reveal the ancient links between West and South West Africa for both forests and savannas, whilst the Cameroon volcanic line appears to be a region of strong taxonomic and phylogenetic turnover. Generalized dissimilarity models show that Calcium and Phosphorous are important drivers of differences between forests and savannas. In an age where tree planting is being promoted as a viable solution to climate change and woody encroachment is threatening to invade savannas, our study highlights the importance and uniqueness of savanna diversity in Africa.

S.119. PHYLOGENOMICS AND ADAPTIVE EVOLUTION OF THE WOODY PLANT GENUS RHODODENDRON

P.1016 The character evolution of the genus Burmannia (Burmanniaceae)

Supakan Simachai[1], Saroj Ruchisansakun[1], Thaya Jenjittikul[1], Nicha Thawara[1], Vincent Merckx[2]

1 Department of Plant Science, Faculty of Science, Mahidol University, Thailand. 2 Naturalis Biodiversity Center, Leiden, The Netherlands.

Burmannia is a genus primarily mycoheterotrophic plants, with approximately 61 accepted species distributed in tropical and subtropical regions. The interaction between the genus *Burmannia* and mycorrhizal fungi has deep roots in their evolutionary history. This fascinating behavior is generally found among all sister genera in the Burmanniaceae family. The goal of this research is to understand the evolutions of mycoheterotrophic lifestyle and morphological shifts on *Burmannia* through phylogenetic approach. In this study we constructed phylogenies for 27 species, including nine species collected in Thailand and the remaining acquired from GenBank database. Bayesian and Maximum Likelihood trees were generated based on the DNA data of three sources: the internal transcribed spacer (ITS) region for nuclear data, and matK and rbcL genes for chloroplast data. The phylogenies established in BEAST2 for Bayesian inference and RaxML for Maximum Likelihood analysis. Subsequently, ancestral states of some morphological characters, e.g. the presence of rosette leaves, the colors of stem, flower shapes, outer and inner perianth shapes and colors, were reconstructed and mapped onto the phylogenetic trees using in RStudio.

S.120. PHYLOGENOMICS AND EVOLUTION OF GYMNOSPERM

P.1017 The phylogeny of extant gymnosperms poster: a visual overview of diversity and genus relationships

James Byng[1,2], Ehoarn Bidault[3,4], Rogier van Vugt[5], Erik Smets[2,6], Mark Chase[7,8], Maarten Christenhusz[1,8]

1 TU Delft Hortus Botanicus, Delft, The Netherlands. 2 Naturalis Biodiversity Center, Leiden, The Netherlands. 3 Missouri Botanical Garden, St. Louis, USA. 4 Muséum national d'Histoire naturelle, Paris, France. 5 Hortus botanicus Leiden, Leiden, The Netherlands. 6 KU Leuven, Leuven, Belgium. 7 Royal Botanic Gardens, Kew, Richmond, UK. 8 Curtin University, Perth, Australia.

Gymnosperms are widely distributed and commonly encountered plants. Many species can form dominant communities, particularly in the extensive conifer woodlands in the Northern Hemisphere, but phylogenetic diversity is higher among Southern Hemisphere groups. They are usually woody, seed-bearing plants differing from the other group of seed plants — angiosperms (flowering plants) — by lacking an ovule enclosed in a carpel. Despite being a widely studied group, molecular data frequently uncovers new insights into their relationships. There are currently twelve extant families recognised in eight orders following the most recent classification. This poster provides a visual overview of the relationships of all extant gymnosperm families and genera. It shows current phylogenetic relationships of all extant gymnosperm subclasses, orders, families and genera following the most recent literature. Important characters are listed for families and all genera are illustrated with 349 images showing the diverse range of vegetative and reproductive morphology across gymnosperms. It is presented as a comprehensive and useful educational tool for botanists, ecologists, horticulturists and other relevant fields.

P.1018 Application of the genome skimming method to investigate diversity and relationships in the Pinus mugo complex

Joanna Sikora[1], Konrad Celiński[1]

1 Department of Genetics, Adam Mickiewicz University, Poznań, Uniwersytetu Poznańskiego Poznań, Poland.

Species delimitation is an extremely important step in biological research. However, establishing taxonomic relationships solely by examining morphological traits often poses challenges, given issues related to phenotypic flexibility and the absence of distinct morphological features at the species level. The development of advanced next-generation sequencing techniques has revolutionized the rapid study of genetic diversity of entire genomes, greatly facilitating the identification and designation of plant species. Genome skimming is based on the generation of multi-copy and highly repetitive genome sequences, including complete organellar genomes and nuclear ribosomal DNA (nrDNA) clusters, through shallow genome sequencing. This allows for a large amount of genomic data to be obtained with relatively low genome coverage and at a reasonable price. In recent years, the usefulness of the genome skimming method in obtaining genomic data from herbarium samples has been demonstrated and its effectiveness in distinguishing taxonomically complex plant species has been proven. The *Pinus mugo* complex consists of closely related pines of various taxonomic ranks and morphological forms occurring in peat bogs and mountain areas of Central and Southern Europe. Numerous studies on the *Pinus mugo* complex do not fully explain the mutual relations between these taxa. The present study used a genome skimming approach to identify genetic diversity and determine taxonomic relationship in closely related taxa of the *Pinus mugo* complex – *Pinus mugo, Pinus uncinata, Pinus uliginosa, Pinus rotundata, Pinus × rhaetica*, from Polish, Czech and German populations, based on the obtained chloroplast and mitochondrial coding sequences, chloroplast intergenic spacer sequences and the complete nuclear cistron (nrDNA).

S.121. PHYLOGENOMICS AND SYSTEMATICS OF LILIACEAE

P.1020 Chromosomal evolution, environmental heterogeneity, and immigration drive spatial patterns of species richness in Calochortus

Nisa Karimi[1,2], Christopher P. Krieg[2], Daniel Spalink[3], Alan R. Lemmon[4], Emily Moriarty Lemmon[5], Evan Eifler[2], Adriana I. Hernández[6], Patricia W. Chan[2], Aarón Rodríguez[7], Jacob B. Landis[8,9], Susan R. Strickler[9], Chelsea D. Specht[8], Thomas J. Givnish[2]

1 Science and Conservation, Missouri Botanical Garden, St. Louis, USA. 2 Department of Botany, University of Wisconsin-Madison, Madison, USA. 3 Department of Ecology and Conservation Biology, Texas A&M University, Texas, USA. 4 Department of Scientific Computing, Florida State University, Tallahassee, USA. 5 Department of Biological Science, Florida State University, Tallahassee, USA. 6 California Academy of Sciences, San Francisco, USA. 7 Departamento de Botánica y Zoología, Universidad de la Guadalajara, Zapopan, Jalisco, Mexico. 8 School of Integrative Plant Science and the L. H. Bailey Hortorium Herbarium, Cornell University, Ithaca, USA. 9 Boyce Thompson Institute for Plant Research, Ithaca, USA.

Geographic variation in species diversity within a lineage reflects both evolutionary processes (speciation, extinction, geographic spread, selection for reproductive and ecological isolation) and ecological processes (e.g., the ability of individual pairs of competing species to coexist). The number of locally co-occurring species in any given area should reflect the net rates of species diversification in the lineages found there, the amount of time since divergence, the extent of pre-existing reproductive barriers, and the range of local environmental conditions that can be partitioned. The genus Calochortus (~68 spp.) provides an outstanding opportunity to test these ideas. Here we investigate whether the number of species co-occurring locally is predicted by increasing environmental heterogeneity (e.g., elevational and climatic ranges) and/or base chromosome numbers, which presumably provides the basis for immediate reproductive isolation. We test these ideas using the first nuclear phylogeny for the genus Calochortus based on targeted sequence capture of hundreds of loci. Results suggest the six major lineages within Calochortus correspond to broad geographic areas and have diverged in climate and other environmental conditions. As predicted, the number of species co-occurring locally increases with both environmental heterogeneity and number of chromosomal clades. In addition, the extent of species overlap in geographic distribution increases with phylogenetic distance, supporting the idea that local sympatry occurs after secondary contact following divergence in climate or fine-scale patterns of habitat distribution. Hotspots of Calochortus diversity – within the California Floristic Province (CFP) and the mountain ranges of central Mexico – are marked by substantial elevational and climatic diversity. The most diverse regions for Calochortus – in parts of the CFP – correspond to areas where several clades of differing chromosome numbers overlap in range, and where substantial topographic relief provides a wide range of environmental conditions to be partitioned.

S.123. PLANT AWARENESS RESEARCH AND CHALLENGES IN SCHOOL EDUCATION

P.1021 Plant-A-Question: Promoting environmental education through a new engaging board game

Andrea Fernández-Gutiérrez[1], Raquel Alonso-Redondo[2], Aitor Álvarez-Santacoloma[2], Sara del Río González[3], Giovanni B. Ferreiro-Lera[2], Norma Y. Ochoa-Ramos[2], Ángel Penas[2], Alejandro González-Pérez[2]

1 Department of Molecular Biology, Faculty of Biological and Environmental Sciences. University of Leon, León, Spain. 2 Department of Biodiversity and Environmental Management, Faculty of Biological and Environmental Sciences, University of Leon, León Spain. 3 Department of Biodiversity and Environmental, Faculty of Biological and Environmental Sciences, University of Leon, Mountain Livestock Institute CSIC-UNILEON, León, Spain. agonp@unileon.es; apenm@unileon.es; gferl@unileon.es; ralor@unileon.es; nochor00@estudiantes.unileon.es; aalvas@unileon.es; anfeg@unileon.es; sriog@unileon.es

The development and implementation of the educational board game PLANT-A-QUESTION aims to address the challenge of student engagement in environmental sciences while simultaneously contributing to the Sustainable Development Goals (SDGs). Targeting students aged 10 to 17 and extendable to the general public, the game incorporates principles of active learning, collaborative problem solving, and thematic content related to biodiversity, climate change, and botany. The methodology involved a thorough review of the curricular content, categorization of questions by difficulty levels, and formulation of group participation rules. Expociencia Unileón events provided a dynamic platform to test the effectiveness of the game with diverse student groups. Survey results from 86 participants indicated a positive reception, with the majority expressing a desire to replay the game and willingness to purchase it for family or social play. The inclusive design of the game, ensuring equal opportunities for all genders, and its ability to foster teamwork and a holistic understanding of environmental concepts received highly favorable feedback. PLANT-A-QUESTION has proven to be an engaging and effective educational tool with potential for broader adoption. Its contribution to SDGs 13 and 15 underscores its significance in promoting students' awareness of plants, climate change, and sustainable development. Future research should focus on refining the game and explore its impact across different age groups and educational settings.

P.1022 A "positive-action" approach to paleoart: Pleistocene vegetation landscapes in the Mediterranean Basin

Gabriela Amorós[1], Victoria Sánchez-Giner[1], Ariadna Amorós[1], Juan Ochando[2,1], Manuel Munuera[3], Juan Manuel Jiménez-Arenas[4], Ana Belén Marín-Arroyo[5], José Carrión[1]

1 University of Murcia, Murcia, Spain. 2 University of La Sapienza Roma, Italy. 3 University Polytechnic of Cartagena, Cartagena, Spain. 4 University of Granada, Granada, Spain 5. University of Cantabria, Santander, Spain.

The pictorial representation of past ecosystems has, since its inception, been an activity with a strong zoocentric bias. We speak of a zoocentrism that historically had deeply permeated the praxis of evolutionary sciences. In everyday reality, an overwhelming majority of works, whether published or displayed in museums or exhibitions, depict the habitat as context, ornament, or simply the background of the painting to position animals in intentionally more conspicuous perspectives. The details of anatomy or morphology are sometimes genuine zoological studies. However, plants are occasionally depicted vaguely, leaving the botanist unable to identify the species or group of species. In other instances, the botanical record is well-defined but clearly insufficient. Very often, this is the case even when paleobotanical data exist, allowing for a more precise paleoecosystem adjustment. It becomes pertinent to reconsider this zoocentrism in light of the future of paleoartistic research. Here, we present paleoartistic works for different Pleistocene sites in the Mediterranean basin linked to the presence of *Homo*. We reconstruct the plant landscape with attention to taxonomic and structural components through a paleoecological speculation based on paleobotanical information from the study sites. Regardless of the aesthetic success of the artistic design and the uncertainties associated with the scientific inquiry method, we believe that such representations of the past can contribute to the development of paleobotanical vocations. Simultaneously, they can help understand the historically contingent serendipity of each species or living form, each plant community, and each ecosystem as a result of a set of fortunate circumstances. This perspective can strengthen the conservation impulse in the general public and, above all, in future generations who will have to confront challenges of social survival in a scenario of accelerated environmental change.

P.1023 Ethnobotany as a tool: presentation and evaluation of a game-based didactic proposal to teach the scientific method and botanical contents

Lorena Gutiérrez-García[1], José Blanco-Salas[2], Isaac Corbacho-Cuello[1], Jesús Sánchez-Martín[1]

1 Area of Didactics of Experimental Sciences, Faculty of Education and Psychology. University of Extremadura, Badajoz, Spain. 2 Area of Botany, Faculty of Sciences, University of Extremadura, Badajoz, Spain.

The perception of science by Spanish society clearly needs to be improved, especially when there is a widespread idea that learning science is boring and difficult. In addition to this, Botany usually is among the science subjects one of the least valued by students. Therefore, different approaches and methodologies are being implemented to fight against the rejection of scientific contents. Moreover, since the publication of the SDGs, educational methodologies aimed at promoting sustainable education have been implemented, and ethnobotany has a high potential as didactic tool. The objective of this paper is to evaluate a game as a didactic tool, and to analyse the emotions aroused by the activity. This proposal, tested with primary school prospective teachers at the University of Extremadura, consists in a game whose main objective is to motivate about science, understand the scientific method, and learn botanical contents. First of all, participants were informed that the game, called "Morisk Holmes", had already been used in an previous experience carried out during the Science Week of Extremadura with students from the "Los Moriscos" High School in Hornachos (Badajoz) with excellent results. Subsequently, the development of the game was explained, highlighting that the game was structured following the scientific method, based on contents about aromatic and medicinal plants and the traditional knowledge linked to them. Then, the activity was carried out, and right at the end, the participants filled in a form to assess the didactic proposal and explain the emotions they felt. Positive results were obtained related to content's acceptance and assessment, methodology and proposal design, both from a didactic and sustainable point of view, awakening activating emotions such as curiosity and fun, to the detriment of others with a negative connotation such as rejection.

P.1024 Digital games as a strategy to reduce botanical unawareness and value biodiversity

Juçara Bordin[1], Elisa T. Aires[1], Vanessa P. C. Oliveira[1], Cassiano R. Oliveira[1], Talita S. Dewes[2], Felipe Gonzatti[3], Daiana Maffessoni[1], Paulo H. Ott[1], Camilo V. Rebouças[4]

1 State University of Rio Grande do Sul, São Francisco de Paula, Brazil. 2 Federal University of Rio Grande do Sul, Porto Alegre, Brazil. 3 University of Caxias do Sul, Rio Grande do Sul, Brazil. 4 Lastlighthouse Games, São Paulo, Brazil.

Brazil has incredible biodiversity with more than 39 thousand species of plants. However, plant unawareness makes people unable to perceive the presence and importance of plants in their daily lives. Botanical unawareness is the result of teachers' difficulty in addressing plant-related topics due to countless concepts, difficult nomenclature or simply the fact that plants attract less attention. Furthermore, there are few resources available for teaching Botany. Aiming to provide an accessible educational resource of interest to students, we developed four digital games with an environmental theme through which teachers use in a playful way, raising students' awareness of environmental issues and reducing botanical unawareness. The games are available for free on Google Play Store. Content was carried out through research in literature and technical visits to specific locations. All games are played by the character Laura, who travels through different environments, knows species and faces some challenges. The species represented have an informative table with name, general characteristics, geographic distribution and if endangered. The *Jornada Biomas* game presents Brazilian terrestrial biomes, emphasizing the heterogeneity of the landscape due to the vegetation and presenting endemic and endangered species. *Jornada bryophytes Pampa* highlights hornworts, liverworts and mosses in the context of the ecosystems of the Pampa biome. The *Jornada Aratinga* aims to promote an important protected natural area in southern Brazil which is home to endangered species such as *Araucaria angustifolia*. *Jornada Cânions do Sul* (in prep.) discloses the natural aspects of the UNESCO World Geopark Caminhos dos Cânions do Sul and among the species represented is *Gunnera manicata*, distributed in southern Brazil, Africa and Australia. The games can be used in formal and non-formal education spaces and we intend to sensitize players to develop a new look at plants, perceiving them in the environment and thereby mitigate botanical unawareness.

P.1025 What's in your greenhouse? The who, what, where, when and why of living plant collections

Hilary S Callahan[1], Nicholas Gershberg[1], Carolyn Dolt[1], Jared Meek[2], Aneeza Asif[1,3], Tiffany Vo[1]

1 Department of Biological Sciences, Barnard College, Columbia University, New York, USA. 2 Department of Ecology, Evolutionary and Environmental Biology, Columbia University, New York, USA. 3 Department of Computer Science, Fu Foundation School of Engineering and Applied Science, Columbia University, New York, USA.

A few North American universities and colleges maintain full-scale botanical gardens with glasshouse conservatories, and many more have greenhouses supporting diverse living collections, including Barnard College's Arthur Ross Greenhouse. Beginning in 2018, we began comparing its taxonomic inventory to counterpart collections at 31 other institutions. Analyses were conducted in an undergraduate summer mentoring program complementing a course in plant systematics and floristics. Students pursued projects aligned with personal interests while training in herbarium practice, APG4 classification, and tenets of open and reproducible science. Our compilation totalled 16,000+ accessions, 7,366 taxa at the species level, 2,091 genera, 326 families and 85 orders. A Jenks natural breaks classification binned collections based on species-level richness: large (> 1,500, 3 institutions), medium (~500–1,000, 9 institutions) and small (< 450, 20 institutions). We discerned eight orders and eight families present in all collections, and *Euphorbia* and *Tradescantia* tied for most ubiquitous genera, missing from two collections. All collections but two had at least one taxon uniquely held, sometimes at the level of genus (820), family (63) and order (8), and generally skewing toward institutions with more ambitious and formal collection management policies and larger holdings. Phylogenetic diversity within each collection and category was, generally, over-dispersed rather than neutral or clumped. To further contextualize these contemporary education-oriented collections, we compared them with lists of species displayed in the Enid Haupt Conservatory at the New York Botanical Garden and in Harvard's 19th century Ware Collection of Blaschka Glass Models of Plants. Next steps include re-updating Barnard's inventory and partial re-compilation of 2024 data, to examine trends through time in species gain or loss. We also aim to analyze these educational collections relative to the 10 plant-use categories of the recent report on the Global Distribution of Plants Used By Humans (S. Pironon *et al.* 2024).

P.1026 Exploring the Wood Collection of UENF (HUENFw) as an Informal Learning Environment in Botanical Collections

Maura Da Cunha1, Camilla R. Alexandrino[1], Gustavo D. Franco[1], Amanda A. Vento[1], Amanda S. Victorino[1], Gleice K. C. M. Ferreira[1], Cleiton Q. Bastos; Gabriel A. Ferreira[1]

1 Laboratório de Biologia Celular e Tecidual, CBB - Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, Brazil.

The informal learning environment encompasses educational spaces outside the traditional system, providing a valuable learning experience. A wood collection records biodiversity and serves as an essential source for species identification and inventory development, acting as a tool for local community outreach. Teaching in botanical collections is enriching, allowing for a practical and engaging exploration of plant diversity. This study aims to highlight the scientific collection of the "Dra. Cecília Gonçalves Costa" Wood Collection and promote playful teaching to students, contributing to human resources development and engaging with diverse audiences in the region's municipalities. Our wood collection, gathered from fieldwork in the North/Northwest region of Rio de Janeiro and various parts of Brazil, results from the Wood Collection team's field efforts (HUENFw), including collaborations with other institutions. The HUENFw houses 903 specimens, utilizing the space as a training center and offering the workshop "Unveiling the Incredible World of Woods" and a booklet on the importance of the Wood Collection. These resources not only disseminate scientific knowledge and the significance of species preservation but also serve as learning environments and connections between students, the University, and the community. Exhibitions in schools and public squares expand knowledge while the space maintains the botanical collection, enhancing understanding of regional tree diversity and contributing to regional conservation efforts.

P.1027 Rethinking strategies for native plants conservation in urban areas: A case in Oaxaca Valley, Mexico

Elvira Duran[1], Liceth Hernández-Olguín[1], Sandra Idrogo[1], Mayra Cerero[1]

1 Instituto Politécnico Nacional (campus CIIDIR-Oaxaca), Oaxaca, Mexico.

Urban areas concentrate large part of the human population around the world; here, the infrastructure transform, diminish or eliminate the original ecosystems and, elements like the native plants (NP). When NP reduce their presence a cascade of ecological implications results, mainly in the pollinators impact. With the global pollinator's crisis awareness, governmental and citizen strategies for promote pollinator gardens (PG) are being implemented almost everywhere. The PG represent opportunities for: 1) being reservoirs of native wild and ornamental plants into the urban infrastructure (like schools, streets, parks and neighborhoods) and 2) for improve ecological conditions in the almost inhospitable urban system. In Mexico, for three years ago, there is a National Strategy for the Conservation and Sustainable Use of Pollinators (ENCUSP by the acronym in Spanish), and a national record of PG. One of them is the Club-POLI PG, located in the National Polytechnic Institute campus Oaxaca. It has around 70 m2, and it is surrounded by buildings and conventional green areas (dominated by grass, bougainvillea, and cypresses). Here, by the collective action of the scholar community, at least 50 native plants are being harbored, included wild plants, which commonly were removed during the pruning grass. These wild plants included some Asclepiadaceae family members, like *Asclepia curassavica*, *A. glaucescens* and *A. oenotheroides*, which are important for butterflies' species like the monarch endangered, *Danaus plexippus*. Also, in the Club-POLI PG, the butterfly monitoring exhibited the presence of 50 different species that egging, eat as larvae and adults, refuge, and adult mating. This study case showed that transition from conventional green areas to PG in urban areas, is a fast opportunity for the conservation of plants and insect-plant interactions, resulting in improve the social-ecological resilience in school spaces and better nature appreciation among students.

P.1028 Plant awareness and botanical sense of place in biology education students in Frankfurt/Main (Germany)

Marilú Huertas de Schneider1, Volker Wenzel[1]

1 Goethe-University, Frankfurt, Germany.

The concept of Botanical Sense of Place (BSP) was introduced by Wandersee et al. (2006) to improve students' botanical understanding and prevent the lack of plant awareness, also known as 'plant blindness'. By the means of a writing template, students' affective and intellectual relationships with plants were explored. This template includes the writing of small essays about childhood memories and the selection of biological concepts in association with the students' own BSP. It was intended to be a useful tool to help botany teachers to estimate the BSP of their students for a further development of their botany courses. Nevertheless, few data about the applicability of this template exists. As a part of school garden seminars for biology education students, the applicability of this concept was evaluated in 66 students. They responded an expanded and modified form of this questionnaire. A list of the most minting plants in their childhood, an analysis of students' personal reflections regarding plant awareness, and their suggestions to increase it at school and university education, are presented.

References: Wandersee, J., Clary, R.M, and Guzman S.M. (2006): A Writing Template for Probing Students' Botanical Sense of Place. The American Biology Teacher, 68:7, 419–422.

P.1029 Incorporating nature-based solutions in schools: evaluation of student learning, climate adaptation and environmental awareness.

Raquel Marijuan Cuevas[1], Esther San José Carreras[1], José Fermoso Domínguez[1], Miguel A. Vega Ruiz[2], Jesús Muñoz[2], Sara Tena Medina[3], Miguel Angel Anton Gamero[3]

1 CARTIF Technology Centre, Valladolid, Spain. 2 Royal Botanical Garden (CSIC), Madrid, Spain. 3 Provincial Government of Badajoz, Badajoz, Spain.

The inclusion of vegetation in schools provides numerous benefits associated to hands-on experiential learning. This approach ranges from plant identification to an in-depth comprehension of their uses, evolution, and life cycles. Moreover, it promotes understanding of the ecosystem services provided by plants, their fundamental role in sustainable development and environmental preservation. In particular, the incorporation of Nature-based Solutions (NbS) in educational buildings extends these advantages, addressing climate change adaptation, enhancing well-being and environmental conditions. However, students are presented with little plant and innovative systems content, contributing to our separation from the natural world, ignorance of the biodiversity crisis and an inability to restore it. Therefore, it is important to include NbS in schools, not only for climate adaptation and thermal comfort but also to encourage botanical education and students' knowledge of ecosystem services. Within the LIFE -my BUILDING is GREEN project, we evaluated the environmental and social impacts resulting from NbS implementation and related educational workshops and demonstration activities at Gabriela Mistral school in Solana de los Barros, Badajoz, Spain. To assess how NbS influences students' understanding of ecosystem service provision and their comfort perception, we conducted surveys in the initial and final stages of the project. Additionally, to complement the information collected from the surveys, we measured the impact of NbS on indoor, outdoor and surface temperatures, and local biodiversity, comparing pre- and post-implementation conditions. Survey results indicate an enhancement in students' awareness of NbS benefits throughout the Project, coupled with an improvement in thermal comfort perception. Temperature measurements confirm a reduction in both indoor and surface temperatures within the school and biodiversity samples showed an increase in the presence of pollinators and bio-indicator species. Therefore, NbS proves to be an effective approach not only for enhancing ecosystem services in schools but also for fostering botanical knowledge through active learning based on experience.

P.1030 Botanical University Challenge: supporting botany students through quizzing

Jonathan Mitchley[1]

1 University of Reading, Whiteknights, Reading Berkshire, UK.

Botanical University Challenge (BUC) was devised in 2016 by academic botanists in the UK and has since grown into an exciting new way to celebrate plants and the next generation of botanists and other plant-aware students. BUC brings together students in a friendly and fun annual plant-focussed contest celebrating the diversity of ways to be fascinated by plants. It connects institutions offering plant-related courses in UK and Ireland and highlights the urgency to educate future generations in botany and plant science to meet global needs. The early rounds are held online and the finals are held live and combined with a student botany festival including a range of hands on plant-focused activities, and is offered free of charge to all student participants thanks to support from our dedicated funders. Twenty-eight teams from across the UK and Ireland registered for BUC 2024, and the early rounds ran online in February 2024 and the live finals will be held at the University of Oxford in August 2024. All the quiz rounds are livestreamed to our BUC YouTube channel and the videos of the contest have been viewed by 1000's of people in more than 30 countries around the world. BUC has stimulated similar approaches in Spain, Switzerland and the USA and we will present a short online questionnaire to explore the options and potential for rolling the BUC model out more widely and developing an international BUC.

P.1031 Lichen blindness – is traditional knowledge reflected in recordings of the citizen science? Case of Lithuania

Jurga Motiejūnaitė[1], Vita Džekčioriūtė[2], Reda iršėnaitė[1]

1 Nature Research Centre, Vilnius, Lithuania. 2 Institute of Lithuanian Literature and Folklore, Vilnius, Lithuania.

In temperate regions of Europe, lichens are little used and therefore little recognised in the traditional knowledge. While investigating the traditional knowledge of macrofungi in Lithuania, we have included three photos of common lichens (*Cetraria islandica, Cladonia rangiferina* and *Xanthoria parietina*) along with 50 photos of macrofungi. Of the 103 respondents, 15 said they had never seen any of the lichens shown and did not know what to call them; three recognised at least one species but did not know what it was; 85 knew at least one species and had a traditional name for it (usually a generalised and taxonomically incorrect one, e.g., mosses). *C.islandica* and *C. rangiferina* were better recognised than *X. parietina*. The former two species were also traditionally used (19 and 27 respondents identified the uses of *C. islandica* and *C. rangiferina*, respectively). The word 'lichen' was used by 14 respondents to refer to non-lichenised bracket fungi (e.g. *Fomes fomentarius*). In contrast to lichens, there were no respondents who did not identify and name (at species level) at least a few mushrooms. Meanwhile, the citizen science records (iNaturalist.org) only partially reflected traditional knowledge. There are 17,557 observations of lichens (Lecanoromycetes, Lichinomycetes, Arthoniomycetes and Verrucariales) by 1,099 observers (of the total 368,567 observations and 7,453 observers). Macrofungi (Agaricomycotina) are represented by 27,583 observations and 1,864 observers. *X. parietina* is the most recognised and most observed lichen species in Lithuania (1,358 observations, 536 observers), while *C. islandica* (163 observations, 82 observers) and *C. rangiferina* (150 observations, 87 observers) do not even rank among the most observed lichens. The reasons for the differences between traditional knowledge and citizen science recording are: 1) the age of the respondents/observers; 2) the areas where the lichens are observed/sighted; 3) the purposes for which the species are observed or recognised.

P.1032 Promoting plant awareness and educational self-regulation in undergraduate students of Pharmacy

Lourdes Rufo[1]

1 Instituto de Investigaciones Biosanitarias, Facultad de Ciencias Experimentales, Universidad Francisco de Vitoria, Madrid, Spain.

At present, there is no degree in Spain specifically aimed at training future botanists, although botany or plant biology is included in the curricula of some university degrees of different types, including pharmacy. The approach to this discipline may vary depending on the degree, the profile of the graduate and the entry profile. In most cases, botany is considered basic and/or compulsory and is usually included in the first courses. Although the specialization in this science is framed in postgraduate education, the initial approach is of vital importance to sow the interest in this discipline. On the other hand, the student entering university is very different from the student of a few decades ago in terms of competencies, acquired knowledge, particular interests, and vision of reality. Among the peculiarities is their low capacity for self-regulation, which hinders their autonomous study and their resilience in the face of unattained goals. In response to this, an educational experience has been carried out for three consecutive years with an adaptation of the program of the subject Plant Biology, of the first year of the degree in Pharmacy, in order to attract students to the discipline based on i) the deep knowledge of plants as sensitive living organisms; ii) the importance of knowing and preserving their diversity; iii) the reasons why plants have been, are and will continue to be medicinal sources. The development of the program is based on the pedagogical methodology of the flipped classroom to promote the self-regulation of the students. The results indicate that, in terms of the students' perception, they improve their understanding of the subject and their interest in it. The activities carried out, especially those aimed at thinking about plants as living beings, help the students to increase their level of awareness of plants.

P.1033 Angiosperm diversity in Miraflores, Colombia, and analysis of leaf morphology as teaching strategies in Botany

Yessica A. López1. Diana M. Arias [1]. Andrea L. Simbaqueba[2], Liliana Rosero[2]

1 Facultad de Educación. Universidad Pedagógica y Tecnológica de Colombia. 2 Facultad de Ciencias Básicas. Universidad Pedagógica y Tecnológica de Colombia.

Floristic diversity refers to the assembly of plant species coexisting in a specific geographic region, while foliar morphology encompasses the physical and structural characteristics of leaves. We assessed floristic diversity and variation in foliar morphology of angiosperm species in the Sub-Andean Forest (1,000-2,500 m) in the municipality of Miraflores, Boyacá. Sampling was conducted during both dry and rainy seasons between 2022 and 2023 as part of Botany II field practices. Specimens with reproductive structures were collected in accordance with international curatorial standards, and data on locality, geographic coordinates, elevation, vegetation type, collectors, site description, and human interventions were recorded. Taxonomic keys and online collections were utilized to identify the minimal taxonomic categories. For foliar variation analysis, characteristics such as organization, arrangement, adhesion, shape, size, base type, venation, apex, margin, and texture were examined. A total of 105 species were recorded, distributed across 40 families and 86 genera, with 15% classified as Liliopsida and 85% as Magnoliopsida. Families with the highest genera richness included Asteraceae (15), Rubiaceae (9), Orchidaceae (7), Solanaceae (7), and Euphorbiaceae (6). Regarding leaf organization, 99 species exhibited simple leaves (Asteraceae 14.28%, Rubiaceae 8.57%), while six species had compound leaves (Fabaceae, Mimosoideae 28.56%). Alternate arrangement predominated (53%) over opposite (44%). As a strategy to enhance Botany II teaching and learning processes, an interactive key for family identification based on evaluated vegetative characters was developed. Preliminary results suggest that Miraflores harbors high biological diversity, facilitating the analysis of adaptations to the environment, teaching of the subject, and development of pedagogical tools to enhance learning and disseminate scientific knowledge.

P.1034 Hands-on botany! Instructional material for botanic classes

Aline S. Tajima[1], Flora A. G. de Queiros[1], Alessandra I. Coan[2]

1 Universidade Estadual Paulista, Rio Claro, São Paulo, Brazil. 2 Departamento de Biodiversidade, Instituto de Biociências de Rio Claro, Universidade Estadual Paulista, Rio Claro, São Paulo, Brazil.

Botany teaching in Brazil is often associated with boring and uninteresting classes, even in college. Mainly because teachers rather use examples linked to zoology to teach basic biology principles. The use of didactic material, such as games, is a strategy to make content more interesting during classes and motivate active participation from students. Our aim was to develop instructional material for basic education teachers and professors to use them during botany classes. Points widely applied in botanical identification, including typology of both phyllotaxis and inflorescences were chosen as the theme. A practice manual, a crochet model kit, and a deck of cards were created. The crochet models represent different types of phyllotaxis or inflorescences; a set of cards contains morphological definitions of types of phyllotaxis and inflorescences and another set contains photos of plants that are commonly present in everyday life. The manual contains recipes for crochet models, diagrams of both phyllotaxis and inflorescences, description of activities and games that can be worked on in the classroom with the material. The games were applied in undergraduate classes of Biological Sciences and Ecology courses at Unesp in Rio Claro. The students showed a lot of interest, the feedback was positive regarding the use of the game, and they had an active learning process during practice. The incorporation of games and hands-on activities was particularly effective in stimulating interest during class and helped students to grasp complex concepts more easily.

P.1035 Fighting plant blindness at school: educational resources for high school students

Beatriz Vigalondo[1,2], Belén Albertos[3], Juan Antonio Calleja Alarcón[2,4], Isabel Draper[2,4], Ricardo Garilleti[3], Francisco Lara[2,4]

1 IES Jose Luis Sampedro, Tres Cantos, Madrid, Spain. 2 Universidad Autónoma de Madrid, Madrid, Spain. 3 Universidad de Valencia, Valencia, Spain. 4 Centro de Investigación en Biodiversidad y Cambio Global (CBIC-UAM), Madrid, Spain.

Secondary education classrooms reflect societal attitudes towards botany, revealing its limited recognition among students and even teachers, despite its fundamental role in our daily life and ecosystems. The lack of familiarity with common plant species, let alone lesser-known ones like bryophytes, mirrors a broader oversight of women's contributions to science, particularly in botany and bryology. To address this plant blindness, engaging educational resources are essential. These resources should integrate students' personal interests and everyday experiences while employing active discovery methodologies to teach botany effectively. Moreover, combining the study of botany with recognition of women's scientific achievements can help address social blindness on both fronts. This communication outlines three educational experiences aimed at high school students: i) integration of Pokemon into botany lessons as an introduction to the study of biodiversity; ii) knowing plant diversity and taxonomy by the contributions of women in botany; and iii) practical laboratory sessions on bryophytes diversity and their role in ecosystems. Through these initiatives, we aim to foster a deeper understanding and appreciation of botany while highlighting the significant role of women in science.

S.124. PLANT CONSERVATION GENETICS: FROM INSITU AND EXSITU CONSERVATION TO REINTRODUCTIONS AND RESTORATIONS.

P.1036 Drivers of plant translocation outcome: an analysis of more than 3000 translocation cases from Europe

Sandrine Godefroid[1,2,3], Timmy Lacquaye[1], Hannah Branwood[4], Sarah E. Dalrymple[4], Andreas Ensslin[5], Thomas Abeli[6]

1 Meise Botanic Garden, Meise, Belgium. 2 Fédération Wallonie-Bruxelles, Service général de l'Enseignement supérieur et de la Recherche scientifique, Brussels, Belgium. 3 Université libre de Bruxelles, Laboratory of Plant Ecology and Biogeochemistry, Brussels, Belgium. 4 Liverpool John Moores University, School of Biological and Environmental Sciences, Liverpool, United Kingdom. 5 Conservatory and Botanical Garden of the City of Geneva, Chambésy, Switzerland. 6 Department of Science, Roma Tre University, Rome, Italy.

Plant translocations are a conservation technique increasingly used around the world. In Europe, many initiatives have taken place without having been published, with the result that the information remains very scattered in grey literature to which access is not easy. This represents a major obstacle to the exchange of information and experience among scientists and practitioners. To help fill this gap, we launched a large-scale continent-wide survey with 39 questions relating to methods, motivations, problems encountered and outcomes, supplemented by a screening of scientific publications, grey literature and national/regional databases. This made it possible to locate and gather data on 3,220 plant translocations across the European continent carried out on 1,185 taxa in 28 countries, which represents the largest dataset ever collected globally. Target species most often were forbs from grassland habitats and they had a higher threat status nationally than globally. Practitioners mainly used plug plants (less than 100) originating from a single source (geographically closest to the target site). Weather events and plant disease were the unanticipated problems most often noticed by respondents. Monitoring revealed that most populations did not survive more than 5 years, demonstrating the challenge translocations are still representing for conservationists. However, this large database allowed us to identify the most relevant drivers of translocation outcome in terms of plant survival and recruitment that will inform future plant translocations.

P.1037 Population genomics of the threatened Verbascum charidemi (Scrophulariaceae) provides insights for conservation management

Serafín Olías-Valencia[1], Hedwig Schwarzer[2], Rocío Juan[1], Encarnación Rubio[1], Sara Martín-Hernanz[1,3], Mario Fernández-Mazuecos[4], Jose Luis Blanco-Pastor[5], Abelardo Aparicio[1]; Clara de Vega[1], Rafael G. Albadalejo[1]

1 Universidad de Sevilla, Seville, Spain. 2 Red Andaluza de Jardines Botánicos y Micológicos en Espacios Naturales, Almería, Spain. 3 Universidad Complutense de Madrid, Madrid, Spain. 4 Universidad Autónoma de Madrid, Madrid, Spain. 5 Universidad de Cádiz, Puerto Real, Spain.

Many taxa at risk of extinction are exclusively categorized using demographic and ecological factors. However, the use of genomic information to evaluate the genetic diversity of endangered species is increasingly being advocated for a more precise conservation management. We conducted a genomic study of the endangered *Verbascum charidemi*, a species strictly endemic to the littoral area of Sierra del Cabo de Gata, SE Spain. The species is seriously threatened by the low number of individuals (about 100) distributed in five population nuclei in a very small extent of occurrence. We collected and genotyped almost all individuals of this species using the genotyping-by-sequencing technique and implemented phylogenomic and population genomic approaches. This allowed us to provide new insights on the taxonomy and relationships of this species within the taxonomically complex genus *Verbascum*, and to determine population genetic structure and diversity for prioritization of *in situ* and *ex situ* conservation measures. Our preliminary results support the monophyly of *V. charidemi*as a species sister to *V. nevadense*, also endemic to SE Spain. *Verbascum charidemi* is characterized by very low levels of genetic diversity in all population nuclei, with slightly higher diversity levels in the North. It also shows evidence of significant levels of inbreeding, very likely due to mating among relatives within family clusters, since this species is allogamous and lacks mechanisms for vegetative reproduction. The five population nuclei were poorly connected by gene flow. Clustering analyses indicate population structure (geographically discrete nuclei), separating populations from the North, Centerand South areas. Based on this genomic information, we suggest cultivation in botanical gardens for future reintroductions and reinforcement actions of wild populations, and translocations in suitable locations.

P.1038 A new era for cycad genomics – custom cross-species marker set

James A. R. Clugston[1,2], Rachael V. Gallagher[1], Vanessa Handley[2], Jian Liu[3], John S. Donaldson[4], Matt G. Johnson[5], Michelle Van der Bank[6], M. Patrick Griffith[2]

1 Hawkesbury Institute for the Environment, Western Sydney University, Penrith, Australia. 2 Montgomery Botanical Center, Coral Gables, USA. 3 Yunnan Key Laboratory for Wild Plant Resources, Kunming, Yunnan, China. 4 Department of Plant and Soil Sciences, University of Pretoria, Pretoria, South Africa. 5 Department of Biological Sciences, Texas Tech University, Lubbock, Texas, USA. 6 African Centre for DNA Barcoding, University of Johannesburg, South Africa.

The Cycadales represent an enigmatic group of seeds plants with an interesting evolutionary history. But many cycads exist in small, fragmented populations, thus quantifying patterns of genetic diversity is critical for understanding their population biology and to support conservation efforts. Cycads are one of the most threatened groups of organisms globally, with continuing declines in populations driven by natural and human meditated activates. Therefore, new tools are urgently required to help understand genetic diversity and conserve this unique lineage, as existing genomic approaches do not provide sufficient depth and clarity on the genetic structure of cycads. This is primarily due to genetic complexity of cycads which makes repeatable genomic level sequencing intractable and not cost effective. Thus, to help in joint conservation efforts for cycads a universal approach for answering genomic level questions is needed, that can be applied using fresh and degraded genetic material.

Here we seek to create a new standard approach for conservation of cycads using genomics to generate a custom target enrichment probe set. The design of this universal probe will be set to work across all extant cycad lineages (Cycadaceae and Zamiaceae) and will combine with universal maker sets designed for angiosperms. The use of targeted enrichment has quickly become the standard for both phylogenomics, population genomics and for population genotyping. The use of target enrichment has many advantages including very is very consistent maker recovery and the ability to recover from highly degraded herbarium specimens or stem fragments from illegal trade. The probe set we are developing will be used to address conservation related questions, with a main aim to differentiate interspecific and intraspecific level differences in populations to better understand species boundaries, evolutionary relationships, detect hybridisation and create forensic applications for tackling illegal trade in cycads.

P.1039 In situ & Ex situ conservation of imperiled plant species in the Southeastern United States

Emily E.D. Coffey[1], Laurie Blackmore[1], Carrie Radcliffe[1], Lauren Eserman-Campbell[1], John Evans[1], Loy Xingwen[1], Jason J. Ligon[1]

1. Atlanta Botanical Garden, Southeastern Center for Conservation, Atlanta, USA.

At the Atlanta Botanical Garden (ABG), the Southeastern Center for Conservation (SECC) leads in advancing plant conservation science through innovative research collaborations, native species recovery programs, and sophisticated horticultural practices. ABG specializes in propagating often under-represented endangered plant groups, restoring and managing their habitats, and focusing on the conservation genetics of these rare taxa. Both in situ and ex situ conservation methods are employed, encompassing field collection, laboratory research, and conservation horticultural practices of imperiled species. With over 30 years of experience, ABG has honed a comprehensive strategy for conserving rare and threatened species. This strategy includes propagation, habitat management, and collaborative restoration efforts, extending across the southeastern United States to the Neotropics. The goal is to address the urgent need to protect imperiled species through diverse conservation approaches. A pivotal part of ABG's conservation work involves diversifying ex situ collections. This includes extensive living collections tracked by maternal line, a seed bank with both conventional and cryopreservation techniques, micropropagation, and tissue and DNA banks. These measures ensure a holistic approach to species preservation. ABG also focuses on capacity building, organizing workshops, providing in situ training, and setting up tissue culture laboratories in biodiverse regions. These initiatives develop plant material for in situ augmentation at protected sites, aid in the outplanting of plants, and assist in monitoring natural populations. ABG's multifaceted approach integrates state-of-the-art science with practical conservation measures, aiming to ensure the survival and stability of imperiled plant species in both natural and managed settings.

P.1040 A translocation project for Geum rivale L. in the Guadarrama Mountains

Aitor García Goyenechea[1], Isidoro Colmenero Martín[2], Felipe Martínez García[1]

1 Polytechnic University of Madrid. Madrid, Spain. 2.-Rural, Agrarian, and Food Research and Development Institute from Madrid. Madrid, Spain.

Geum rivale L. is an eurosiberian herbaceous plant from the Rosaceae family, which is very rare in the Iberian peninsula. Its main Spanish populations are located in the north, in the Cantabrian Ledge, where the climate has an Atlantic character (eurosiberian). However, the populations located in the south are situated in small microclimatically favourable areas, where they can be protected from the characteristic mediterranean climate of the most part of the peninsula. Therefore, these populations are relictual and very isolated from each other, which survive in wet settlements, such as those located in the Guadarrama and Ayllón mountains (both located in the Madrid and Segovia provinces). For these reasons, *Geum rivale* is protected by the Regional Catalogue of Endangered Species from the Madrid Community. This protection implies the responsibility for elaborating a specific conservation plan for this species. The objective of this study is to contribute to this plan by designing a translocation project. In order to achieve our objective, we have done germination tests for establishing which pretreatment allow us to producing individuals *ex situ* in the most efficient way. Subsequently, we have elaborated a potential distribution model for the species (niche model) using the MAXENT program, which allowed us establishing the ideal places where the translocation project could be accomplished: where to do a population reinforcement or, on the other hand, where to introduce or reintroduce this species. Finally, we have elaborated the translocation design, considering the results all the analysed parameters (climate, soil, etc) and a first stage has been accomplished, using the individuals produced in the first germination tests.

P.1041 Conservation genomics of the critically endangered Limonium estevei Fern. Casas (Plumbaginaceae)

García-Rodríguez, Rosanna[1,6]; Schwarzer, Hedwig[2]; Rubio-Pérez, Encarnación[1]; Martín-Hernanz, Sara[1,3]; Fernández-Mazuecos, Mario[4]; Blanco-Pastor, Jose Luis[5]; Aparicio, Abelardo[1]; Albaladejo, Rafael G.[1]

1 Universidad de Sevilla, Seville, Spain. 2 Red Andaluza de Jardines Botánicos y Micológicos en Espacios Naturales, Almería, Spain. 3 Universidad Complutense de Madrid, Madrid, Spain. 4 Universidad Autónoma de Madrid, Madrid, Spain. 5 Departamento de Biología, Instituto de Investigación Vitivinícola y Agroalimentaria, Campus de Excelencia Internacional Agroalimentario (ceiA3), Universidad de Cádiz, Puerto Real, Cádiz, Spain. 6 Herbario Erik Leonard Ekman, Universidad ISA, Santiago, República Dominicana.

The conservation of endemic species is of utmost importance as they are often at risk of extinction, primarily due to habitat alteration and fragmentation and low genetic diversity. Genomic analyses are increasingly used in biodiversity conservation to provide unparalleled resolution on patterns of genetic diversity and structure, offering new tools to explore for conservation applications and management. *Limonium estevei* Fern. Casas (Plumbaginaceae) is a species strictly endemic to Sierra de Cabrera and the nearby coastal area of Mojácar, SE Andalusia (Spain). This species occurs in a single population in increasingly fragmented nuclei, with an estimated census of only 7000 individuals and an area of presence ca. 1.7 km². Anthropogenic habitat loss and fragmentation, and low reproductive success, have brought the species to Critically Endangered status. Furthermore, natural hybridization with its widely distributed congener, *L. cossonianum* Kuntze, is considered a potential threat to *L. stevei*, as it faces the possibility of genomic swamping. In this study, we sampled all known extant nuclei of *L. stevei* and used genotyping-by-sequencing to assess levels of population genetic diversity and implemented Bayesian approaches to infer the population structure, demographic history, and degree of introgression with *L. cossonianum*. We aim to present insights on the genomic variation of *L. estevei* to provide important information for its conservation and the application of in situ and ex situ strategies, and the suitability of potential reintroductions and reinforcement actions.

P.1042 Validating priority areas for the conservation of Butia (Arecaceae) genetic resources

Gustavo Heiden[1,3], João Iganci[2,3]

1 Embrapa Clima Temperado, Pelotas, Brazil. 2 Universidade Federal de Pelotas, Pelotas, Brazil, 3 Pampa Singular

Butia (Arecaceae) is a palm genus of 24 South American species, occurring in Brazil, Argentina, Paraguay and Uruguay. According to the historical records, the distribution of Butia palm groves was greatly reduced in the last decades compared to the current area occupied by the last remnants. We mapped the specimens' records with natural occurrence in South America and are reevaluating the conservation status of the species and their respective threat criteria based on historical records to map priority areas for conservation. The results based on historical records are guiding the search of recent populations visible in satellite images. Then, fieldwork is being conducted to confirm and validate the current persistence of *Butia* palm groves in the priority areas, validating the proposition of these areas for in situ and ex situ conservation. According to preliminary data, ten species were evaluated as Vulnerable (VU), seven species as Critically Endangered (CR), three species as Endangered (EN), two species were assessed as Near Threatened (NT) and one species could not be assessed due to Deficient Data (DD). The priority areas for in situ conservation chosen based on the species distribution and threat status are being validated as viable or not. Thus, current persistence of remaining viable populations is the first condition to validate an area as priority for the in situ conservation of genetic resources and as a source of germplasm for ex situ conservation, restoration and rewilding projects.

P.1043 Genetic diversity of the critically endangered endemic Tripleurospermum heterolepis (Asteraceae): a preliminary assessment

Fatih S. Beris[1], Rabia Sagan[2], Huseyin Inceer[2]

1 Department of Biology, Faculty of Arts & Sciences, Recep Tayyip Erdogan University, Rize, Turkey. 2 Department of Biology, Faculty of Sciences, Karadeniz Technical University, Trabzon, Turkey.

Tripleurospermum heterolepis (Asteraceae) is known only from the type locality in Gumushane provience from Türkiye. It is a local endemic species classified as CR (critically endangered) category of IUCN (The International Union for Conservation of Nature) and is facing high risk of extinction due to several anthropogenic threats. In this study, we analyzed the genetic diversity of this species using five inter simple sequence repeats (ISSR) markers in thirteen individuals to contribute with information useful for the establishment of conservation actions. Within the population, the similarity indices among thirteen genotypes were between 0.396 and 0.700, according to the cluster analysis based on UPGMA. The present results obtained from ISSR analysis indicate that the conservation of *T. heterolepis* requires *in situ* strategies, such as implementing a monitoring program and establishing a 'botanical reserve', and *ex situ* strategies, such as collection and long-term storage of seeds. Acknowledgments: This study was partly supported by the Scientific and Technological Research Council of Türkiye (TUBITAK, project no.122Z845) in the frame of 2519-COST CA18201 "An integrated approach to conservation of threatened plants for the 21st Century".

P.1044 In vitro seeds germination of native endangered Sri Lankan orchid Aerangis hologlottis

Jayalath J.M.S.M.[1], Wijeratne I.L.[1], Maddumage P.M.[1]

1 Royal Botanical Garden, Peradeniya, Sri Lanka.

Among the 193 of Sri Lankan orchid species, 137 are in the threatened categories and 72 species are in the endangered category. Therefore, conservation measures should be taken focusing on native and endemic orchid species. *Aerangis hologlottis* orchid species native to Sri Lanka and distributed in Kenya, Mozambique, Sri Lanka, and Tanzania. It is growing as an epiphytic subshrub. Populations of the species have been recorded in Royal Botanical Garden, Nalanda and Aluthgama in Sri Lanka. The species is in the endangered category according to the IUCN 2020 Red List. The study aims to develop an in-vitro seed germination medium for A. *hologlottis*. Mature seed pods of A. *hologlottis* were collected from a naturally grown plant population at the Royal Botanical Garden, Peradeniya. Seeds were used to grow using five different treatment methods and five replicates as a completely randomized design under laboratory conditions at the Royal Botanic Gardens. Different media were used in this experiment to test the most suitable medium for further use. Successfully germination was observed after 115 days in the medium supplemented with BAP P.02 mg/l, NAA P.01 mg/l, and IBA P.01 mg/l, 250 ml of coconut water. The study supports identifying a method to multiply this plant in vitro and introduce the industry of floriculture use. Hence this plant is small in size it can be suggested to use as a terrarium plant. Since it's under the category of endangered, it's important to find methods to develop the population in ex-situ conservation. This type of study provides the intention to develop new methods to conserve this kind of plants further.

P.1045 Population genetics of rare and threatened Cardamine serbica in the Balkan Peninsula

Mira Fiškalović[1], Judita Zozomová-Lihová[2], Marek Šlenker[2], Ivana Džaković[3], Predrag Lazarević[1], Maja Lazarević[1]*

*1 University of Belgrade, Faculty of Biology, Belgrade, Serbia. 2 Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovakia. 3 Public Enterprise for National Parks of Montenegro, Podgorica, Montenegro. *Contact: majat@bio.bg.ac.rs.*

Cardamine serbica Pančić (Brassicaceae) is a critically endangered plant species inhabiting steep screes in mountains and gorges in only several places in the Balkan Peninsula. Survival of the species in its *locus classicus* near Lake Perućac (Mt. Tara), which is the only known locality in Serbia, is under threat due to habitat destruction and the extremely small population size. Implemented conservation measures, based on the removal of surrounding vegetation, ex-situ seed propagation, and translocation of these individuals to the original population, led to an improvement in habitat quality and an increase in the number of individuals. This study aimed to investigate the genetic structure and diversity in all populations of *C. serbica*, consider their genetic suitability in the case reinforcement with individuals from other populations is needed, and investigate the impact of the implemented conservation measures on the genetic diversity of the population in Serbia. Microsatellite and ddRADseq analyses were performed on 114 individuals of *C. serbica* originating from seven populations throughout the species' range. The results show that the population in Serbia is genetically highly impoverished and distinct from all other populations of the species, even from the geographically closest one on the other side of lake Perućac in Bosnia and Herzegovina. Strong genetic bottlenecks and genetic drift in this small population have probably led to its genetic uniqueness. Recent habitat restoration and translocation of individuals (from 2019 to 2023) have kept the diversity stable with minor fluctuations, but the real impact can only be expected over a longer period of time.

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P.1046 Deciphering the role of ecological, geographical and climatic factors on genetic structure of T. baccata in the Iberian Peninsula

Eudald Bach[1], Miquel Riba[1,2], Carmen Bouza[3], Javier Ferreiro[4], Francesco Maroso[3], Paulino Martínez[3], Pablo Ramil-Rego[4], Manuel Vera[3], Maria Mayol[1,2]

1 CREAF, Cerdanyola del Vallès, Spain. 2 Univ. Autònoma Barcelona, Cerdanyola del Vallès, Spain 3 Departamento de Zooloxía, Xenética e Antropoloxía Física, Facultade de Veterinaria, Universidade de Santiago de Compostela, Campus de Lugo, Lugo, Spain. 4 IBADER (Instituto de Biodiversidade Agraria e Desenvolvemento Rural), Universidade de Santiago de Compostela, Campus de Lugo, Lugo, Spain.

English yew (*Taxus baccata* L.) is a long-lived dioecious gymnosperm presently found in a variety of habitats throughout most of the European continent. Despite its wide distribution, populations are often small and isolated, particularly in the Mediterranean area. Therefore, it is included in several conservation actions and laws in European countries. As a result of its fragmented distribution, gene flow among English yew populations is limited, and genetic diversity is highly structured both at the local and the regional scale. Inference based on distinct molecular markers support a consistent demographic decline of English yew populations, suggesting that habitat suitability for this species has been worsening during the last millennia. In East-Central Europe, it has been suggested that the overall genetic variation of yew populations tends to decrease with mean tree size/age, due to a greater impact of founder effects in younger populations. This is consistent with the theoretical predictions for a metapopulation with extinction-recolonization dynamics, and fits well the expected recolonization history of northern latitudes after the last glaciation. Genetic diversity in populations from southern refugia, however, might reflect different and more complex evolutionary scenarios. Identifying the main factors that determine the distribution of genetic diversity in this area is fundamental to guide conservation and management actions, as well as to predict the species' response in the future. To further investigate the main factors affecting genetic diversity in southern English yew populations, we used SNPs and nuSSRs to disentangle the relative contribution of ecological, geographical and climatic factors on the genetic structure of English yew in the Iberian Peninsula. Contrary to northern latitudes, genetic patterns were not determined by tree size/age. Instead, genetic diversity patterns were mainly explained by past and current climatic conditions experienced by populations, particularly by the amount and variability in precipitation.

P.1047 Genetic diversity and structure of natural Shorea robusta populations in India as revealed by microsatellites markers

Garima Mishra[1], Shailesh Pandey[2], Rama Kant[1], Rajendra K. Meena[1], Maneesh S. Bhandari[1]

1 Genetics and Tree Improvement Division, Forest Research Institute, Dehradun, India. 2 Forest Protection Division, Forest Pathology Discipline, Forest Research Institute, Dehradun, India.

The foundation for effective selection practices, breeding, and conservation of forest trees lies in understanding genetic variations, which can be evaluated through the use of molecular markers. *Shorea robusta*, a wind-pollinated timber species of significant commercial value in southern Asia, has experienced a sharp decline in stocks. It is attributed to factors such as excessive logging, inadequate natural regeneration, overexploitation, and habitat fragmentation. Consequently, there is an urgent requirement to develop robust genetic conservation approaches. In this study, we investigated the genetic diversity and structure of fifteen populations using microsatellite-based marker in the state of Uttarakhand (India). Out of 60 primers, 24 showed polymorphisms. Notably, ten primers were used omitting 14 null alleles. Estimates of genetic diversity (NA=3.69, HO=0.377, HE=0.555) were similar when compared to other tropical tree species. The polymorphism information content (PIC) was noted as 0.252. Also, the gene flow estimate was Nm=0.728 migrant per generation that suggested a very limited gene flow with very low value of genetic differentiation (FST=0.281). In the structural analysis, bar plot for estimated Q-matrix at K=2 for different sampled populations revealed two distinct clusters. Moreover, the AMOVA revealed that most of the genetic variation (76%) was confined within population. The accessibility of sequence information and novel SSR markers through our study, potentially enriches the current knowledge of the genomic background for *S. robusta* and for implying conservation programme when extrapolated on a large scale. Based on results, protection of populations is recommended for the sustainable conservation of genetic resources and rare alleles.

P.1048 Critical carnivores: The conservation potential of Nepenthes in ex situ collections

Olivia G. Murrell[1,2], Philip J. Esseen[2], Rebecca N. Lewis[2], Jennifer K. Rowntree[3], Leah J. Williams[2], Francis Q. Brearley[1]

1 Manchester Metropolitan University, Manchester, UK. 2 Chester Zoo, Chester, UK. 3 University of Plymouth, Plymouth, UK.

The monotypic *Nepentheaceae* is the largest family of pitcher plants, with its center of diversity in Southeast Asia. Many species of *Nepenthes* are endangered at some level, given their often narrow endemism, threats to native habitats, and prevalence in the illicit plant trade. Despite their precarious position in the wild, this genus is widely held in botanic garden collections worldwide, though little is known about its *ex situ* status. The objective of this study is to determine which species are held in collections and to what extent they represent the genus in the wild. To achieve this objective, we have adapted the zoological model for endangered species conservation by consolidating known accession-level data about *Nepenthes* in collections, with the aim of informing breeding decisions and material exchanges. In this first stage of research, we gathered accession data from 55 institutions worldwide, with the largest collections held at Chester Zoo (Chester, UK) and the Royal Botanic Gardens, Kew (Richmond, London, UK). We found that 66% of the genus is represented in gardens, but 40% of these represented species have fewer than 5 individuals in living collections. Additionally, 81% of the species evaluated for the IUCN's Red List are represented. While this indicates good coverage in terms of number of species, there are still relatively few individuals in collections. Populations are small and are at risk of inbreeding depression if not managed effectively. An action plan for the long-term sustainability and conservation value of these collections is needed, and this research begins to address that need.

P.1049 Genetic characterisation and conservation of New Zealand Pimelea

Jessica M. Prebble[1], Rob Smissen[1], Carina Davis[1]

1 Manaaki Whenua – Landcare Research, Lincoln, New Zealand.

Rapid species radiations often present challenges for species delimitation, and the genus *Pimelea* (Thymelaeaceae) in New Zealand is a good example of this. A recent taxonomic revision identified c. 54 taxa, but despite being based solely on morphology these can still be difficult to identify in the field. More than 60 percent of the species are considered threatened or at risk of extinction, and additional un-named entities have been identified, which if they prove to be species would also be endangered. Prior attempts to resolve the phylogeny using ITS and plastid markers have shown the New Zealand species plus several Australian endemics form a clade nested within the main Australian phylogeny, but these markers do not have sufficient variation to aid in species delimitation. We have developed a set of low copy nuclear markers in an attempt to help resolve species boundaries, and are using these to test the morphological species hypothesised in the recent revision. The first example, the *P. villosa* complex, is a coastal species group that has undergone a significant decline, and there are numerous community groups involved in its conservation and restoration around New Zealand. We compare the genetic diversity of in situ wild remnant populations to those being cultivated ex situ for conservation. In addition, *Pimelea* in New Zealand is it a host to several endemic *Notoreas* moths, which are themselves endangered.

S.125. PLANT CONSERVATION IN MEDITERRANEAN AND MACARONESIAN ISLANDS

P.1050 Biogeography and genetic diversity of the range-restricted species Diplotaxis ibicensis based on genotyping-by-sequencing (GBS)

Lucía Bezares[1], Mario Fernández-Mazuecos[1], Emilio Cano[2], Joana Cursach[3], Joshua Borràs[3], Pablo Vargas[2]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Real Jardín Botánico (CSIC), Madrid, Spain. 3 Universidad de las Islas Baleares, Palma, Spain.

Population genetic analyses are essential in order to design conservation measures for threatened species. Here, we investigate *Diplotaxis ibicensis* (Pau) Gómez-Campo, a range-restricted species distributed in the western Mediterranean Basin, specifically in the Balearic Islands (Mallorca, Ibiza, Formentera and Cabrera) and eastern Iberia (Alicante). It has a conservation interest as it is protected by national law (Real Decreto 139/2011) and international conventions (European Council Directive 92/413/CEE). Sixteen populations distributed in five geographic areas were sampled, and three objectives were addressed: (1) to evaluate the geographical and evolutionary origin of the populations; (2) to estimate the levels of genetic diversity and differentiation among populations; and (3) to reconstruct colonization patterns explaining its current distribution range. On the one hand, the ITS region was sequenced for this species and *Diplotaxis* relatives, and phylogenetic analyses were conducted (objectives 1, 3). On the other hand, genome-wide DNA polymorphisms were obtained using a high-throughput sequencing technique, genotyping-by-sequencing (GBS), and analysed using phylogenetic and population genetic approaches (objectives 2, 3). Taking into account both phylogenetic and population genetic results, we propose specific measures useful to enhance conservation strategies for the studied species.

P.1051 Feral goats and flora conservation: A study of herbivory impact in insular Mediterranean landscapes

Joshua Borràs[1], Miquel Capó[2], Miguel Ibañez[3], Jordi Bartolomé[4], Elena Baraza[1]

1 Research Group of Plant Biology under Mediterranean Conditions. Departament de Biologia. Universitat de les Illes Balears, Palma, Spain. 2 Plant & Animal Ecology Lab. Centro para la Conservación de la Biodiversidad y el Desarrollo Sostenible. Departamento de Sistemas y Recursos Naturales. Universidad Politécnica de Madrid, Madrid, Spain. 3 Forest Research. Forestry Commission, Roslin, United Kingdom. 4 Grupo de Investigación en Rumiantes, Departamento de Ciencia Animal y de los Alimentos. Universitat Autònoma de Barcelona, Bellaterra. Spain.

Changes in land use have led to an increase in ungulate populations in Mediterranean landscapes and, in some cases, negatively affecting plant communities. This issue is exacerbated on islands where native herbivores are extinct, and the present are of domestic origin. Mallorca's mountain ranges are home to feral goat populations (*Capra hircus* L.). Our study aimed to analyze the relationship between the presence of ungulates, and plant diversity and community composition. We established 80 plots of 25m² using a random sampling method, evaluating herbivory pressure (using the number of fecal pellet groups as a proxy), plant species diversity, habitat type, altitude, trees' basal area, NDVI, slope, and orientation. Our data did not reveal a significant effect of the number of fecal pellets on plant diversity and composition. However, we observed a significant positive relation with species number in pine forests. The number of plant species increases signifyingly with attitude and decreases with adult tree density. One hypothesis is that the Mediterranean flora, well adapted to herbivory, presents a high degree of resilience against the pressure from wild goats on our plots. On the other hand, it could also happen that plots currently with no or low presence of ungulates have been grazed in past years, currently presenting a plant community already modelled by herbivory. Otherwise, we could be observing a selection by goats for higher-altitude areas that are also areas with greater species richness.

In conclusion, despite the possible negative effects that the presence of feral goats can have on the conservation of certain vulnerable species, at the level of plant diversity, the pressure levels observed in our study plots do not have a negative impact. Therefore, the management of feral populations in the Tramuntana mountains must be adapted to each area according to flora characteristics.

P.1052 Conservation status of Limonium (Plumbaginaceae) in Greece: an updated synthesis

Efstathios Apostolopoulos[1], Nikolaos Gkournelos[1], Anna-Thalassini Valli[2], Theophanis Constantinidis[1]

1 National and Kapodistrian University of Athens, Athens, Greece. 2 Agricultural University of Athens, Athens, Greece.

Limonium Mill., the largest genus of the Plumbaginaceae family, incorporates annual or perennial herbaceous plants. It is represented in Greece by 85 species, inhabiting predominantly coastal environments and found in salt-rich soils and rock crevices. Currently, there are no Greek *Limonium* species in the IUCN Red List, but 13 species are included in National Red Data Books. Our involvement in the project "Compilation of Red List of Threatened Species of Plants of Greece" conducted by the Natural Environment & Climate Change Agency in collaboration with the IUCN, allowed us to assess the conservation status of all Greek *Limonium* species, register the threats they face, and focus on targeted conservation measures. Our assessment utilized data from the bibliography and our fieldwork and revealed that 56.5% of Greek *Limonium* species are under threat. Specifically, 29.4% are classified as Vulnerable (VU), 21.2% as Endangered (EN), and 5.9% as Critically Endangered (CR). Additionally, 4.7% are categorized as Near Threatened (NT), while 38.8% are deemed Least Concern (LC). When considering endemic species alone, the threat level increases to 60.5% (32.0% VU, 23.0% EN, 5.5% CR), with 5.5% NT and 34% LC. In contrast, non-endemic species exhibit lower threat levels, with 18% classified as threatened (9% VU, 9% EN, 9% CR), and 73% deemed LC. The primary threats identified are residential and commercial development (including tourism) affecting 56.2% of the threatened species, followed by the impact of invasive species (37.5%), and human intrusions and disturbance (18.8%). Notably, 15% of the threatened species possess extremely narrow distribution ranges. This, coupled with the high vulnerability of their coastal habitats, underscores the pressing necessity for effective conservation measures. Regarding the

LC *Limonium* species, 48% of them are widespread, and 52% are range-restricted but not currently facing any known threat.

P.1053 Pollination and reproductive success of the range-restricted species Diplotaxis ibicensis in two different coastal habitats

Miquel Rodríguez[1], Marcello Dante Cerrato[1], Antoni J. Far[1], Miguel Á. González-Estévez[2], Samuel Pinya[1], Joana Cursach[1]

1 Universidad de las Islas Baleares, Palma, Spain. 2 Instituto Mediterráneo de Estudios Avanzados (UIB/CSIC), Esporles, Spain.

Deeping on the knowledge of the reproductive biology of plant species is a key issue in conservation biology. This study focuses on *Diplotaxis ibicensis* (Pau) Gómez-Campo, a taxon endemic to Mallorca Island, Pityusic Islands and Alicante coast (western Mediterranean Basin), located mainly in satellite islets, that has a conservation interest as it is protected by national law (Real Decreto 139/2011) and international conventions (European Council Directive 92/413/CEE). It is an entomophilous species, although there is no information about its reproductive biology. Two study populations were selected in Mallorca: in a rocky coastal habitat in the west of the Island (El Toro) and on fixed dunes in the south (Es Marquès). During the flowering peak of the species, pollinators were collected for taxonomical identification and focal censuses were carried out to gather information related to the visitation rate. Reproductive success was evaluated through fruit set and seed set. During autumn, 385 plant-pollinator interactions were observed in Es Marquès (40 h of censuses) and 364 in El Toro (29 h of censuses). Overall, we identified more than 20 pollinator species, and *Hylaeus (Paraprosopis) taeniolatus* Forster, 1871 (Colletidae; Hymenoptera) was the most frequent pollinator in both studied populations. Although the visitation rate was similar between populations (0.24 (± P.8) (n=16) visits per flower and for 10 minutes in Es Marquès vs. 0.31 (± P.7) (n=16) in El Toro), the fruit set was higher in Es Marquès (55.56% ± 7.13) (n=18) than El Toro (35.83% ± 4.96) (n=17) (p-value P.31) as well as the seed set (29.72% (± 6.01) (n=15) in Es Marquès vs. 11.20% (± 5.15) (n=16) in El Toro; p-value P.26). Further analyses of collected pollinators' pollen load will reveal their specific contribution to the reproductive success of this range-restricted species.

P.1054 An inventory of assessing the conservation status and extinction risk of the endemic plant species in Egypt: Mediterranean coastal

Mohamed M. El-Khalafy[1], Yassin M. Al-Sodany[1], Dalia A. Ahemd[2], Heba Bedair[2], Soliman A. Haroun[1], Salma K. Shaltout[2]

1 Botany and Microbiology Department, Faculty of Science, Kafrelsheikh University, Egypt. 2 Botany and Microbiology Department, Faculty of Science, Tanta University, Tanta, Egypt.

Having valid and up-to-date information on the ecological and conservation status of threatened species is one of the most important elements in the establishment of an effective conservation programme The IUCN Red List is a critical indicator of the health of the world's biodiversity which provides information about range, population size, habitat and ecology, use and/or trade, threats and conservation actions that will help to inform necessary conservation decisions. The Plant diversity in the Mediterranean region depends heavily on endemism. The majority of species belonging to this area are narrow endemic species. The present study aims at evaluating the conservation status, degree of risk to extinction of Mediterranean plant species in Egypt and changes of these species over the past 50 years. Twenty Field visits have been carried out from between February 2017 till September 2022 including different locations in the Mediterranean region for investigation as well as evaluation of all studies in the investigated area, scientific literatures, and different herbaria were visited. Main habitats, coordinates and threats were recorded through visits, while evaluation of conservation status was based on IUCN Red List Categories and Criteria. A complete IUCN assessment for 15 Mediterranean endemic taxa was conducted including: Geographic range, population characteristics, habitat, ecology, threats and Conservation actions. Assessment showed that 13 taxa are threatened (7 endangered, 2 critically endangered and 4 believed to be extinct). On the other hand, two species as Data Deficient. Human impacts (especially urbanization and tourism) and climate changes (especially drought and extreme temperature) are the most severe threats that impacted the taxa in this region. taxa. The present study has the priority for complete evaluating these taxa according to IUCN categories.

P.1055 Plant site preparation and population reinforcements within the Life+ SEEDFORCE in Sardinia: first results and lessons learnt

Mauro Fois[1], Maria E. Boi[1], Alba Cuena-Lombraña[1], Ludovica Dessì[1], Andrea Lallai[1], Francesca Meloni[1], Lina Podda[1], Marco Porceddu[1], Gianluigi Bacchetta[1]

1 Department of Life and Environmental Science, Cagliari State University, Cagliari, Italy.

Developing successful plant conservation projects is a challenging task and requires an inclusive and multidisciplinary approach, bringing together diverse expertise to address all critical issues. The Life+ SEEDFORCE project aims to improve the conservation status of 29 threatened plant species from Italy, Malta, Slovenia and France through an integrated approach that includes *in situ* and *ex situ* studies and conservation actions. Six endemic plants listed in Habitats Directive 43/92/EEC from Sardinia were targeted: *Astragalus verrucosus* Moris, *Centranthus amazonum* Fridl. & A.Raynal, *Limonium strictissimum* (Salzm.) Arrigoni, *Linaria flava* (Poir.) Desf. subsp. *sardoa* (Sommier) A.Terracc., *Linum mulleri* Moris and *Ribes sardoum* Martelli. Threats to each *taxon* were initially identified and addressed, followed by the establishment and implementation of protocols for propagating the species and reinforcing populations. Although the project is still ongoing, early results have shown that: 1) preliminary actions, such as reproductive biology, demographic, and ecological niche modelling studies, are critical to better identify target populations and sites, and to enhance the reintroduced plants' survival; 2) establishment of germination protocols in the laboratory improves the success of larger-scale replications; 3) site preparation, such as alien species removal and population reinforcement, achieve better results in terms of awareness and cost-effectiveness by involving local stakeholders. The here presented activities are increasingly needed in the Anthropocene Era. However, the growing crisis in many areas of the planet leads to better use the limited resources devoted to plant conservation. It is therefore imperative to monitor and share the experiences gathered from this and similar projects.

P.1056 10 years of monitoring of threatened vascular flora in Menorca: some results and conclusions

Pere Fraga i Arguimbau[1,2]

1 Institut Menorquí d'Estudis, Maó, Menorca, Spain.
2 Jardí Botànic Marimurtra, Fundació Privada Carl Faust, Blanes, Spain.

In 2015, the Menorca threatened flora monitoring program was launched, promoted by the Menorca Biosphere Reserve Agency of the Menorca Insular Council. Its main objective is to continuously assess the level of threat and the state of conservation of the taxa of the vascular flora under threat, to have solid information for a better long-term management time limit. The selection of the taxa to be monitored was based on their rarity in the island territory, that is, those with less than five known populations. For all of these, a first assessment has subsequently been made according to the IUCN criteria, those that have been classified as threatened (VU, EN, CR) have been included in the monitoring program. The monitoring consists of periodic in-situ visits in which a census is taken of the cash, the threats are determined, the possible negative effects of these and the conservation status of the habitat and the surrounding environment are also assessed immediate Based on this data, the state of conservation is determined annually according to the criteria established by the AFA project and the level of threat according to the criteria established by the IUCN. Based on these results, the information collected in situ and the evolution of the taxon's situation, management measures are proposed to improve the state of conservation and reduce the level of threat. A total of 151 taxa have been evaluated so far. In the most up-to-date information, the distribution by threat level is: 37% VU, 13% EN, 58% CR, while for the state of conservation, 20% is worrying and 18% is alarming. In the most critical situation categories (CR and alarming), non-endemic taxa predominate (90% and 85%) compared to endemics (10% and 15%).

P.1057 Conserving pale flax (Linum bienne) in the Mediterranean Basin

Yong-Bi Fu[1]

1 Plant Gene Resources of Canada, Saskatoon Research and Development Centre (AAFC).

Pale flax (*Linum bienne*) is long known to be the wild progenitor of cultivated flax (*L. usitatissimum*) and is expected to harbor an important source of genetic variability for flax genetic improvement. Literature review shows that little exploration has been done, particularly regarding its utilization and conservation. Currently, there are only 350-400 accessions available in seed genebanks worldwide and 114 less duplicated pale flax accessions with GPS coordinates. Clearly, the existing germplasm collections have poor coverage in the European and Mediterranean regions and large geographical gaps in the species distribution. No germplasm was collected from the regions of northern Africa, Jordan, Iraq, Syria, and Iran. Also, no reports were found on the development of in situ conservation strategies to protect pale flax natural populations. Thus, urgent actions are clearly needed to assess the species' vulnerability, particularly in those regions without any collected germplasm, and to develop effective in situ conservation strategies.

P.1058 Phylogenetics, phylogeography and conservation of Chaenorhinum rodriguezii, a neoendemic species from the island of Mallorca

Francisco Gómez Prieto[1], Llorenç Sáez[2], Mario Fernández-Mazuecos[1]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Universitat Autònoma de Barcelona, Barcelona, Spain.

Chaenorhinum rodriguezii (Porta) L. Sáez & Vicens (Plantaginaceae, Antirrhineae) is an endangered endemic species from the Tramuntana mountain range, in the north of the western Mediterranean island of Mallorca. It is classified as a narrow endemic, as only three extant populations are known, each with a very small number of individuals. Some authors consider it a subspecies of *Chaenorhinum origanifolium* (L.) Kostel., but morphological and reproductive traits support its consideration as a distinct species. In this study, we conducted a phylogenetic analysis of the genus *Chaenorhinum* using the nuclear ITS region and the plastid *rpl32-trn*L region to clarify the evolutionary origin of *C. rodriguezii* and its relationship with *C. origanifolium*. A phylogeographic study of the three populations of *C. rodriguezii* was also carried out using the plastid DNA regions *trn*Q-*rps*16 and *trn*V-*ndh*C. Results show that *C. rodriguezii* belongs to a recently diversified clade of *Chaenorhinum* species from the western Mediterranean Region, with *C. origanifolium* as one of the closest relatives. The divergence of *C. rodriguezii* is estimated to have occurred during the Pleistocene, and therefore it should be considered a neoendemic species. The phylogeographic study indicates relatively high plastid DNA variability (considering the small population sizes) and significant isolation among the three populations. Based on these patterns, conservation measures are suggested for this endangered species.

P.1059 GO-Argan: operational group rescuing argan tree, an alternative crop for climate change Mediterranean agriculture adaptation

Yalbeiry Labarca-Rojas[1,2,4], Esteban Hernandez-Bermejo[1,2,4], Francisca Herrera-Molina[2,3,4], Jose L. Quero[1,3,4], Rocío Hernández-Clemente[1,2,4], Alfonso Jiménez Ramírez[4]

1 University of Cordoba. Córdoba, Spain. 2 Red CultIVA – CYTED (www.cyted.org/es/cultiva). Cordoba, Spain. 3 Andalusian Plant Germplasm Bank (BGVA). Cordoba, Spain. 4 Go-argán Andalusian Operational Group supported by Operational Groups of the European Innovation Partnership in the field of agricultural productivity and sustainability.

Argania spinosa (L.) Skeels is a species with current natural distribution in Morocco and Algeria. It has been mainly introduced in Tunisia, Israel, and Spain for productive purposes, although it is still underutilized in these countries today. The species is highly spiny and has a high genetic diversity showing high polymorphism in size, shape, and size of leaves and fruits. Nowadays, argan can still be considered non-domesticated due to the difficulties in propagation, variety selection, and direct harvesting (from the tree canopy) in part because of the peculiarities of its biology, ecology, and phenology. This high economic-value oilseed species is collected from the trees that make up forest formations and pastures. Collectors extract it from the ground, but almost always after the fruit has been consumed by livestock (goats, camels). Recent studies about argan distribution models and its presence in circum-Mediterranean countries have extended its strategic value compared to other species more sensitive to climate change. For this reason, it has been established in Andalusia, Spain, as a species with a high potential for economic development. According to this, the Andalusian Argan Tree operational group was set up in Spain in 2019, bringing together various academic and scientific institutions, and joining them with agricultural and breeding companies, with the common aim of advancing the processes of domestication of the species for its cultivation. The cluster is working on the construction of predictive models regarding the future evolution of its natural formations and the analysis of its potential cultivation or agroforestry use in other territories. This communication presents some of the results in the last five years, including several publications, experimental cultivations, advances in propagation protocols, analysis of its genetic diversity in *ex situ* populations, and identification of new uses and industrial and medicinal properties.

P.1060 Reproduction biology of the narrow endangered endemic Scrophularia oxyrhyncha Coincy as first step to its conservation

Eusebio López Nieto[1], Tomás Rodríguez-Riaño[1], Francisco J. Valtueña Sánchez[1], Josefa López Martínez[1], José L. Pérez-Bote[1], Ana Ortega-Olivencia[1]

1 Universidad de Extremadura, Badajoz, Spain.

Scrophularia oxyrhyncha is a narrow endemic species from SW Iberian Peninsula with few and, generally, small populations habiting areas with major anthropic disturbance (habitat fragmentation, grazing disturbance, among others). It is classified as "Vulnerable" in Andalusia, Castilla-La Mancha and Extremadura, and as "Insufficient Data" at the national level. Therefore, knowing its reproductive biology is essential for initiating conservation processes. Its reproductive biology has been analyzed in an Extremaduran population subjected to intense grazing by sheep during 2019 and 2021. We selected five inflorescences in each of 15 different individuals. Each inflorescence was designed for a different pollination test: spontaneous self-pollination, hand-geitonogamous pollination, hand-cross pollination and agamospermy, as well as a control. Additionally, we carried out a forced xenogamy in another individual with a single inflorescence to check if fruit/seed set was limited by pollinators. We evaluated fruit and seed set from each of the pollination tests and control. Both parameters varied significantly among treatments and years. Fruit set after hand geitonogamy and xenogamy was about 74%, clearly demonstrating that this species is self-compatible. By contrast, it was practically null after spontaneous self-pollination, highlithing the pollinator importance for sexual reproduction and the effectiveness of protogyny. Seed set after control and hand-xenogamy was significantly higher than those from forced xenogamy and geitonogamy demonstrating pollinator limitation and greater reproductive success with cross-pollen. These results highlight not only pollinators necessity for the survival of this species, but also to achieve greater reproductive success, by facilitating cross-pollination. In recent decades, both climate change and intensive grazing, are greatly reducing the presence of pollinators, posing a serious danger to the survival of endemic, rare and endangered species. In our case, the pollinators are being displaced and without them the plant cannot reproduce sexually, endangering its survival.

P.1061 Conservation translocations of Anchusa sardoa (Illario) Selvi & Bigazzi, a critically endangered Sardinian endemic species

Emmanuele Farris[1], Arianna Amadori[1], Antonella Cosseddu[1], Martina Deplano[2], Alfredo Maccioni[1,*], Mariano Mariani[3], Sergio Ortu[3], Marco Porceddu[2], Gianluigi Bacchetta[2]

*1 University of Sassari, Sassari, Italy. 2 University of Cagliari, Cagliari, Italy. 3 Azienda Speciale Parco di Porto Conte, Alghero, Italy. *Presenting author. amaccioni@uniss.it*

Plant translocations are rising as a common conservation practice, and are needed when the conservation status of a given taxon falls in one of the IUCN threatened categories. *Anchusa sardoa* (Boraginaceae) is a narrow endemic plant that grows only on coastal sandy dunes in the Regional Park of Porto Conte (NW Sardinia). Previous research demonstrated a dramatic decline of its population size > 80% in < 10 years, mainly caused by increasing mass tourism pressure. Due to the very restricted range and evidence of Allee effects caused by habitat fragmentation, more pronounced on juveniles, the plant was categorized as CR. A dramatic decline of the total population was observed from 2005 to 2015, when -92.1% of the individuals disappeared (from 9,200 to 725) and six out of 14 population patches underwent extinction. To contrast decline processes, a first attempt of translocation was undertaken in winter 2015: 104 adult individuals, obtained from wild seeds, were planted in five sites, of which two where the plant experimented extinction and three with already present individuals. After two years, 0% of the planted individuals survived in the first two sites and 0.3 new individuals per each planted adult were found near these areas, whereas in the last three sites survival was 94.4% with 1.52 new individuals per adult plant. A further translocation plan was planned in 2023-24, because, based on detailed total counts of remnant population patches and despite an increase of the total population, the number of adult individuals did not vary in eight years. To reinforce extant populations and reintroduce extinct populations, a total of 3,634 seeds was collected in spring-summer 2023: the majority was stored *ex-situ* at the Sardinian Germplasm Bank (BG-SAR), whereas ca. 100 were used for multiplication and the juvenile plants will be translocated in the winter 2024-25.

P.1062 Restoration of potential vegetation in degraded semi-arid areas on the island of Tenerife, Canary Islands, Spain

Victoria Eugenia Martín Osorio[1], Wolf H. Wildpret Martín[2], Rocío González Negrín[1], Alberto de la Rosa Padilla[1], Alejandro T. Martín Umpierrez[1], Wolfredo Wildpret de la Torre[1]

1 Universidad de La Laguna, La Laguna, Spain. 2 Georg-August-Universität Göttingen, Göttingen, Deutschland.

The EU Biodiversity Strategy 2030 sets targets to further protect nature in the EU. However, it stresses that protection alone would not be enough, in order to reverse the loss of biodiversity, efforts must be redoubled and nature restored across the Union, both in protected areas and beyond. The Commission therefore committed to proposing legally binding targets to restore the EU's degraded ecosystems, especially those with the greatest potential for carbon capture and storage, as well as to prevent natural disasters and reduce their impact. The territory being restored on the island of Tenerife, is characterized by being a degraded area due to the multiple interventions and disturbances of anthropic origin that have been carried out in the area, having been predominantly used for agricultural and currently being in a state of abandonment, greatly affected by changes in topography and soil properties. Its natural values are focused on the coastal strip, with the presence of a protected habitat classified as of "community interest" made up of fragments of vegetation formed by potential species of the coastal halophilic belt, although it is also heavily affected by anthropogenic impacts. The purpose of the project is to be able to restore the territory to a more natural state, with the different units of the plant landscape that must have existed before the successive anthropic interventions and with this, contribute to the natural regeneration of one of the most altered areas of the Canary Islands, such as the coastal strip. Furthermore, it supports a typical halophilic geopermaseries vegetation and habitats that represent a very appropriate biotope for the establishment of ornithological fauna, crustaceans and mollusks, and on the other hand, the area corresponding to succulent shrubs, typical of the arid basal zones with Infra- and Thermo-Mediterranean bioclimate of Tenerife, of great endemicity value.

P.1063 Comparison of the climate change tolerance of native species from arid zones of the Iberian Peninsula with potential use as orname

Pilar Soriano[1], Elena Estrelles[1], Marina Martín[1], Reyes Mora[1], Mariola Monllor[1], José Aparici[1], M. Isabel Martínez-Nieto[1,2]

1 ICBiBE – Jardí Botànic, Banco de Germoplasma, Universitat de València, Valencia, Spain. 2 Depart-

ment of Agroforestal Ecosystems, EPSG, Universitat Politècnica de València, Valencia, Spain.

As consequence of climate change, temperature and rainfall regimes are being modified, threaten the survival of the current gardening concept in many areas of the world. This situation highlights the need to investigate the potential of other interesting species, especially in more sensitive areas such as the Mediterranean Basin. For this reason, the aim of this study is to promote sustainable gardening with adapted species. The use of native Mediterranean flora offers a good opportunity to find plants that are resistant to the current conditions of increasing temperatures and decreasing water availability. To achieve this objective, four autochthonous species from arid zones of the Iberian Peninsula, with potential use as ornamentals, were selected to compare their tolerance in the germinative phase to different levels of temperature and water stress. The species were *Salsola oppositifolia*, *Mesembryanthemum nodiflorum*, *Mesembryanthemum crystallinum* and *Halogeton sativus*. Germination tests were carried at constant temperatures between 10 and 40°C. The effect of water stress was studied by creating a low osmotic potential environment with PEG 6000 between -0.10 and -3 MPa. Germination percentage, mean germination time, base temperature, thermal time, base water potential and hydrotime (Tb, S, Ψb and ϴH) were calculated. The results showed an extremely good response to high temperature and low osmotic potential for *Salsola oppositifolia*.

P.1064 Biogeography and ecology of the Algerian island flora

Mohamed Hamimeche[1,2], Errol Véla[3], François Gillet[4], Riadh Moulaï[1]

1 LZA lab, Abderrahmane Mira university, Bejaia, Algeria. 2 Mohammed Seddik Ben Yahia university, Jijel, Algeria. 3 AMAP lab, University of Montpellier/CIRAD/CNRS/INRAE/IRD, Montpellier, France. 4 University of Franche-Comté, Besançon, France.

In spite of their proximity to the coast, the flora of the Algerian islands and islets had been poorly studied. This work is the first to provide an overall view of the richness and the determinants of the Algerian island flora, based on a compilation of original and recently published floristic data. Two independent classifications of 30 islands and islets were derived from PCA and HCPC performed on a matrix of physiographic variables (longitude, latitude, elevation, area, isolation, steepness index and area/perimeter ratio) and a matrix of flora descriptors including species richness, functional traits (life form, seed dispersal, pollination) and biogeographic range. We performed an RDA to explain the variation in flora characteristics by a set of physiographic, biotic and survey variables. The floristic inventory encompassed a total richness of 288 vascular plant taxa. Three main groups of islands and islets can be distinguished from either intrinsic botanical descriptors or physiographic descriptors, resulting in two different typologies. RDA revealed that the combination of five variables (seabird density, longitude, area, isolation and survey duration) explained 16.1% of the variation in flora characteristics. Taken alone, the density of yellow-legged gull colonies and the island area were the main drivers of this variation. Results showed that floristic richness was associated with larger island area and distance to mainland, with importance of some plant functional traits, such as zoochory and entomogamy, and with a lower proportion of Mediterranean species. In the context of island flora conservation, some of these small islands can be considered as “modern refuges” from human pressures, and this pattern is particularly important in the context of Mediterranean ecosystems characterised by a quasi-permanent human impact in various habitats. Two new important plant areas (IPA) for Algeria are proposed following the results of these floristic inventories.

P.1065 Patterns and processes of extinction in the flora of Macaronesia

Raúl Orihuela-Rivero[1,2], Javier Morente-López[1], J. Alfredo Reyes-Betancort[3], Hanno Schaefer[4], Alfredo Valido[1], Miguel Menezes de Sequeira[5], María M. Romeiras[6], Carlos A. Góis-Marques[5,7], Marcos Salas-Pascual[8], Alain Vanderpoorten[9], José María Fernández-Palacios[2], Jairo Patiño[1,2]

1 Instituto de Productos Naturales y Agrobiología (CSIC), La Laguna, Spain. 2 Universidad de La La-

guna, La Laguna, Spain. 3 Jardín de Aclimatación de La Orotava, Instituto Canario de Investigaciones Agrarias, Puerto de La Cruz, Spain. 4 Plant Biodiversity, Department Life Science Systems, Technical University of Munich, Freising, Germany. 5 Madeira Botany Group, Faculty of Life Sciences, University of Madeira, Funchal, Portugal. 6 Universidade de Lisboa, Lisboa, Portugal. 7 CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Ponta Delgada, Portugal. 8 Universidad de Las Palmas de Gran Canaria, Las Palmas de Gran Canaria, Spain. 9 University of Liège, Liège, Belgium.

The number of studies on plant extinction have so far been very limited compared to other taxonomic groups such as animals. In addition, these studies reveal relatively lower extinction rates. However, extinction debt (i.e., the extinction of species in the future due to events that occurred in the past), together with the lack of exhaustive studies, could have led to an underestimation of its magnitude. Under this framework, oceanic islands are particularly important environments as they are home to numerous endemic species, which contribute significantly to global biodiversity and which, besides, are particularly vulnerable to extinction processes. In this study, we carry out an exhaustive review of both plant extinction and extirpation events that have occurred in Macaronesian islands as well as a biological trait characterization of all the native flora of the Canary Islands and Azores. Specifically, we analyze (i) which geographic and biological intrinsic factors potentially influence the risk of disappearance of a taxon, and (ii) the existence of temporal-altitudinal patterns of extinction/extirpation linked to socioeconomic changes in the islands. Among the biological traits analyzed, the endemicity, habit and pollination mechanism were closely linked to a high risk of extinction. Besides, the island's geological age and the human population density were the most important factors explaining the number of extinction events for each island. We identified the existence of differentiated patterns of extinction in the altitudinal gradient over time, highlighting a recent coastal hotspot of extinction possibly associated with tourism development and expansion of invasive species. Through this work, the need to increase knowledge about the functional traits of the island floras is highlighted to predict possible future extinction events more efficiently and accurately.

P.1066 Genetic characterization of Teline stenopetala in the Canary Islands: a new approximation.

Verónica Pérez[1], Miguel A. Padrón-Mederos[1], J. Alfredo Reyes-Betancort[1]

1 Jardín de Aclimatación de La Orotava, Instituto Canario de Investigaciones Agrarias. Puerto de la Cruz, Tenerife, Spain.

In the Canary Islands, a young volcanic oceanic archipelago, all plant species arrive through diverse dispersion mechanisms. Once established, these plants undergo diversification or radiation in adaptation to new ecosystems. An example is *Teline stenopetala* (Webb & Berthel.) Webb & Berthel., a wild shrub legume species traditionally used for animal feeding and natural ecosystems regeneration. This species has five endemic subspecies in the Canary Islands (*microphylla, pauciovulata, sericea, spachiana* and *stenopetala*), identified in a morphological study (Del Arco, 1981) and distributed across the four westernmost islands (Tenerife, La Gomera, El Hierro and La Palma). Genetic data about this species (considered in this work as Teline despite that this genus shows inconsistency as a monophyletic group) provides insufficient support for the infraspecific taxa considered (Percy & Cronk, 2002; Pardo et al. 2004). Consequently, a new approach will be performed with chloroplast DNA analysis to detect pronounced differences, and ISSR genetic markers to detect subtler variations. The objective is to clarify the taxonomy and diversity within this group, while also exploring their potential as fodder.

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P.1067 Impact on the wild vegetation of the Balearic Islands (Spain) of the phytopathogenic bacterium Xylella fastidiosa

Juan Rita[1], María Cañellas[1], Mauricio Ruiz[1], Francesc Adrover[2], Diego Olmo[2], Andreu Joan[2], Margarita Gomila[1]

1 Universitat de les Illes Balears, Palma, Spain. 2 Conselleria d'Agricultura, Pesca i Medi Natural. Govern Balear, Palma, Spain.

Xylella fastidiosa is a Gram-negative aerobic plant pathogenic bacterium. It multiplies inside the xylem vessels, clogging them and obstructing the flow of water. It is transmitted naturally by insects that feed on xylem sap. *X. fastidiosa* seriously affects a many different plants species, some of great economic interest (olive, vineyard, citrus, almond, etc.), but also many wild species. The latest update of the host plant database (EFSA, 2023, EFSA Journal 21(6):8061) rise to 690 species. An assessment of the impact of this bacterium on the natural vegetation of the Balearic Islands (Spain) has been carried out within a broader project developed by the Department of Agriculture, Fisheries and Natural Environment of the Government of the Balearic Islands. 1,857 samples of 147 plant species, 24 of them endemic to the Balearic Islands, have been collected in 236 locations on all the islands. All tests were performed followingEPPO PM 7/24 standard usingqPCR Harperet *al.* 2010 protocol. 190 samples have been found that have tested positive, which represents 10% of the samples. We have located 24 affected plant species, 18 were wild species, 3 of them endemic and another 6 cultivated as ornamentals but which are also naturalized. 10 of these species were not known until now to be sensitive to *X. fastidiosa*. The wild olive (*Olea europea* var. *sylvestris*), with a positivity rate of 46.2% of the symptomatic trees, and the ash (*Fraxinus angustifolius*), with 37.1%, are two of the most affected species. No oak (*Quercus* ilex) sample has tested positive so far. Regarding endemic species, we have found a worrying affectation of Santolina magonica on the island of Menorca, with plants seriously affected both wild and cultivated plants. The endemics *Genista valdes-bermejoi* and *Phlomis italic* are also sensitive to this bacterium.

P.1068 Considering plant-plant interactions to improve the restoration of plant communities

Jairo Robla[1], Inés Ibáñez[2], Alejandro Rodríguez[1]

1 Doñana Biological Station (EBD-CSIC), Seville, Spain. 2 School for Environment and Sustainability, University of Michigan, Ann Arbor, USA.

Active restoration is a commonly employed practice for reclaiming disturbed and degraded areas. This approach typically aims to expedite the establishment of plant communities, leading to self-sustaining ecosystems over time. However, many restoration efforts lack ecological considerations, focusing solely on plant identity in relation to abiotic factors. Understanding how interactions between plants (i.e., facilitation or competition) can influence the survival and growth of neighbouring plants presents a beneficial opportunity to enhance restoration programs and achieve greater success. To advance this understanding, we conducted a study along the 36 km-long Guadiamar Green Corridor, an area impacted by a mine toxic spill in 1998 that underwent a comprehensive restoration program during 1999 and 2000. Ninety-four plots of 20 x 20m were designated, where all existing woody plants were geolocated and monitored for growth and survival from 2009 to 2018. We analysed the growth performance of various target species based on the identity of neighbouring plants and their distance from the focal plant. Additionally, we examined the recruitment of new woody plants in 2018 in relation to the existing plant community in 2009, as well as the size and distance among them. Results revealed high survival rates for all species, probably because all plants in our sample had passed the critical period for survival during the early years after the plantation. Neighbourhood effects on growth indicated that neighbours can exert either positive or negative influences on various growth parameters (height, crown area, diameter). Recruitment was shaped by the identity and size of existing plants. Compositional changes suggested that diversification in community composition could take place inly in the mid- to long-term. Examining plant-plant interactions through neighbourhood analysis emerges as a valuable tool for crafting more effective restoration plans. Recognizing the impacts of these interactions during revegetation efforts could inform and optimize future programs.

P.1069 Morphometric analysis of the Canarian juniper (Juniperus cedrus subsp. cedrus): Exploring adaptations to ecological gradients

Guillermo Sicilia-Pasos[1, 2] , Agustín Naranjo-Cigala[3] , Javier Morente-López[2] , AbrahamPadilla[1] , David P. Padilla[1] , Javier Martín-Carbajal[1] , Manolo Marrero-Gómez[4] , Jairo Patiño[1, 2]

1 Instituto de Productos Naturales y Agrobiología (CSIC), La Laguna, Spain. 2 University of La Laguna, La Laguna, Spain. 3 University of Las Palmas de Gran Canaria, Las Palmas de Gran Canaria, Spain. 4 Teide National Park, Santa Cruz de Tenerife, Spain.

The Canarian juniper (*Juniperus cedrus* Webb & Berthel.) is a species endemic to the Canary Islands. The distribution of this gymnosperm taxon is thought to have been much more extensive in the past. However, logging, fires, and the presence of wild herbivores have led to a significant reduction in both its range size and abundance. Despite the current declining situation, it is evident that this species maintains a broad distribution across the most important elevational vegetation belts in the Canary Islands. Surprisingly, there is a lack of studies investigating potential morphological adaptations that might indicate the species' ability to adapt to diverse ecological conditions within the Canarian archipelago. To fill this gap, we conducted measurements using morphometric tools, focusing on life traits such as leaves and reproductive structures. These are traits that are hypothesized to play a role as indicators of potential adaptation of this species to the strong ecological conditions across *Juniperus cedrus*' distribution. To achieve such a goal, samples were collected from different populations across the islands where the species occurs, including La Palma, La Gomera, Tenerife, and Gran Canaria. The ultimate goal was to explore potential signatures of morphological diversification and their relationship to environment and geography. Compiling information about these key aspects related to the Canarian juniper is crucial for implementing effective conservation measures tailored to the specific environments where it thrives in the archipelago.

P.1070 Phylogenetic framework and genomic diversity of an endangered endemic species (Silene migjornensis) from the Balearic Islands.

Inés Herrero[1], Mario Fernández-Mazuecos[2], Emilio Cano[1], Joana Cursach[3], Lorenzo Gil[3], Pablo Vargas[1]

1 Real Jardín Botánico (CSIC), Madrid, Spain. 2 Universidad Autónoma de Madrid, Madrid, Spain. 3 University of Balearic Islands, Palma, Spain.

Silene migjornensis (≡ *Silene sericea* var. *balearica*) is a recently recognized species endemic to southeastern Mallorca Island (western Mediterranean Basin) that belongs to *Silene* sect. *Dipterospermae*, which includes 15 species from small geographical areas of the Mediterranean Basin. This annual plant is a narrow endemic occurring on maritime sandbanks and catalogued as Vulnerable (VU) in the Red Book of the vascular flora of the Balearic Islands. Indeed, it is known from a single locality in a protected area (*Parque Natural Marítimo-terrestre d'Es Trenc Salobrar de Campos*). To advance in the conservation of *S. migjornensis*, three objectives were addressed in the present study: (1) To perform a phylogenetic analysis and evaluate its systematic status, (2) to study the genetic diversity of the only extant population, and (3) to propose management and conservation measures for the species. We studied the genetic diversity using ITS sequences of *Silene* sect. *Dipterospermae* species, we obtained genome-wide nucleotide polymorphisms by high-throughput DNA sequencing using the genotyping-by-sequencing (GBS) technique, and we investigated whether the population structure is better characterized by a panmictic model or by within-population differentiation. The endemic flora of the Balearic Islands, especially coastal plants, is particularly vulnerable to habitat degradation and loss due to anthropogenic activities. Therefore, conservation studies using genomic data like this one are of paramount importance.

P.1071 Epiphytic invasive species on the Canarian palm tree, Phoenix canariensis H.Wildpret, in the Canary Islands and Andalusia, Spain.

Wolfredo Wildpret de la Torre[1], Victoria Eugenia Martín Osorio[1], Wolf H. Wildpret Martín[2]

1 Universidad de La Laguna, La Laguna, Spain. 2 Georg-August-Universität Göttingen, Göttingen, Germany.

Over the years we carried out a study and monitoring of epiphyte vascular plants installed naturally in the trunk of the Canarian palm tree. The Canarian Palm Tree, *Phoenix canariensis* H.Wildpret., is an endemic species of the Canary archipelago distributed by the world as an ornamental plant. In the Canaries their artificial distribution extends from sea level up to 1,000 m.a.s.l. Exceptionally some specimens have reached 1,600 m.a.s.l. (Vilaflor, Tenerife). There are some semi-anthropic palm groves that are renewed naturally. It corresponds to the terminal community of the arid to semiarid Inframediterranean and semiarid to dry Thermomediterranean edaphohygrophilous colluvial and riparian series of the Canary Palm (*Periploco laevigatae-Phoenico canariensis sigmetum*). *Phoenix canariensis* is also a characteristic species of *Juniper* thermo-sclerophyllous woodland *Junipero canariensis-Oleo cerasiformis sigmetum* preferably located in island medium elevation in the company for example, *Dracaena draco*, *Olea cerasiformis*, *Juniperus turbinate* ssp. *canariensis*, *Pistacia lentiscus*, *Pistacia atlantica, Gymnosporia cassinoides*. We have explored more than five thousand individuals of palm trees in the Canary Islands and about six hundred in the province of Málaga, Andalusia. Epiphytic species growing on the Canarian Palm Tree, base, trunk, treetop and occasionally on the ascending roots of old specimens of large size have been inventoried. Epiphytism on the palm tree has been detected in over 2,000 specimens from near sea level on coastal walks to those in the midlands. At these altitudes they are subject to the humid climate of the trade winds and there are a higher number of epiphytic species of cyanobacteria, briolichenic communities and even some basidiomycetes. Until now we have recorded some eighty different vascular plant species established on the stipe phorophyte mentioned. The high presence of three invasive species stands out: *Ficus microcarpa*, *Ficus rubiginosa* and *Nicotiana glauca*.

S.126. PLANT DIVERSITY IN SPECIALIZED HABITATS ECOLOGY TO EVOLUTION

P.1072 Geobotanical characterization of plant communities used in traditional sheep pastoralism

Raquel Alonso-Redondo[1], Ángel Penas[1], Alejandro González-Pérez[1], Sara del Río González[2]

1 Department of Biodiversity and Environmental Management, Faculty of Biological and Environmental Sciences, University of Leon, León, Spain. 2 Department of Biodiversity and Environmental Management, Faculty of Biological and Environmental Sciences, University of Leon, Mountain Livestock Institute CSIC-UNILEON, León, Spain. ralor@unileon.es; apenm@unileon.es; agonp@unileon.es sriog@unileon.es.

The work presented herein is part of a research project entitled: *Ecosystem Services of Traditional Grazing: Biodiversity, Carbon Footprint, and Socioeconomic Sustainability* (ECOSPAS) (TED2021-131388B-I00). This project, classified as a Strategic Initiative for Ecological Transition, is funded by the Ministry of Science and Innovation, along with European NextGeneration funds. It is led by the Institute of Biodiversity Research (IMIB) under the Spanish National Research Council (CSIC) and involves collaboration with 16 national and international institutions. The primary objective of the project is to investigate how pasture management can promote biodiversity, minimize carbon footprint, and ensure socio-economic sustainability. In Spain, there is limited information across extensive regions regarding grazing intensity, grazing patterns of traditional pastoralism, and their impact on biodiversity. The study encompasses 489 farms located throughout the nine provinces of Castilla y León (Spain). The region has a longstanding tradition of livestock farming, with the ovine sector, primarily through milk and meat production, exerting significant socio-economic influence on the territory. It represents nearly one-third of livestock production and 60% of sheep milk production in Spain. To assess the impact of traditional pasturing on the landscape, it is essential to understand the diversity of the flora and vegetation associated with the plant communities exploited by sheep. This study conducts geobotanical characterization of the plant communities present on each farm, incorporating a 2 km buffer. It was applied the latest approaches in Bioclimatology, Phytosociology and Biogeography. The results highlight that the plant communities most palatable for sheep farming in Castilla y León belong to the phytosociological classes of grasslands and natural and semi-natural meadows. These include: *Poetea bulbosae*, *Stipo-Agrostietea*, *Molinio-Arrhenatheretea*, *Nardetea strictae*, *Festuco-Brometea*, *Festuco-Ononidetea*, *Lygeo-Stipetea* and *Tuberarietea*. It is noteworthy that, from a bioclimatic perspective, these communities predominantly exhibit a Mediterranean character.

P.1073 Geographical gradients and ecological factors determine the diversity of mycorrhizal fungi associated with Orchis italica

Marco G. Balducci[1], Karl J. Duffy[1]

1 University of Naples Federico II, Naples, Italy.

The distribution and abundance of plant populations are often linked to the availability of mutualists. Semi-anthropogenic grasslands are havens of plant diversity, and in the Mediterranean, frequently contain many orchid species and the mutualists on which they depend. As their seeds lack endosperm, orchids depend on mycorrhizal fungi for seed germination and subsequent development. These orchid mycorrhizal (OrM) fungi are free-living saprotrophs; hence their distributions may vary according to both abiotic and biotic variables. We investigated the abundance and diversity of OrM communities associated with *Orchis italica*, which has a distribution limited to Mediterranean grasslands. We used metabarcoding of the ITS region to identify OrM fungi associated with adult individuals in 23 populations of *O. italic* across the Mediterranean. We used both multivariate analyses and joint species distribution models (JSDMs) based on geographical, climate, and soil variables, to test how both common OrM fungi and their communities vary according to geographical and ecological factors. 79 OrM OTUs were found associating with *O. italica*, 35 of which were members of the Tulasnellaceae. Five Tulasnellaceae OTUs and one Ceratobasidiaceae OTU were found in every population. Abundance of these OTUs, as measured by number of reads, increased from west to east and decreased from south to north. OrM community composition varied according to precipitation, annual mean temperature, and soil phosphorous content. This indicates that OrM fungi are influenced by a combination of soil chemical and climatic variables. Likewise, JSDMs revealed that OrM OTUs responded differently to ecological variables, but that there were both positive and negative co-occurrences among OrM. Thus, the occurrence of OrM may be determined by interactions beyond the influence of abiotic factors. Taken together, these results highlight the importance of quantifying and identifying the distribution of belowground mutualists, such as mycorrhizas, in understanding and predicting plant distributions.

P.1074 Towards a comprehensive cartography of the riparian vegetation of Spain

Juan A. Calleja[1,2], Francisco Lara[1,2], Ricardo Garilleti[3], Carlos Gonzalo Gil[4], Marina Coca de la Iglesia[4], Carmen Andrés[4], Álvaro Prado[4], Alba Romero[4], David G. del Olmo[1,4], Macarena Cuerdo[1,4], Eduardo Ballesteros[4], Juan C. Veláquez[4], Ruth Martín[4], Elena Bermejo[4], Cristina Moreno[5], Blanca Ruiz[5]

1 Universidad Autónoma de Madrid, Madrid, Spain, juan.calleja@uam.es. 2 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain. 3 Universidad de Valencia, Valencia, Spain. 4 Tragsatec, Madrid, Spain. 5 Ministerio para la Transición Ecológica y el Reto Demográfico, Madrid, Spain.

The Spanish riverine vegetation is extraordinarily diverse due to the floristic and environmental heterogeneity present throughout the territory. The remarkable set of riparian forests and scrublands includes a high proportion of unique communities in the European context. To date, their distribution in Spain has been approached with different methodologies and represented very partially at both the state and regional levels, usually including only some riparian communities located within the Natura 2000 Network. The Nature Data Bank (MITECO) of Spain, through Tragsatec, has promoted the development of the first comprehensive and homogeneous cartography of habitats of the entire national territory including those characterized by riparian forests and shrublands. The project involves experts in riparian communities from CBIC-UAM and UV and focuses on mapping the plant communities of rivers, streams, and wadis. It contributes to the objectives of the Spanish Inventory of Natural Heritage and Biodiversity, which seek to organize and harmonize information on the biodiversity of the country. The cartography integrates two habitat typologies: i) 65 types of riparian communities recognized in the *Spanish Standard List of Habitats* (known in Spain as LPEH and based on the European EUNIS habitat classification) that covers both native (e.g. *Alnus glutinosa* forests, *Salix cantabrica* groves) and exotic communities (e.g. *Populus x canadensis* and *Robinia pseudoacacia* stands); and ii) 8 types of riparian Habitats of Community Interest (HIC). Its recognition (presence and occupied surface) is addressed by extensive field work and photointerpretation. The collected data are feeding the 33.701 riparian polygons previously defined in the *Forest Map of Spain* (MFE). Likewise, new sections (1,459) with riparian vegetation are being set in numerous fluvial courses. To date, more than 18,000 polygons have been covered from most provinces of the different Autonomous Communities of Spain. As detailed example, the cartography of Castilla-La Mancha is presented.

P.1075 Wetlands: diversity and conservation status of vascular plants - Buenos Aires Argentina

Aldana M. Elisei[1, 2], María A. Ficher[3], Renée H. Fortunato[1, 2]

1 Instituto de Botánica Darwinion, San Isidro, Buenos Aires, Argentina. 2 Escuela Superior de Ingeniería, Informática y Ciencias Agroalimentarias, Universidad de Morón, Morón, Buenos Aires, Argentina. 3 Instituto de Clima y Agua, Hurlingham, Buenos Aires, Argentina.

Wetlands are ecosystems that are covered by water (salt, fresh or intermediate) on a seasonal or permanent basis. In recent years these environments have been increasing their studies, especially in benefit to the society. According to that, in Argentina the wetlands are going to be considered of National interest, however until now there is no legislation in the province of Buenos Aires that includes their protection and conservation. With the objective of collaborating with the National initiative for the preservation of wetlands, the aims of this work focus on the record and conservation status of vascular flora associates in that ecosystem in Buenos Aires region. For this purpose, the species registered in platforms (i.e. GBIF, IRIS Darwinion, DBHERB), bibliography and herbaria (i.e. BA, BAA, BAB, BBB, CORD, CTES, SF, SI) was analyzed. The research included georeferenced specimens (Map of Wetland Distribution a Deep-Water Bodies in the Argentine Republic - version 1.0 - INTA) examined with open-access QGIS program, and the geographic data and wetland areas for further analyses were associated. The result of this study has identified: 144 Families, 517 genera and 853 species, increasing the number of taxa and new records to the previous works cited. Furthermore, our evaluation as novelty included Gymnospermae and Poaceae taxa and it is the first florist inventory with an integrative work covering all wetland systems in the province of Buenos Aires. The ecosystem services and the rich biodiversity present in wetlands are the main focus that encourages conservation awareness. Our results are a source of information about the vegetation cover currently present in these environments and serve as a tool for decision-making at a national and international level.

P.1076 Spaciation of Anaphalis (Asteraceae) to the islands of Japan

Toshifumi Kataoka[1], Katsuhiro Yoneoka[1], Tao Fujiwara[2], Shun K Hirota[3], Yoshihisa Suyama[4], Tetsukazu Yahara[5], Noriaki Murakami[1]

1 Makino Herbarium, Tokyo Metropolitan University, Tokyo, Japan. 2 Center for Molecular Biodiversity Research, National Museum of Nature and Science, Tokyo, Japan. 3 Botanical Gardens, Osaka Metropolitan University, Osaka, Japan. 4 Graduate School of Agricultural Science, Tohoku University, Miyagi, Japan. 5 Kyushu Open University, Kyushu, Japan.

Japan archipelago, with its many islands, is known as one of the world's most biodiverse regions with diverse environments. Three species of *Anaphalis* (Asteraceae) are distributed in Japan and are also found on some Islands. The presenters have conducted molecular phylogenetic analysis of the

Jananese *Anaphalis* species, and have shown that several taxa may be recognized as new species. In this presentation, we examine the actual status of *Anaphalis* species growing on the islands of Rishiri and Rebun in Hokkaido, the Izu-Island in Honshu, and Yakushima in Kyushu. In this study, molecular phylogenetic analysis based on nuclear ITS and ETS region sequences, genome-wide SNPs analysis by MIG-seq method utilizing a next-generation sequencer, and comparison of morphological traites were conducted. As a result, the Hokkaido population, including Rishiri and Rebun Islands, was genetically differentiated from the Honshu population, forming a clade distinct from the conventional *Anaphalis margaritacea*. The Mikurajima (Izu-islands) population, although a taxon closely related to the Japanese *A. margaritacea*, was genetically and morphologically distinct from any of the *A. maegaritacea* varieties. *Anaphalis sinica* var. *yakushimensis* from Yakushima Island, which has been considered a variety of *A. sinica*, is genetically related to *A. margaritacea*, but is genetically and morphologically distinct from both vareties of *A. margaritacea*, and is differentiated at the species level. Thus, different species of genus *Anaphalis* are distributed on each of the Japanese Islands.

P.1077 The flora of Zuid Limburg: documenting a botanically diverse region of valleys at the edge of the Netherlands

Phil Klahs[1]

1 Maastricht University, Maastricht, Limburg, Netherlands.

The Dutch province of Limburg is located in the southeast of the Netherlands. Plant biodiversity is positively influenced by a combination of topological variation, the presence of different soil strata, and regional proximity to other European countries. Dutch Limburg contains the highest elevation point (322.4 m) in the European section of the Netherlands. This increase in elevation, although small, provides a different environment than the coastal / lowland habitats available across much of the rest of the Netherlands. Unique growing situations are also afforded by exposed limestone, which support a distinctive plant community known as chalk grasslands. Together these characteristics make the Dutch province of Limburg an interesting intersection of plant distributions, and a worthy locale for floristic research. To support future science and education the herbarium of the Natuurhistorisch Museum Maastricht (MAAS) is expanding to include a satellite teaching collection at the Maastricht Science Programme.

P.1078 Quantitative Assessment of Nurse Species' Influence on Tree Regeneration and Biodiversity in Socotra Island

Dario La Montagna[1], Michele De Sanctis[1], Petr Maděra[2], Kay Van Damme[3], Fabio Attorre[1], Luca Malatesta[1]

1 Department of Environmental Biology, Sapienza University of Rome, Rome, Italy. 2 Department of Forest Botany, Dendrology and Geobiocoenology, Faculty of Forestry and Wood Technology, Mendel University in Brno, Brno, Czechia. 3 Centre for Academic Heritage and Archives and Ghent University Botanical Garden, Ghent University, Ghent, Belgium.

The intriguing role of thorny or poisonous shrubs as nurse plants in promoting tree regeneration is evident in the ecosystems of Socotra Island. There is, nevertheless, a lack of information in the quantitative evaluation and identification of the best nurse species for tree regeneration. Six shrub species were chosen and carefully examined in this study in order to fill this gap. Phytosociological surveys were carried out in randomly chosen shrubs to evaluate species abundance and shrub characteristics. Corresponding control plots were also established. Multivariate analysis and weighted means at the community level were utilised to analyse functional traits, and the Relative Interaction Index (RII) was utilised to comprehend the dynamics between the shrub and its surroundings. Plot positions and nurse species significantly affected the results of multivariate analyses. Different patterns of plant communities were revealed by the Indicator Species Analysis, with graminoids predominating outside shrubs and forbs being more common inside. The diversity indices showed that species' levels of biodiversity varied, and the RII results helped in the selection of beneficial nurse shrubs. The facilitation effect of nurse species on tree and shrub growth forms is highlighted in this study and it has been determined that some species are less effective at preventing overgrazing. Endemic tree species on Socotra are endangered due to the lack of natural regeneration with the majority of individuals over-matured. This work provided a thorough grasp of the facilitation potential of multiple nurse species. The next step will be focused on planting seeds within this nurse species, checking the survival of seedlings. This will be useful for future ecological restoration project on the island, implementing this nature-based intervention fostering climate resilience and sustainable ecosystem management on Socotra Island.

P.1079 Composition and structure of plant communities in the moist temperate forest ecosystem of the Hindukush Mountains, Pakistan

Matiullah1, Amjad U. Rahman[2], Zahid Ullah[3], Rahmatullah Qureshi[1], David F. R. P. Burslem[4], Zia-ur-Rehman Mashwani[1]

1 Department of Botany, PMAS Arid Agriculture University Rawalpindi, Pakistan. 2 University of Swabi, Department of Botany, Swabi, Pakistan. 3 University of Swat, Centre for Plant Sciences and Biodiversity, Swat, Pakistan. 4 University of Aberdeen, Department of Plant and Soil Science, Aberdeen, United Kingdom.

We investigated the relationship between Plant communities and the environment from the moist temperate vegetation of Lakoo mountainous forest District Swat. We sampled data from 162 sampling units (Quadrates) using1x1m2 for herbs 5x5m2 and shrubs, while 10 x10m2 for trees, systematically considering six elevation gradients between the altitudinal from 1970m to 3095m. We performed statistical analysis like Canonical correspondence analysis (CCA) and TWINSPAN (two-way indicator species analysis) for ecological assessment and clustering of plant communities. To check upon the correlation of species (CR) with topographic and edaphic variables we used statistical software PC-ORD version 7. We recognized 264 species plants belonging to thirty families. We recorded key sampling measurements of density, frequency, and cover for all these species which are vital for community description. The results showed Shannon-Winner's, and Simpson diversity values as 19.18 and 3.17respectively. The importance value indexes (IVI) were used to identify the leading and rare species of plant in each community or cluster group. In total we recognized eleven different communities as: *Berberis-Abies-Bergeni, Picea-Indigofera-Poa, Abies-Parrotiopsis-Poa, Quercus-Viburnum-Poa, Picea-Salix-Primula, Abies-Viburnum- Poa, Viburnum-Taxus-Poa, Pinus-Viburnum-Lithospermum, Abies-Berberis-Carex, Pinus- Viburnum-Poa* and *Parrotiopsis-Picea-Poa* through hierarchical cluster analysis (TWINSPAN). CCA analysis revealed that of all studied edaphic and topographic variables altitude, silt, calcium carbonate, and organic matter were the strongest factors determining plant community diversity and composition in each microclimate of the eleven communities. Visually the vegetation of the forest was dominated by small-sized trees followed by shrubs, and regenerates indicating the stage of secondary regeneration. We found severe human interference in disturbing the existing biodiversity, which requires immediate conservation to ensure sustainable management and utilization of natural resources of the Lalkoo moist temperate forest.

P.1080 Population Structure of Shorea robusta across thirteen Indian domains: A key indicator for regeneration and conservation

Garima Mishra[1], Shailesh Pandey[2], Rama Kant[1], Rajendra K. Meena[1], Maneesh S. Bhandari[1]

1 Genetics and Tree Improvement Division, Forest Research Institute, Dehradun, India. 2 Forest Protection Division, Forest Pathology Discipline, Forest Research Institute, Dehradun, India.

In developing countries, numerous people depend on woody resources for their livelihoods. Monitoring human impact on the populations of socio-economically vital species is therefore imperative for the conservation of vulnerable trees. *Shorea robusta* (Sal) is a valuable forest timber and has innumerable uses in global livelihood. In order to assess the population structure and regeneration patterns of this multipurpose species in the distribution range of Uttarakhand (India), we used size-class distribution method (SCD). Diameter at breast height (DBH) of adult individuals were sampled on 100 m^2 (10m*10m) plots (total 387) in each domain. Recorded DBHs were distributed among thirteen size-classes of 10cm intervals. The slope of the ordinary least-squares regression (OLS) of SCD was considered to be an indicator of the population structure. The regeneration status of species was determined based on population size of seedlings and saplings in all the sites. This was observed to be quite adequate with an average of 1056 seedlings per site. The species had significant ($p<P.01$) negative SCD slopes with an inverse J-shaped distribution in all the expanses; characterizing stable populations with good regeneration encompassing more individuals in the smaller than in the larger size-classes. Thus, the dynamics indicate an overall steady population trend for Sal, which foretells future expansion and stability. Nevertheless, the species is still exposed to borer attack, mortality, dieback phenomenon, anthropogenic interferences etc. We therefore recommend that conservation campaigns be used to encourage the sustainable resource management practices to healthify the establishment and growth of Sal.

P.1082 The Betpakdala desert is the centre of concentration of endemic Chenopodiaceae of Kazakhstan

Polina V. Vesselova[1], Gulmira M. Kudabayeva[1], Bektemir B. Osmonali[1]

1 Institute of Botany and Phytointroduction, Almaty, Kazakhstan.

Endemic species, reflecting the specificity of the flora, play an important role in the development of biodiversity protection issues. 44% of the territory of Kazakhstan lies in the zone of deserts, in which representatives of Chenopodiaceae predominate, accordingly, the issue of its endemism deserves close attention. Among Kazakhstani desert regions high endemism of Chenopodiaceae is characterised by the flora of Betpakdala. The analysis of distribution of its representatives showed concentration here of 8 of 12 species endemic for Kazakhstan. Here is the list of the corresponding herbarium specimens (with the inventory number): - *Anabasis gypsicola* Iljin: LE00054884-LE00054887; - *Arthrophytum balchaschense* (Iljin) Botsch.: AA - Western Betpak-Dala. Tamgaly-jar tract, at foot of chink, near spring on solonchaks (Kubanskaya Z.V., 22.08.1946); - *Arthrophytum betpakdalense* Korovin et Mironov: AA - Betpakdala, Sarysu r. Red clays (Baitenov M.S., 24.09.1954); Eastern part of Betpak-Dala desert, vicinity of Sary-Tuma springs (Kubanskaya Z.V., 21.09.1941); Central Betpak-Dala. Kok-Ashik tract, (Rubtsov N.I., 3P.8.1940); South-eastern Betpak-Dala, (Kubanskaya Z.V., 25.08.1949); Betpak-Dala, Kogashik r. (Katyshevtseva V.G., 17.07.1952); MW0823233-MW0823235; East Betpak-Dala, Keshir-mola settlement, (Mironov B., 21.08.1933 (isotype)). (LE); TASH000807-TASH0008089; TASH000819- TASH000821; - *Arthrophytum pulvinatum* Litv.: TASH00005659; - *Arthrophytum subulifolium* Schrenk: AA - Southeastern part of the Betpak-Dala Desert. Kurmanchite Mountains, on stony-rubble slopes (Kubanskaya Z.V., 03.08.1941); TASH000000005746; TASH00005748; - *Halimocnemis mironovii* Botsch.: Eastern Betpakdala (Pratov U., 1972); - *Petrosimonia hirsutissima* (Bunge) Iljin: Betpakdala (Pratov U., 1972); Betpakdala (Smirnov V.I., 14-19.08.1929); - *Climacoptera kasakorum* (Iljin) Botsch: Betpakdala (Pratov U., 1972); (AA0001827-AA0001829). Thus, there are 5 endemic species in the western part of Betpakdala and 4 in the eastern part. Acknowledgments: This study was carried out within the framework of grant AR19679078.

P.1083 Molecular ecology of endemic shrubs in isolated OCBIL populations

Peter Pemberton[1], Rose L. Andrew[1], Manu Saunders[1], John Hunter[1], Liz Wandrag[2]

1 University of New England, Armidale, Australia. 2 University of Tasmania, Hobart, Australia.

Old Climatically Buffered Landscapes (OCBILs) often exist as terrestrial islands that are isolated in a larger landscape matrix, and plants confined to OCBILs have a high incidence of endemicity and rarity. Shrubs are a significant component of OCBIL vegetation, yet many have restricted gene flow due to a lack of seed dispersal mechanisms, and a reliance on insect pollinators with limited ranges. We hypothesise that the persistence of these shrub species in small and isolated populations limits the adaptive potential that arises from gene flow between populations. We conducted a systematic review of molecular ecology papers on OCBIL species to identify where the research has occurred and what the molecular ecology revealed about OCBIL flora. We identified geographic gaps and a paucity of studies focusing on shrubs, whilst species pollinated by insects alone tended to have highly structured populations with low gene migration rates, underlining the need to understand how OCBIL shrubs diversify and persist. On the basis of this review, we will now research the genetic diversity and gene flow at multiple scales in the New England Tableland region of Australia, a region with relatively understudied OCBILs. Fine-scale analysis of relatedness and spatial autocorrelation at centimetre precision will investigate patterns of gene flow and dispersal within granite outcrop populations. In concert with observations of flower visitors, comparisons among age cohorts will illustrate the influence of geography and insect-mediated pollination on gene flow at the finest scale. Using coalescent estimates of migration rates and population divergence in OCBIL and non-OCBIL taxa, we can begin to understand the demographic history and adaptations of terrestrial island flora. This research sheds light on the mechanisms by which small, isolated populations persist, and their capacity to adapt to novel conditions under global climate change.

P.1084 Salicornioideae in Western Europe and North Africa: exploring diversity, ecological traits, and biogeography of perennial taxa

Esteban Ramírez[1], Irene Sánchez-Gavilán[1], Lourdes Rufo[2], Daniel Sánchez-Mata[3], Nuria Rodríguez[4], Ricardo Amils[5], Vicenta de la Fuente[1]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Universidad Francisco de Vitoria, Madrid, Spain. 3 Universidad Complutense de Madrid, Madrid, Spain. 4 Centro de Astrobiología (CSIC), Madrid, Spain. 5 Centro de Biología Molecular Severo Ochoa, Madrid, Spain.

This study aims to understand the distribution and ecological behavior of the main genera and species within the subfamily Salicornioideae (Chenopodiaceae-Amaranthaceae) in the Mediterranean and Atlantic territories of the Western European areas and North Africa which show a woody habit. Specifically, we focus on *Arthrocnemum*, *Halocnemum*, and *Sarcocornia* genera. In this contribution, we provide new data and perspectives on two *Arthrocnemum* species (*A. macrostachyum*, *A. meridionale*), seven *Sarcocornia* species (*S. alpini*, *S. carinata*, *S. fruticosa*, *S. hispanica*, *S. lagascae*, *S. perennis*, and *S. pruinosa*) and two *Halocnemum* species (*H. strobilaceum* and *H. cruciatum*). In addition, we include ecological requirements, vegetation units, biogeographical data, and some taxonomical and nomenclatural comments. This comprehensive analysis will contribute to a deeper understanding of these plant groups and their conservation implications.

P.1085 Taxonomic list and conservation status on the beach forest flora of Homonhon Island, Philippines

Roanne Benesisto Romeroso[1,2], Danilo Niem Tandang[3], Ian Ausa Navarrete[4,5]

1 The Graduate School and Research Center for the Natural and Applied Sciences, University of Santo Tomas, Manila, Philippines. 2 Department of Biology, University of Eastern Philippines, Catarman, Philippines. 3 Philippine National Herbarium, Botany and National Herbarium Division, National Museum of Natural History, Manila, Philippines. 4 Department of Environmental Science, Southern Leyte State University-Hinunangan Campus, Hinunangan, Philippines. 5 Center for Smallholder Horticulture and Agroforestry Research and Extension, Southern Leyte State University-Hinunangan Campus, Hinunangan, Philippines.

A total of 44 families, 89 genera and 103 beach forest species were identified. The most numbered family is Euphorbiaceae (9), Leguminosae (8) species, Compositae and Poaceae (7) and Rubiaceae (6), Malvaceae (5) Araceae, Convolvulaceae (4), while the rest of the genera have three to fewer species. Among the sites, Habag beach forest is the most diverse with 38 families, 80 genera, 95 species followed by Pagbabangnan beach forest with 25 families, 32 genera and 32 species and Casuguran beach forest with 21 families, 30 genera, 33 species. Thefindings of the study would be a great help to at least fill the gap on the scarcity of data on the beach flora species on the Philippine Island. The forest of Homonhon Island is affected by mining activities, with the depressing threats of extinction at hand. It is hoped that the findings of this study will encourage more researchers to perform a floristic survey of the Philippine beach forest to catalogue the species before they become prey to extinction.

P.1086 Checklist of the Ecuadorian Páramo vascular flora

Katya Romoleroux[1], Priscilla Muriel[1], Petr Sklenář[2], Carmen Ulloa Ulloa[3], David Espinel[1,4] Chaquira Romoleroux[1], Joel Calvo[5]

1 Laboratorio de Botánica Sistemática, Herbario QCA, Facultad de Ciencias Exactas y Naturales, Pontificia Universidad Católica del Ecuador, Quito, Ecuador. 2 Department of Botany, Charles University of Prague, Faculty of Science, Prague, Czech Republic. 3 Missouri Botanical Garden, St. Louis, USA. 4 Bonn Institute of Organismic Biodiversity, University of Bonn, Bonn, Germany. 5 Conservatoire et Jardin Botaniques, Département de la Culture et de la Transition Numérique, Geneva, Switzerland.

The Páramos is a neotropical mountainous biome of the northern and central Andes that plays an essential role in regional and global cycles of water, carbon and nutrients. The Páramos and their plants act as water reserves, delivering water and environmental services to communities and settlements at lower altitudes. The Ecuadorian Páramos are integrated by several ecosystems, whose plant composition vary according to climate, altitude, geology, biogeographic history, and disturbance degree. The present investigation is based on field work, bibliographic data and search of collections in herbaria. We have recorded 1,865 vascular plant species, which is the highest number of species cited for this biome in Ecuador (1,649 Angiosperms, 211 Pteridophytes and five Gymnosperms), of which 1,119 are native, 708 are endemic to Ecuador, and 38 are introduced. We have found that the five most diverse families in this biome were: Asteraceae, Orchidaceae, Poaceae, Melastomataceae, and Campanulaceae; whereas the five richest genera are: *Epidendrum*, *Elaphoglossum*, *Phlegmariurus*, *Calceolaria*, and *Senecio*. Ecuadorian Páramos have a high percentage of endemism (40%), especially in the narrower and more fragmented altitudinal belt, these unique species contribute to the formation of complex communities that change from north to south and along altitudinal gradients. Although these Páramos contain one of the highest numbers of native and endemic species in relation to their area, they are very vulnerable to environmental changes and other anthropogenic processes, that is why most of these species are now endangered. It is necessary to continue with the study of the Páramos to have a complete and updated checklist of the flora species, which will serve as a basic tool for conservation and decision-making processes in this important Andean landscape.

P.1087 Water ecological requirements of Characeae taxa in Spain and their variations at infraspecific and geographical levels

Borja Sanz[1], Herminio Boira[1], María Ferriol[1]

1 Instituto Agroforestal Mediterráneo, Universitat Politècnica de València, Valencia, Spain.

Characeae are basic components of continental underwater meadows. Their presence is strongly influenced by quality and chemical composition of water. Spain has a great variety of water ecosystems with different hydric conditions. The aim of this study is to assess the ecological requirements of Characeae taxa growing in different Spanish water basins, and to analyse whether infraspecific levels or localities affect these requirements. Single pairs of the presence of a given Characeae taxon in a given location and the chemical composition of water at that location were searched in the literature. More than 600 pairs data were obtained from 25 publications, which included 33 different taxa belonging to genera *Chara*, *Lamprothamnium*, *Nitella*, *Nitellopsis*, and *Tolypella*. Water electric conductivity, which correlated to concentrations of salt, chloride, and magnesium, was one of the most determinant parameters for the distribution of Characeae taxa. The most tolerant species to salinity was *L. papulosum*. *Nitellopsis obtusa* and some taxa of *Tolypella* and *Chara* showed an intermediate tolerance, while the rest of the taxa could not tolerate salinity. Most taxa developed in alkaline, basic waters although some were able to grow in slightly acidic waters in some locations. Although the water concentrations of calcium could also affect the distribution of some Characeae taxa, Ca^{2+}/Mg^{2+} was more able to detect ecological differences. Differences in water electric conductivity among locations from central Spain and the south-east coast was detected for *T. hispanica*. Water in which *C. hispida* populations grew showed different levels of electric conductivity and Ca^{2+}/Mg^{2+} according to geographical areas and irrespectively of varieties, probably due to a high phenotypic plasticity in this species. The opposite occurred for *C. vulgaris*, in which more differences were found among varieties than among locations.

P.1088 The contribution of old and new residential areas in urban flora diversity: A case study in Bucharest, Romania

Mihaela Urziceanu[1,2], Petronela Camen-Comănescu[1,3], Alina Georgiana Cîşlariu[1], Ioana-Minodora Sîrbu[1], Eugenia Nagodă[1,3], Daniela Clara Mihai[1], Maria Raicu[3], Paulina Anastasiu[1,3]

1 University of Bucharest, Faculty of Biology, Bucharest, Romania. 2 Research Institute of the University of Bucharest, Bucharest, Romania. 3 University of Bucharest, Botanic Garden "D. Brandza", Bucharest, Romania.

Urban biodiversity research has gained global recognition for its positive impact on human well-being and ecosystem services. Our study addresses the increasing importance of urban flora in the context of a rapidly changing society. Urban environments, characterized by both native and introduced species, offer favorable conditions for diverse plant species. In this study, we focused on understanding the floristic diversity in old and new residential environments, including the historical center and areas with houses, apartment buildings and boulevards in Bucharest, Romania. A comprehensive floristic inventory was conducted during the year 2023, covering a 1 ha plot in each designated area. The results revealed a total of 560 plant taxa, including 260 alien species, and also 20 native species of conservation value. Comparative analyses using various biodiversity metrics revealed different levels of resemblance and disparity among the areas. Old residential areas, especially old houses and apartment buildings, exhibit higher homogeneity, while the historical center shows similarities with new residential zones, differing from new or old boulevards. Correlation analyses reveal negative correlation between the age of residential areas and the total species richness and alien species richness, respectively. In contrast, a positive correlation exists between the age of residential zones and the number of species of conservation value, indicating an increase in rare species richness with the aging of residential areas. Notably, new residential areas predominantly feature horticultural ornamental species; surprisingly, there are also occasional appearances of spontaneous native species, even though they may be few, maintaining a touch of naturalness in the urban landscape. Our findings emphasize the influence of human urban management on plant diversity and richness. This study contributes valuable data to the understanding of urban flora in Bucharest, offering insights that can inform conservation policies and urban development strategies.

S.127. PLANT DIVERSITY, BIOGEOGRAPHY AND EVOLUTION IN THE TROPICS FOR CONSERVATION, RESTORATION AND SUSTAINABLE USE.

P.1089 Linking beta diversity of plant community composition with anthropogenic actions in tropical high-elevation peatlands

Carlos Victor Mendonça Filho[1], Alexandre Christófaro Silva[2], Diego Tassinari[2], Fabiane Nepomuceno Costa[1], Lucia Porto[1], Yasmine Antonini[3]

1 Departamento de Ciências Biológicas, Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, Brazil. 2 Laboratório Integrado de Pesquisas Multiusuário dos Vales do Jequitinhonha e Mucuri, Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, Brazil. 3 Departamento de Biodiversidade Evolução e Meio Ambiente, Universidade Federal de Ouro Preto, Ouro Preto, Brazil.

The plant community of peatlands is poorly studied in the tropical regions. Nonetheless, these environments provide valuable ecosystem services, including supporting biodiversity. In these habitats, an apparent environmental filtering effect limits non-adapted species from occurring, generating a taxonomic-functional mismatch. Despite being very rich in species, these

environments have been vectors of human activities that can contribute to the destruction of peatlands, but they can also have different effects on the different groups of plants. Little is known about the drivers that determine plant distribution patterns in peatlands. To fill these knowledge gaps, we conducted vegetation surveys at 12 peatland sites both in protected and impacted areas in the high elevations of Espinhaço Mountain Range in Brazil. To test whether the dissimilarity of plants between protected and impacted peatlands is driven by species turnover or nestedness over impacted and protected peatlands, we calculated the beta (β) diversity of plants using the multiplicative partitioning of diversity. In addition, to test whether the β-diversity of the plant is determined by the variation of abiotic conditions (C, Slope, Fertility, and Elevation) we built Generalized Linear Models (GLM). The total beta diversity was significantly different between protected and impacted bogs due to the changes in C content, fertility, and slope. Also, species turnover was explained by changes in C content and fertility. In summary, our investigation into the plant communities of tropical peatlands has uncovered critical insights into the ecological dynamics of these poorly studied ecosystems. Despite their inherent biodiversity and the provision of valuable ecosystem services, tropical peatlands are facing a pressing challenge due to anthropogenic activities that contribute to their degradation. Our study reveals a notable taxonomic-functional mismatch in these environments, highlighting an environmental filtering effect that shapes the morphological similarity of phylogenetically diverse peatland species while limiting the occurrence of non-adapted species.

P.1090 Preliminary phylogenetic and taxonomic studies of the genus Hypoestes (Acanthaceae) with a focus on Malagasy species.

Wendy L. Applequist[1], Michael Landis[2], Emily Warschefsky[1]

1 Missouri Botanical Garden, St. Louis, U.S.A. 2 Washington University in St. Louis, St. Louis, U.S.A.

Hypoestes Sol. ex R.Br. (Acanthaceae, Justiceae) is a herbaceous to shrubby genus characterized by resupinate corollas and monothecal anthers. It is widespread in the Old World tropics but most diverse in Madagascar, with 91 endemic species in the flora area. The last taxonomic work on *Hypoestes* in Madagascar was done by Benoist, who described many new species between 1920 and 1962 but never published a key. The difficulty of identifying *Hypoestes* has meant that the genus is undercollected, and most Malagasy collections are not identified to species level. While numerous floral and vegetative characters useful for species delimitation exist, they do not vary in concert; homoplasy appears to be widespread. Here, we present a phylogenetic and biogeographic study of *Hypoestes* using the Angiosperms353 universal probe set to amplify DNA extracted from over 200 herbarium specimens, with outgroups including species of *Rhinacanthus* Nees, *Dicliptera* Juss., and *Justicia* L. We conducted preliminary studies of herbarium material to provide determinations for as many sampled specimens as possible, and briefly describe the unpublished identification resources created for this purpose. However, many Malagasy specimens remain unidentifiable, and it appears that a significant number of undescribed species are present in herbarium material. Our preliminary phylogenetic results identify monophyletic subclades and demonstrate that some names have been misapplied to distinct lineages, both in Madagascar and elsewhere, particularly in Africa. These results will facilitate future taxonomic studies in the group and provide us with a more complete understanding of the diversity of Malagasy *Hypoestes*.

P.1091 Exploring acoustic features of buzzing bees as an indicator of bee diversity and their efficiency in poricidal flower pollination

César A. Arvelos[1], Vinicius L. G. Brito[1]

1 Universidade Federal de Uberlândia, Uberlândia, Brazil.

Biodiversity is often measured by species richness and abundance, yet indirect methods like acoustic analysis can offer an alternative approach to studying communities and the role of species in their ecosystem. Bee acoustics are relatively understudied but provide a vital functional contribution to ecosystems. Sonicating bee species produce different sounds during their interactions with flowers. In this study, we investigated the relationship between the acoustic features of bee sonication and the diversity of visiting species on pollen release. We observed and recorded bee visits in a population of *Rhynchanthera grandiflora*, calculated acoustic indices, and examined their associations with bee diversity as well as the amount of pollen released from the anthers. The acoustic indices proved to be reliable predictors of bee diversity. However, we believe these indices better predict functional diversity rather than species diversity. Pollen release is positively related to acoustic diversity when there are few bee visitors, but this relationship becomes inverted when visitors are abundant. In summary, this study highlights the utility of vibrational features of sonicating bees in assessing functional diversity within the community and its effect on pollination.

P.1092 New floristic records and phytogeographical notes on the vascular flora of the Maamora-Zemmour-Zaer region

Benkhnigue Ouafae[1,*], Boudik Soukayna[2], Zidane Lahcen[2], Moujahdi Chouaib[1], El Oualidi Jalal[1]

*1 Department of Botany and Plant Ecology, Scientific Institute, Mohammed V University in Rabat, Morocco. 2 Plant, Animal Productions and Agro-industry Laboratory, Department of Biology, Faculty of Sciences, Ibn Tofail University, Morocco. *benkhnigue@gmail.com.*

Morocco, with its geographical and climatic diversity, is one of the Mediterranean countries with the greatest diversity of flora and is home to an exceptionally rich (5280 species according to Fennane et al. (2023). The vascular flora of Morocco seems to be relatively well known in North Africa, but it is still less studied than that of European countries such as Spain, France and Italy. In this context, we provide in this work several information on the systematics, biogeographical distribution and chorology of exotic species newly reported in the Maamora-Zemmour-Zaer region in Morocco. Recent fieldwork in this region, which is a part of the geographical division known as North Atlantic Morocco-3 (Man-3), has enabled us to report for the first time the presence of seven exotic species (*Dysphania multifida* (L.) Mosyakin & Clemants; *Galinsoga quadriradiata* Ruiz & Pav.; *Aphanes australis* Rydb. *Cestrum parqui* (Lam.) L'Hér.; *Ambrosia psylostachya* DC.; *Cotula australis* Hook.f. and *Euphorbia hypericifolia* L.) belonging to five families and seven genera. These taxa have been reported as new in several localities in Man-3, in particular in the two cities of Rabat and Kenitra. According to IUCN Red List criteria, one of these species (*Dysphania multifida*) is Least concern (low risk of extinction) and three species are naturalized weeds in Morocco (*Galinsoga quadriradiata*; *Aphanes australis* and *Cestrum parqui*). The species *Euphorbia hypericifolia*, native to tropical and subtropical America, is mentioned for the first time in Morocco in this work as an introduced species. Information on the distribution, ecology, habitat and conservation status of these taxa are provided. These new data complete the biogeographical distribution of certain taxa of the Moroccan vascular flora.

P.1093 Functional strategies and environmental adaptation: intraspecific variations of Amazon restinga species.

Luane Botelho[1], Mateus C. Silva[2], Handria J. A. da Costa[3], Ely Simone C. Gurgel[3], Grazielle Sales Teodoro[4]

1 Universidade Federal de Lavras, Lavras, Brazil. 2 Department of Geography, Faculty of Environment, Science and Economy, University of Exeter, Exeter, UK. 3 Botany Department, Museu Paraense Emílio Goeldi, Belém, Brazil. 4 Institute of Biology, Universidade Federal do Pará, Belém, Brazil.

Functional morphophysiological characteristics play a crucial role in the life of plants, influencing their growth, establishment, and survival, especially in the face of environmental heterogeneity. Plants adopt various strategies to cope with these variations, such as acquisitive strategies, more associated with forests, and conservative strategies, common in savanna areas. These strategies directly impact the productivity and tolerance capacity of plants in environments with limited resources. Intraspecific variation is essential for plants to adapt to different environments, influencing their distribution and abundance. The restinga, due to its vegetation diversity, serves as an excellent model for investigating intraspecific variation. In this study, we investigated how environmental gradients affect the plasticity of functional leaf and wood attributes of two abundant species in the Amazon restinga: *Clusia grandiflora* Split. (Clusiaceae) and *Anacardium occidentale* L. (Anacardiaceae). We conducted our study in the restinga areas of the Environmental Protection Area (APA) of Ilha de Algodoal, Maracanã, on the coast of Pará state, Brazil. We evaluated attributes such as leaf area, leaf thickness, leaf dry matter content, and wood density in three physiognomies: dunes, shrubland, and forest. We used analysis of variance (ANOVA) and Tukey's post-hoc test to compare functional attributes between species, respecting the assumptions for parametric analyses. We observed that *C. grandiflora* maintains more conservative characteristics, while *A. occidentale* exhibits more acquisitive traits, varying according to physiognomy. Our results indicate that species respond differently to environmental limitations, demonstrating a diversity of responses to environmental heterogeneity. These findings highlight the importance of understanding intraspecific variations in species, which is still poorly studied, and the adaptive strategies of plants for their survival and success in different ecosystems.

P.1094 Commonness as a reliable surrogacy strategy for the conservation planning of rare tree species in the subtropical Atlantic Forest

Guilherme Salgado Grittz[1], Giesta Maria O. Machado[1], Alexander Christian Vibrans[1], André L. de Gasper[1]

1 Universidade Regional de Blumenau, Blumenau, Brazil.

Global biodiversity is declining at rates never seen before. At the same time, resources directed at conservation planning still fall orders of magnitude short. Thus, efficient allocation of resources is needed to prioritize regions that can shelter more biodiversity. A usual approach to identify priority areas for conservation is to map species distribution and use this information as input in spatial prioritization software. Since data on common species are more readily available, final maps of priority areas for conservation are heavily biased towards this group, overlooking rare species. Thus, we created ranking priority maps for common and rare tree species separately, aiming to comprehend if prioritizing areas for the conservation of common trees is enough to protect rare trees all at once. Then, we overlapped our priority maps with maps of current protected areas (PAs) to identify if the latter already cover areas designated in our models. Our results show that common tree species can act as surrogates for rare tree species since both groups priority maps overlap with more than 70% of their area. Yet, most of the current PAs do not cover significant areas for protecting tree species, revealing an urgent need to expand or create new PAs to safeguard the local biodiversity.

P.0944 Fifteen years inventorying: How can a forest inventory improve a small herbarium collection?

André L. de Gasper[1], Alexander C. Vibrans[1], Giesta Maria O. Machado[1], Guilherme S. Grittz[1]

1 Universidade Regional de Blumenau, Blumenau, Brazil.

Since 2007, the Floristic and Forest Inventory of Santa Catarina (FlorestaSC) has been dedicated to studying the subtropical Atlantic forests of Brazil, a shrinking biodiversity hotspot. By employing 449 systematically distributed plots, the project conducted a comprehensive sampling of the entire state's area on two occasions, encompassing all forest vegetational types. In the first cycle of measurements (2007 – 2011), 24,686 specimens were sampled, while the subsequent cycle (2014 – 2020) featured a reduced yet substantial sample size of 6,108 specimens. Despite the sampling decrease, 303 new species were incorporated into the project's findings. Jointly, both measurement cycles amounted to more than 30 thousand specimens, distributed within 2,923 unique species, constituting 40% of the entire state's flora, and encompassing 244 botanical families. FlorestaSC, beyond its extensive representation of 2,501 angiosperms species collected, also gathered 308 pteridophytes, 23 lycophytes, and six gymnosperms. Over 90% of the inventoried flora is native to the region. Taxonomically, the project made significant contributions, including four holotypes, one isoneotype, one isotype, and 16 paratypes. Simultaneously, it distributed more than 20 thousand duplicates to 63 Brazilian herbaria. In addition to its substantial contributions, it is noteworthy that FlorestaSC has played a crucial role in improving a small herbarium collection. Today, the project stands as a major contributor to FURB herbarium collection. Created in 1991 at the Universidade Regional de Blumenau, Blumenau, Santa Catarina, Brazil, the herbarium was named after Dr. Roberto Miguel Klein, a notorious botanist who extensively studied the flora of the region together with Raulino Reitz. Nowadays, nearly half of all FURB herbarium samples originate from FlorestaSC efforts. Evidently, the project stands as a foundational resource for the state's flora studies, further enhancing and enriching the understanding of the region's unique biodiversity.

P.1095 Areas of endemism of the Mexican bromeliads

Ivonne N. Gomez[1], Mario A. Espejo[1], Tania Escalante[2], Claudia Ballesteros[1]

1 Universidad Autónoma Metropolitana, Ciudad de México, Mexico. 2 Universidad Nacional Autónoma de México, Ciudad de México, Mexico.

Mexican bromeliads include 460 species, 70% of them restricted to the country. Many of them have close relationships with their pollinators (hummingbirds, bees and bats), and a high economic and cultural value. Areas of Endemism (AE) are distributional patterns based on homopatry, and their identification allows to identify the areas for bromeliads conservation. In order to identify areas of endemism of bromeliads restricted to Mexico, we used the Endemicity Analysis (EA) by means of the NDM/VNDM software. A data matrix with 6,394 geographic records of Bromeliaceae including 325 Mexican species, was analyzed using three cell sizes (2° latitude-longitude, 1° and 0.5°). The cell with the highest number of records was 799, 370, 198 and a richness of 91, 56, 35 species, in 2°, 1° y 0.5° grades cells respectively. Five consensus AE were identified for Mexican bromeliads for the 2° grid, which are located in the center and northwest of the country. While for the 1° grid, 9 consensus areas were obtained, one located on the borders of Sonora and Chihuahua, and the others in the states that face the Pacific slope, from Jalisco to Chiapas. For the 0.5° grid, 6 consensus areas were obtained, which are located on the limits where the following entities Jalisco-Colima, Guerrero-Morelos, Puebla-Oaxaca-Veracruz join. For each grid size there are Consensus Areas that include the greatest number of species, 17 and 10 endemic species for 2° grids, 16 and 9 for 1°, and 7 and 6 for 0.5. With this preliminary analysis it is observed that the areas of endemism are located in the central and northwest part of the country.

P.1096 The Dry Chaco Forest: multiple facets of plant diversity and ecosystem functioning along a deforestation & precipitation gradient

Axel Gualdoni-Becerra[1], Nathaly Guerrero-Ramirez[1], Holger Kreft[1].

1 University of Göttingen, Göttingen, Germany.

The loss and fragmentation of natural ecosystems caused by the expansion of agricultural frontiers has become one of the main threats to global biodiversity. The rate of forest loss in the South American Chaco Dry Forest is among the highest in the world. Deforestation is mainly due to the expansion of agriculture and cattle ranching, generating highly fragmented landscapes. This land-use change together with regulations that promote the creation of linear forest strips with native vegetation remnants, lead to forest forest fragmentation and create strong edge effects. Yet, the effect of fragmentation on multiple facets of plant diversity remains understudied in the area. Here, we analyse the vegetation of the Dry Chaco forest across a precipitation and deforestation gradient to understand the role of fragmentation and edge effects on the community assembly, the impacts of multiple facets of biodiversity on the functioning of a disturbed ecosystem, and how remote sensing indices capture these disturbances. The main hypothesis is that multifaceted diversity decreases along the precipitation gradient, with a greater decrease in the forest patches than in the forest strips, who initially have a lower diversity than the forest patches. We are conducting comprehensive woody species´ diversity inventories along a 380 km precipitation transect in the Dry Chaco Forest of Argentina. Our study covers forest strips, patches and natural reserves, incorporating taxonomic, phylogenetic and functional diversity, alongside remote sensing indices. Soil parameters are also measured to control for grazing intensity. NDVI is obtained by an Unmanned Aerial Vehicle and structural complexity indices by a LiDAR scanner. The expected findings will provide deeper insights into the processes and mechanisms underpinning biodiversity changes in highly fragmented areas with a strong anthropogenic influence.

P.1097 Nuclear phylogenomic allows breakthrough on taxonomy and evolution on neotropical Hyptidinae (Lamiaceae)

Guilherme Antar[1], Raymond M. Harley[2], Felix Forest[2], Alexandre Zuntini[2], José F. Pastore[3], Arthur S. Soares[4]

1 Universidade Federal do Espírito Santo, São Mateus, Brazil. 2 Royal Botanic Gardens, Kew, Richmond, UK. 3 Universidade Federal de Santa Catarina, Curitibanos, Brazil. 4 Universidade Federal do Rio Grande do Norte, Natal, Brazil.

Hyptidinae is a mostly neotropical subtribe currently with 19 genera and ca. 400 species. When the group was first monographed by Benth, the segregation of *Hyptis* in different genera, was already discussed due the huge diversity of the problematic genus *Hyptis*, which was instead segregated in 20 sections. Two phylogenies based on Sanger sequencing established a new classification for this subtribe, however the recognition of some genera, and the relationships between taxa remained poorly supported and controversial. We present a new phylogeny for Hyptidinae based on a broad sampling and high-throughput sequencing with a target-capture methodology based on the Angiosperms353 probe kit. We recovered sequences for 67 samples, covering all Hyptidinae genera, plus nine outgroups obtained via PAFTOL project or available transcriptomic data. The species tree was inferred using multispecies coalescence (in Astral), based on individual gene trees inferred with maximum likelihood. Our results support the subtribe as monophyletic and most of genera proposed in previous studies with the exception of *Hyptis* and *Hypenia*. *Hyptidendron* is recognized as monophyletic for the first time and the backbone relationships between genera are improved. Based on all the phylogenies produced and morphological data, we provide a new key to Hyptidinae genera as well as an update to the taxonomic status of the subtribe, with the proposition of the new monospecific genus *Myriohyptis*. Additionally, three new species combinations and one reestablishment are proposed. Our results highlight the potential of genomic data to solve poorly supported phylogenies and the need of a solid morphological base to propose taxonomic decisions based on phylogenetic results.

P.0098 The Costa Brava (coast of NE Spain) as a focus of plant invasions: floristic novelties resulting from the first steps of the LIFE

Carlos Gómez-Bellver[1], Neus Ibáñez[1], Neus Nualart[1], Arnau Bosch-Guiu[1], Jordi López-Pujol[1]

1 Botanic Institute of Barcelona, CSIC-CMCNB, Barcelona, Spain.

The Costa Brava, the coastal strip of ca. 250 km stretching from the French-Spanish border to Blanes, is known for its rugged appearance, with abundant sea cliffs, in clear contrast to other nearby coastal areas characterized by long sandy beaches. As a result of the interaction of various factors, including a complex topography, a profound transformation of the habitat and an enormous tourism development, the Costa Brava has become a focus of plant invasions, probably the most important in the whole Iberian Peninsula. In order to prevent new introductions of alien plants and improve the management of invasive species already present, a project within the LIFE Program of the European Union is underway. This project is focused on Vegetated sea cliffs of the Mediterranean coasts with endemic *Limonium* spp. (EUNIS, 2019). The initial phase of this project (LIFE medCLIFFS; https://lifemedcliffs.org/es/) required the design of a set of transects (about a hundred) of 0.5–1 km in length distributed throughout the coast of the Costa Brava; these small strips of coastline are being monitored by volunteers (trained citizen scientists) with the aim of early detection of new invasive plants and monitoring the different species already observed. Since early 2022, as a result of the fieldtrips derived from the design of the transects and the volunteers' observations, we were able to detect a large number of species observed as subspontaneous for the first time in this coastal region, some of which are novelties even at a European scale (such as *Agave parryi* and *Heptapleurum arboricola*).

P.1098 Assessment of sample completeness and species diversity of woody plants in Angola

Edwin Imfumu[1], Tsutomu Enoki[2], Buntarou Kusumoto[3]

1 Graduate School of Bioresources and Bioenvironmental Sciences, Kyushu University, Japan. 2 Ashoro Research Forest, Faculty of Agriculture, Kyushu University, Japan. 3 Kasuya Research Forest, Faculty of Agriculture, Kyushu University, Japan.

Angola has been identified as one of the tropical African nations with the most limited data availability on biodiversity. To evaluate the current state of knowledge of woody plants in Angola, this study seeks to quantitatively assess the extent of available data by i) quantifying sample completeness and ii) estimating species diversity. We compiled species occurrence data for woody plants from the existing databases, including Global Biodiversity Information Facility, and other published materials. The final dataset included 14,364 occurrence points from 2,865 woody species of 146 families. We estimated the sample completeness and species diversity at province level using the Hill number approach based on species incidence data at a scale of 10 km × 10 km grid cells. We evaluated the woody plant data by a four-step framework: 1) assessing sample completeness with changing sensitivity to species incidence frequencies, 2) drawing sample-size-based rarefaction/extrapolation curves, and comparing empirical and asymptotic diversity profiles, 3) performing non-asymptotic coverage-based rarefaction/extrapolation analysis, and 4) evaluating evenness among species incidence frequency distributions. The sample completeness profile shows substantial variability in the coverage rate of detected species across the 18 provinces ranging from 12% in Zaire to 46% in Luanda Norte and Lunda Sul, and 89% in Huíla, suggesting that each dataset contained many undetected species. Focusing on the highly frequent species group, the undetected species range from 31 to 342 for Cuando Cubango and Lunda Norte, respectively. Unsaturated sample-diversity curves indicate the existing data is not sufficient to accurately infer the true woody species diversity at the province level. The evenness profile shows that the species are evenly distributed in each province. The results provide insights into the need for more botanical collections across the country with a high priority in the Eastern half of the country.

P.1099 Characterization, kinetics and catalytic application of silver nanoparticles (AgNPs) synthesized from Crinum moorei

Sailee S. Raut[1], Utkarsha M. Lekhak[1]

1 Dr. Homi Bhabha State University, Mumbai, India.

Nanoparticles such as carbon, metal, bio-originated, etc. have been synthesized by a variety of physical, chemical and biological methods. Biological methods that employ bacteria, fungi and plants for the synthesis of metal nanoparticles are sustainable and eco-friendly. Among the biological methods, plants being acleaner and greener source are widely accepted. We studied the synthesis of silver nanoparticles (AgNPs) using the root and leaf extract of 15 different *Crinum* species. Among all the species, the highest synthesis was observed in the case of *Crinum moorei* which was detected by a peak at 390 nm under a UV-visible spectrophotometer. The optimization of AgNP synthesis from *C. moorei* root extract was performed based on extract concentration (1 %), salt concentration (1.5 mM), pH (9) and temperature (30°C). The kinetics study of AgNPs exhibited a rate constant of P.609 h^{-1}. AgNPs were also characterized using TEM, SEM, FTIR, XRD, NTA and DLS. AgNPs catalysed the decolorization of Congo red, an azo dye. Our studies provide an additional approach for controlling pollution caused by dyes and colorants. These green synthesized nanoparticles are biocompatible and therefore can be used in various fields such as food industry, medicine, cosmetics, textile, etc.

P.1100 An integrated approach to the classification of potential vegetation in western Mexico

Norma Y. Ochoa-Ramos[1], Miguel Á. Macías-Rodríguez[2], Joaquín Giménez de Azcárate[3], Alejandro González-Pérez[1], Sara del Río González[4]

1 Department of Botany, University of Leon, Leon, Spain. 2 Department of Environmental Sciences, University of Guadalajara, Jalisco, Mexico. 3

Department of Botany, University of Santiago de Compostela, Lugo, Spain. 4 Department of Botany, University of Leon, Mountain Livestock Institute CSIC-UNILEON, Leon, Spain.

Western Mexico includes the states of Jalisco, Michoacán, Nayarit, Colima and Aguascalientes, covering an area of 178,000 km² with an altitude range from sea level to 4260 m (Nevado de Colima). The region is characterized by mountain ranges and volcanoes that converge in two directions: one parallel to the Pacific Ocean coast, consisting of the Western Sierra Madre and the Southern Sierra Madre, and the other running east to west, known as the Trans-Mexican Volcanic Belt. The geographical location and physiographic diversity of the area contribute significantly to its bioclimatic diversity and phytocenosis. This study aims to identify different types of vegetation or plant formations and establish the characteristic climacic domain of the study area using a hierarchical system. The domains were defined by considering dominant species, biogeography and bioclimatic characterization. This approach is based on the information from the land use and vegetation map of Mexico, INEGI Series VII. We also considered works proposed for Mexico by Miranda and Hernández X., Rzedowski, and González-Medrano, as well as the Worldwide Bioclimatic Classification System by Rivas-Martínez and other complementary sources of information. The proposal provides a comprehensive and up-to-date perspective, improving the understanding of the present biological wealth. Furthermore, this methodology could be effectively applied throughout Mexico.

P.1101 Urban ecological restoration of a coastal vegetation: the Fundão island

Gisele Paixão[1,2], Dulce Mantuano[2]

1- UERJ, Brazil. 2 - Plant Ecophysiology Lab, UFRJ, Brazil.

The restoration of urban restingas requires specific techniques due to extreme modifications in biotic and abiotic factors in the urban ecosystem, in addition to contemporary environmental changes in coastal environments. Until 2016, the city of Rio de Janeiro had a significant shortage of remaining restinga vegetation areas, representing only 0.78% of the municipality's natural coverage. The aim of this study was to develop methodology and assess the effectiveness of restoring a closed creeping psammophilous and shrubby restinga area in an urban environment. We conducted a preliminary floristic survey and selected restinga species based on functional attributes of water resistance and pollution resistance. Fifteen native restinga species were planted in the sandy coastal line on Ilha do Fundão. The location is heavily impacted by the arrival of solid waste during tidal variations. Its urban use includes fishing, ritualistic use, sports use, and pedestrian traffic. Exotic species and native species of herbaceous and arboreal life forms were found. Planting included a diversity of life forms, was done in clumps, the seedlings were not fertilized. Survival rates varied among species, with *Eugenia uniflora*, *Senna pendula*, *Guapira opposita* being the most successful and *Ouratea cuspidata* having the highest mortality rate (22%). The rates of individual loss were low despite the high summer temperatures and the absence of irrigation. The choice of specific restinga species appears to play an important role in the success of reforestation in this environment, although the availability of seedlings is a challenge prior to planting. It is urgent to preserve and restore coastal ecosystems, as the occurrence area of native vegetation contributes to environmental resilience, biodiversity, and urban quality of life. Reforestation of Ilha do Fundão's restingas creates a new area of occurrence for this flora on the coast of Rio de Janeiro, where this ecosystem is virtually nonexistent.

P.1102 Understanding carbon storage dynamics in Ayeyarwady Delta's mangrove ecosystem in Myanmar: insights for restoration efforts

Bikram Pandey[1], Saroj Koirala[2,3], Htay Aung[4], Li Rong[1], Arbindra Timilsina[5], Soe Thaw Thaw Htun[4], Joacim Kontny[3], Htun Thiri Naing[3]

1 CAS Key Laboratory for Plant Diversity and Biogeography of East Asia, Kunming Institute of Botany, Kunming, Yunnan, China. 2 University of Jyväskylä, Finland. 3 Worldview International Foundation, Yangon, Myanmar. 4 Department of Marine Science, Pathein University, Pathein Township, Myanmar. 5 Hebei Key Laboratory of Soil Ecology, Center for Agricultural Resources Research, Institute of Genetics *and Developmental Biology, Chinese Academy of Sciences, Shijiazhuang, China.*

Mangroves are highly valued for their ecosystem services, providing a wide range of ecological, social, and economic benefits, including their role as carbon-rich ecosystems. Recent research suggests that preserving mangrove forests can offer a cost-effective strategy for mitigating CO_2 emissions. However, extensive deforestation has placed mangrove ecosystems under severe global threats. Currently, the assessment of mangrove restoration outcomes, particularly regarding soil carbon stocks, is inadequate. Therefore, this study aims to investigate the impact of restoration on soil organic carbon (SOC) in the Shwe Thaung Yan, Ayeyarwady coastal region of Myanmar. The study aimed to quantify and compare carbon stocks in different soil layers, examine the carbon sequestration potential of various mangrove species, and evaluate the effectiveness of mangrove restoration efforts. Soil samples were collected in 2015 (pre-restoration) and 2021 (post-restoration) at various soil depths and analyzed for SOC concentration, organic matter content, and bulk density using the Loss on Ignition (LOI) procedure. Significant changes in soil properties were observed between 2015 and post-restoration in 2021, with higher SOC and carbon concentrations observed in 2021. The average soil carbon stocks in 2021 (1954.43 ± 33.24 Mg C ha^{-1}) were approximately 2.7 times higher than the estimated carbon stocks in 2015 (732.26 ± 6.99 Mg C ha^{-1}). Furthermore, the study revealed variations in SOC accumulation among different soil depths, with higher carbon stocks found in the upper soil layers. This study highlights the positive impact of mangrove restoration on SOC accumulation and emphasizes the significance of considering soil carbon dynamics in restoration initiatives. The findings offer valuable insights for the conservation and management of mangrove ecosystems, especially concerning their potential for carbon sequestration and their contribution to mitigating climate change.

P.1103 What do recent dated phylogenetic trees tell us about the assembly of the Caribbean flora?

Víctor Pérez-Calle[1], Julissa Roncal[1]

1 Department of Biology, Memorial University of Newfoundland, St. John's, Canada.

The geographic origin and assembly mechanisms behind the rich and unique flora of the Caribbean biodiversity hotspot have been the focus of scientific interest for many years. Four main, non-mutually exclusive mechanisms played a role in the assemblage of Caribbean flora: late Cretaceous vicariance, colonization through land bridges like GAARlandia and GRANOLA, long-distance overwater dispersal, and in-situ speciation. During the last decade, with the development of new sequencing methodologies and biogeographical modelling, the evolutionary knowledge of an increasing number of Caribbean plant groups has improved considerably. However, scant research has merged this new information to elucidate the relative importance of the above mechanisms on the origin of Caribbean flora. We hypothesize that species isolation during the Mid-Miocene climatic optimum could have triggered most of the in-situ speciation events in Caribbean plant lineages. We also hypothesize that long-distance overwater dispersal was the predominant mode of arrival of plant lineages into the Caribbean. To test this, we propose to compile published dated molecular plant phylogenies that sample Caribbean endemic lineages and their proposed areas of origin to estimate speciation and colonization event accumulation through time. BioGeoBEARS will be used for those lineages with an available dated phylogenetic tree but not a formal ancestral area range reconstruction. Our analysis will reveal any period in geological time when speciation and colonization events were high and link this period to specific climatic and geological events. Timeframes of increased speciation and colonization of biota could guide the temporal framework for detailed geomorphological reconstructions in the Caribbean which are incomplete.

P.1104 Note on the morphology and molecular data of the genus Paris in Thailand

Saroj Ruchisansakun[1], Supajit Sraphet[2], Chatchai Yothawut[3], Chompunooch Thamanukornsri[4], Nawarat Suksee[2], Panida Kongsawadworakul[1], Nattaya Srisawad[2], Nicha Thawara[1], Puangpaka Umpunjun[1], Supaporn Rodpradit[5], Winai Sangkaew[6], Kanokporn Triwitayakorn[2]

1 Department of Plant Science, Faculty of Science, Mahidol University, Bangkok, Thailand. 2 Institute of Molecular Biosciences, Mahidol University, Nakhon Pathom, Thailand. 3 Doi Phu Kha National Park, Nan, Thailand. 4 Institute of Science, School of Mathe-

matics, Suranaree University of Technology, Nakhon Ratchasima, Thailand. 5 Queen Sirikit Botanic Garden, Botanical Garden Organization, Chiang Mai, Thailand.

The genus *Paris* presents an important and challenging taxonomic issue, as there is high variation within species and distinguishing between species can be difficult. Consequently, the classification of some taxa has changed over time. In order to bring clarity to the status of *Paris* species for the purpose of plant conservation and effective management of this genus in Thailand, we conducted a comprehensive survey in northern Thailand. We analyzed the morphological characteristics and constructed a molecular phylogenetic tree, which we compared to recently published findings on this genus. Our study reveals that Thailand is home to two species: P. yunnanensis and a newly discovered species, P. siamensis. This study provides detailed descriptions, illustrations, and the phylogenetic position of these two species.

P.1105 Revision on the genus Paris in Thailand

Saroj Ruchisansakun[1], Supajit Sraphet[2], Chatchai Yothawut[3], Chompunooch Thamanukornsri[4], Nawarat Suksee[2], Panida Kongsawadworakul[1], Nattaya Srisawad[2], Nicha Thawara[1], Puangpaka Umpunjun[1], Supaporn Rodpradit[5], Winai Sangkaew[6], Kanokporn Triwitayakorn[2]

1 Department of Plant Science, Faculty of Science, Mahidol University, Ratchathewi, Bangkok, Thailand. 2 Institute of Molecular Biosciences, Mahidol University, Salaya, Nakhon Pathom, Thailand. 3 Doi Phu Kha National Park, Pua Nan, Thailand. 4 Institute of Science, School of Mathematics, Suranaree University of Technology, Mueang Nakhon Ratchasima, Nakhon Ratchasima, Thailand. 5 Queen Sirikit Botanic Garden, Botanical Garden Organization, Mae Rim, Chiang Mai, Thailand. 6 Faculty of Agricultural Production, Maejo University, San Sai District, Chiang Mai, Thailand.

The genus Paris is a taxon of great importance and complexity, primarily due to the high variation observed within species and the challenges in defining boundaries between different species. Consequently, the classification of certain taxa has undergone changes over time. In order to shed light on the status of Paris species for the purposes of plant conservation and effective genus management in Thailand, we conducted an extensive survey in northern Thailand. This study involved the examination of morphological characteristics and the construction of a molecular phylogenetic tree, which we compared to recently published findings on this genus. Our findings reveal the presence of two species in Thailand: P. yunnanensis and a newly identified species, P. siamensis. In this article, we provide detailed descriptions, illustrations, and the phylogenetic position of these two species.

P.1106 State of our knowledge on the evolutionary relationships of Chrysobalanaceae

Cynthia A. Sothers[1], Ghillean T. Prance[1]

1 Herbarium, Royal Botanic Gardens, Kew, Richmond, UK.

Over the last years molecular phylogenetics has played a major role in the changing taxonomic landscape of the Chrysobalanaceae. The well-established morphological classification based on four tribes was upturned and genera previously thought to be close were found to be distantly related. Analyses using plastomes and more recently nuclear genomes show congruent results as well as incongruences across analyses. We investigate these results and propose hypotheses on the evolutionary relationships of the well-supported clades and discuss putative reasons for the incongruence of some genera. Chrysobalanaceae has a pantropical distribution and comprises 540 species in 27 genera. The Neotropics harbours the greatest number of taxa, represented by over 400 species in 16 genera. Africa is represented by ca. 50 species in seven genera and Australasia ca. 60 species in ten genera. The megadiversity of the family in the lowland neotropics is discussed. It is among the top ten most abundant families in terra firme forests of the Amazon region. The flowers of all genera share one distinct and stable character, the gynobasic style, and diversity in floral morphology among genera centres on the position of the ovary on the receptacle (basal, apical, midway on wall of receptacle), number of ovary locules (1- or 2-locular), and presence/absence of petals. *Parinari* and *Maranthes* are the only two pantropical genera in the family and display distinct morphological adaptations for germination, a character lacking in the neotropical genera. The Neotropical-Australasian clade is the most enigmatic of the family, from a morphological and biogeographical viewpoint, and relationships among genera are still unclear.

P.1107 Diversity, endemism and conservation of Pogostemon Desf. (Lamiaceae) in Peninsular India

Ashna Toms[1], P Sunojkumar[1]

1 Department of Botany, University of Calicut, Malappuram, Kerala, India.

Peninsular India (PI), once part of the Gondwana supercontinent, now forms the southern region of the Indian subcontinent. Acting as a biotic ferry, PI facilitated floral exchange from Africa to Asia during its collision with the Eurasian plate, and since then, it has been mediating the African-Asian biota exchange by overland migration or trans-oceanic dispersals. The genus *Pogostemon* (Lamiaceae, Lamiales), originated in Southeast Asia, comprises over 90 species distributed primarily in tropical and subtropical Asia extending to Africa (5 spp.) and northern Australia (1sp). The genus has dispersed, colonized and diversified throughout the Indian subcontinent, thriving with the highest diversity in PI. This study aims to document the diversity and distribution of *Pogostemon* in PI, identifying its major centres of diversification and endemism. Through extensive field surveys and herbarium consultations conducted as part of the study, 24 species and 4 varieties were recorded from PI. The Western Ghats - Sri Lankan biodiversity hotspot emerged as the centre of diversity in PI, hosting all 28 taxa, representing 31% of the global *Pogostemon* diversity. Moreover, PI also showcases notable endemism, with 22 taxa endemic to the region, among them 19 taxa being endemic to the Western Ghats. A preliminary phylogenetic analysis was also performed to explore whether PI served as a secondary centre of origin. The study also assessed the conservation status and threats faced by the narrow endemics, revealing habitat loss as a major threat, attributed to natural calamities, infrastructure development and conversion of natural land for agriculture. These findings contribute to our understanding of plant diversity and evolution in PI, highlighting the significance of the conservation of these regions.

P.1108 Complex evolutionary history of Chusquea, the most diverse genus of Neotropical woody bamboos (Poaceae, Bambusoideae)

Kaio V. A. Vidal[1], Lynn G. Clark[2], Cassiano A. D. Welker[3], Evandro M. Pianissola[1], Reyjane P. Oliveira[1]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Iowa State University, Ames, USA. 3 Universidade Federal de Uberlândia, Uberlândia, Brazil.

Chusquea (Poaceae, Bambusoideae) includes about 200 accepted species widely distributed in montane forests from Mexico to Argentina, Chile, and Brazil. Phylogenies involving this genus recover its monophyly, with five subgenera recognized in its circumscription. Two of them, *C.* subg. *Chusquea* and *C.* subg. *Swallenochloa,* are non-monophyletic and together represent the Euchusquea clade. Our main objective was to investigate internal relationships within the Euchusquea clade based on a molecular study using plastid (*trnD-trnT* and 3' final portion of *ndhF*) and nuclear (ITS) markers, as well as to increase the sampling of species belonging to the subgenera *Chusquea* and *Swallenochloa*, in order to test evolutionary hypotheses that better explain the geographical structuring observed in this clade. Our results corroborated the monophyly of *Chusquea* and its main lineages, especially in the Euchusquea clade. Within this clade, the relationships recovered here do not reflect the traditional classification based on morphology, reinforcing geographical structuring as the main factor in species grouping in this clade. As a novelty, the inclusion in our study of Peruvian species of this genus made it possible to recover a clade containing only these species with high support, named as clade (VII) *C. simplicissima*. Another important result was the inclusion of almost 85% of the accepted species of both subgenera *Chusquea* and *Swallenochloa* from Brazil, confirming the monophyly of clade (VI) *C. meyeriana*, although the interspecific relationships in this clade remain unclear. Additionally, from our data it was possible to hypothesize multiple long-distance dispersal events as an important factor in the radiation and diversification of the main lineages in Euchusquea, which could also explain the grouping of its species based on their geographical proximity. Phylogenomic studies using plastomes are also in progress with members of *Chusquea*, in order to better understand its evolutionary history.

P.1109 The genetic profile of an important oil nut Rubroshorea: plastid genome and MIG-seq analysis of Rubroshorea macrophylla

Wong Sin Yeng[1], Ogary Kinshen[1,2], Malcom Demies[3], Liu Jie4

1 Institute of Biodiversity and Environmental Conservation, Universiti Malaysia Sarawak, Samarahan, Sarawak, Malaysia. 2 Sarawak Forestry Corporation, Kuching, Sarawak, Malaysia. 3 Forest Department Sarawak, Kuching, Sarawak, Malaysia. 4 Kunming Institute of Botany, Kunming, Yunnan, China.

The Dipterocarpaceae is the foremost family of hardwood timber trees of the humid Asian tropics. Despite the seemingly wealth of publication material much remains to be accomplished in the dipterocarps, especially in species which are known to produce Engkabang/Tengkawang/Teglam-fat rich fruits, a high-quality high-melting-point fat. The first aim of the study focused on the phylogenomic analysis of a subset of Rubroshorea species which produce Engkabang fats (R. macrophylla, R. splendida, R. stenoptera, and R. pinanga). Plastid genomic data of eight Rubroshorea and Shorea species (17 out of 18 accessions) were obtained and analysed. For the second part of the study, we have also carried out de novo polymorphism in Rubroshorea macrophylla using multiplexed ISSR genotyping by sequencing (MIG-seq). Ninety-six leaf samples were taken from R. macrophylla grown in five different geographical locations. The number of SNPs reported is 421 polymorphisms with a range of allele frequency from 1P. % to 5P. %. It is hoped that this study will promote non-timber uses among Rubroshorea and Shorea spp. and thus conserve the diversity of these species in Sarawak.

P.1110 Comprehensive population analysis of S. holostea in the herbaceous layer of forest ecosystems in Goettingen forest, DE

Nataliia Yaroshenko[1], Viktoriia Skliar[1]

1 Department of Botany and Ecology, Sumy National Agrarian University, Sumy, Ukraine.

In this study, we conducted plant population investigations in the Goettingen forest, located in Low Saxony, Germany, in 2022-2023. Our research focused on six distinct populations of *Stellaria holostea L.* across six plots within the forest. These plots encompassed varying tree species and forest management conditions, including a managed young beech forest (Plot #1), a virgin beech forest (Plot #2), and four managed old beech forest plots (Plots #3-6) subjected to different anthropogenic influences. To assess these coenopopulations' ontogenetic and vitality structures, we employed a range of scientific methodologies, including geobotanical description, morphometry analysis, complex vitality assessment, and statistical data analysis. Morphometric analyses allowed us to discern the characteristic size parameters of *S. holostea* plants within each specific habitat. Notably, our findings revealed that the ontogenetic spectra of *S. holostea* in areas varying in the intensity of anthropogenic influence exhibited incompleteness, except in the virgin forest plot, where all ontogenetic stages were observed. We conducted a factor analysis to gauge vitality, identifying critical morphological parameters unique to each population. Our results indicated a pronounced level of resilience in coenopopulations residing in areas devoid of forestry activities. Specifically, five of the six *S. holostea populations* were classified as having low vitality (class c). In contrast, the highest vitality class (class a) was predominantly observed among the populations residing in the virgin forest. This study, utilizing *S. holostea* as an exemplar species, highlights the considerable disruption that forestry management imparts upon the herbaceous layer of forest ecosystems and underscores the resultant degradation in population quality.

S.128. PLANT ECOLOGY HOW AND WHY GENOME SIZE MATTERS

P.1111 Larger genomes evolve under temperature-stable environments in allohexaploid Rorippa indica

Ting-Shen Han[1,2], Yao-Wu Xing[1]

1 CAS Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Yunnan, China. 2 Department of Chromosome Biology, Max Planck Institute for Plant Breeding Research, Cologne, Germany.

A common character across organisms is that we all have genomes. However, size and component of genome change hugely. Why genomes vary so largely is an intriguing but less known question. Here we used a group of *Rorippa* species, to decipher the evolutionary and ecological significances of their cytological variation, including natural variation in genome sizes and ploidy levels across populations. Plants of *Rorippa* are naturally distributed in subtropical to tropical areas. Using flow cytometry, genome sizes of multiple individuals were quantified, which showed as large as 128 Mb intraspecific variation among accessions than that of 23 Mb in *Arabidopsis thaliana*. Genome size variation of *Rorippa* plants was positively related with annual mean temperature, but negatively related with temperature seasonality, suggesting larger genome preferred under temperature-stable environments. Furthermore, genome size variation was correlated with genomic repeat content, particular the *Ty1-copia* type belonging to long tandem repeat. Common garden experiment was performed in temperate (SWFU, Kunming) and tropical (XTBG, Menglun) sites to test the adaptive bases of genome size variation in *Rorippa*. The results revealed local adaptation of larger genomes to temperature-stable environments at XTBG. Accessions with larger genomes performed well in terms of several fitness components (e.g., fruit number and plant height) under tropical environment. In summary, study on natural variation of genome size in *Rorippa* suggests that plant genome size may tend to be large due to the expansion of repeat elements and in response to the extended growing period under temperature-stable environments.

P.1112 On the evolutionary significance of Pteronia polyploids in the Greater Cape Floristic Region

Eliška Havlíčková[1,2], Kristýna Šemberová[1], Vojtěch Zeisek[1,2], Terezie Mandáková[3,4], Douglas Euston-Brown[5], Zuzana Chumová[1], Pavel Trávníček[1]

1 Institute of Botany of the Czech Academy of Sciences, Průhonice, Czech Republic. 2 Faculty of Science, Charles University, Prague, Czech Republic. 3 Central European Institute of Technology, Brno, Czech Republic. 4 Masaryk University, Brno, Czech Republic. 5 Independent botanist, Scarborough, Cape Town, South Africa.

The Greater Cape Floristic Region (GCFR) is well known for its enormous biodiversity with a high level of endemism and substantial diversification within limited plant lineages, a phenomenon ascribed to historical radiation events. Polyploidization, generally recognized as one of the major forces in angiosperm evolution, is considered to be infrequent in the Cape flora. This investigation focuses on the South African endemic genus *Pteronia*, a prominent Cape representative of Asteraceae, the most species rich family in the GCFR. *Pteronia* radiated in the Cape and is adapted to main local biomes, fynbos and succulent karoo, with transitions to deserts or Nama-karoo. *Pteronia* species demonstrate a wide spectrum of genome sizes, which are associated with polyploidy (up to the octoploid level) and local adaptation to diverse environmental conditions. In particular, the species complex around *Pteronia adenocarpa* provides a perfect study opportunity with seven closely related species transitioning main biomes where we revealed multiple polyploid origins. Employing next-generation sequencing-based Hyb-Seq and RADseq methodologies, flow cytometry, karyology, and ecological modeling, we scrutinize the intricacies of its polyploid evolution and search for patterns of spatial and ecological distribution of polyploids across Cape in each species and the whole complex.

P.1113 Genome size evolution in the tropical ginger genus Curcuma L.

Bijay Khadka[1*], Marcos V. Dantas-Queiroz[2], Jana Leong-Škorničková[3, 4], Axel D. Poulsen[5], W. John Kress[6], Otakar Šída[7], Eliška Záveská[2], Tomáš Fér[1]

*1 Charles University, Prague, Czech Republic. 2 Czech Academy of Sciences, Institute of Botany, Průhonice, Czech Republic. 3 The Herbarium, Singapore Botanic Gardens, Singapore. 4 National University of Singapore, Singapore. 5 Royal Botanic Garden Edinburgh, Edinburgh, UK. 6 National Museum of Natural History, Smithsonian Institution, Washington, USA. 7 National Museum in Prague, Prague, Czech Republic.*khadkabi@natur.cuni.cz*

Genome size (GS) is an important feature of organisms that impacts cell-level processes and thus determines their biology and ecology. In plants, stochastic genomic processes like whole genome duplication and differential proliferation, and/or removal of repetitive regions of the genome (in particular transposable elements (TEs)) are thought to be potential factors influencing GS variation. Further investigation into the evolutionary and ecological foundations of this variance is an intriguing challenge. In temperate plant groups it has been demonstrated that organisms with smaller genomes are naturally selected in response to drought, which constitute the basis for the 'Large genome constraint hypothesis' (LGCH). Nevertheless, there is limited information regarding the validity of the LGCH in tropical regions and the potential influence of seasonality on the evolution of GS in tropical monsoon-climate plants. Here we aim to test LGCH on tropical rhizomatous herb genus *Curcuma* L. (Zingiberaceae) native to the monsoonal tropical Asia adapted to long periods of drought via dormancy. For this study, GS was measured for *ca.* 387 accessions of the genus *Curcuma* covering all three subgenera and more than 50% of the known species. GS, climatic and soil variables extracted for the localities of the samples were used in the phylogenetically corrected generalized least-square (GLS) model. Results indicate that areas with strongest seasonality (i.e. Western Ghats in India) are not occupied by polyploid species with bigger genomes. Moreover, GLS analysis with and without phylogeny indicate the significant role of precipitation, temperature, evapotranspiration, and soil nitrogen and phosphorus content for seasonal dormant tropical plant GS variation, supporting the LGCH. Furthermore, TEs quantified for 20 species from shallow-level genome sequencing using the RepeatExplorer2 pipeline, revealed a pattern congruent to phylogeny with lineage-specific TEs and satellite composition, and also a relationship with GS, polyploidy and TEs.

P.1114 Patterns of genome size evolution in the genus Helianthemum: relationship with chromosome number, climate, and morphology

Sara Martín-Herranz[1,2], Rafael G. Albadalejo[1], Juan Viruel[3], Rafael Matos[4], Sara Lopes[4], Encarnación Rubio[1], Mariana Castro[4], João Loureiro[4], Abelardo Aparicio[1]

1 Universidad de Sevilla, Spain. 2 Universidad Complutense de Madrid, Spain. 3 University of Coimbra, Portugal. 4 Royal Kew Gardens, Richmond, United Kingdom.

Inferring the patterns of genome size evolution and examining its relationship with ecological and phenotypic traits provide insights into the processes driving the rapid diversification of plants. Recent studies have revealed that variation in genome size can result from adaptive responses to various selective pressures, as well as from neutral evolution. The genus *Helianthemum* is a recently diversified lineage within the Cistaceae family, distributed in the Palearctic region. It comprises three subgenera, 10 sections and over 100 species inhabiting different environmental niches, including subdeserts, Mediterranean regions, subtropical-insular areas, and humid-montane ecosystems. The genus exhibits significant variability in life form, ranging from therophytes to chamaephytes, and diverse breeding systems, including autogamous, facultatively xenogamous and xenogamous plants. However, the underlying causes of their rapid ecological and phenotypic diversification remain enigmatic. In this study, we reconstructed the phylogenetic relationships for approximately 95% of the species using 353 Angiosperms genes. Additionally, we measured nuclear DNA content (2C) through flow cytometry to explore the evolution of genome size variation. Our findings reveal that genome size in *Helianthemum*, irrespective of chromosome number, contains valuable systematic and evolutionary information.

‘Small’ genomes are prevalent in desert specialists (sect. *Eriocarpum*), therophytes (regardless of their taxonomic position), and the species radiation of the Canary Islands (sect. *Helianthemum*), characterized by predominantly autogamous breeding systems. On the other hand, ‘large’ genomes are characteristic of the rest of species of sect. *Helianthemum* and the whole subg. *Plectolobum*, mostly xenogamous chamaephyte species with a Mediterranean and Eurosiberian distribution.

P.1115 Genome size impacts on the functional composition of leaves in species with large genomes

Arezoo Dastpak[1], Guo-Feng Jiang[2], Mae Camacho[1], Kevin Simonin[3], Adam Roddy[1]

1 Institute of Environment, Department of Biological Sciences, Florida International University, Miami, USA. 2 State Key Laboratory of Conservation and Utilization of Subtropical Agrobioresources, and Guangxi Key Laboratory of Forest Ecology and Conservation, College of Forestry, Guangxi University, Nanning, China. 3 Department of Biology, San Francisco State University, San Francisco, USA.

Across diverse taxa, cell size has been recognized as a pivotal factor influencing physiological performance. Notably, species with larger cells typically have lower rates of photosynthetic metabolism. Moreover, beyond the repercussions of cell size on diffusion, the mechanical attributes of a cell may exhibit variance as a function of cell size. As genome size imposes a primary constraint on cell size, species with large genomes may showcase alternative phenotypes to accommodate the physiological and mechanical constraints of enlarged cells. This investigation encompassed an examination of over 300 species of tropical and subtropical gymnosperms and angiosperms, with a specific focus on species with 2C genomes larger than 11 pg. Confirming prior findings, species with larger genomes manifested larger stomatal and epidermal pavement cells. However, a discernible trade-off was observed between genome size and leaf epidermal pavement cell shape, wherein species with smaller genomes exhibited more rounded cells with diminished undulating margins. Such cellular configurations, featuring reduced solidity, likely serve to alleviate mechanical stress on cell walls, thereby mitigating the consequences of cellular enlargement. Furthermore, We also found that cycads revealed unusual and distinctive profiles of stomatal and epidermal pavement cell sizes. Notably, cycad stomatal guard cells exhibited pronounced enlargement relative to their genome sizes, potentially augmenting the rates of CO_2 diffusion into their leaves. This adaptive trait may have been a key innovation that could have facilitated rapid radiation during a period of declining atmospheric CO_2 and increasing aridity. Taken together, these findings highlight the diverse approaches that species with extensive genomes may employ to address the constraints imposed by their big genomes on cell sizes, consequently influencing their physiological and biomechanical capabilities.

P.1116 Genome size diversity and its effects under nutrient limitation in wheat

Sayed Tahir Shah1, Nesrin Orcen2, Lubna Faizullah 1, Joseph Morton 1, Ilia Leitch 3, Simon Orford 4, Andrew Leitch 1

1 Queen Mary University of London, London, United Kingdom. 2 Ege Univeristy, Bornova, Turkey 3 Royal Botanic Gardens, Kew, London, United Kingdom. 4 John Innes Centre, Norwich, United Kingdom.

Wheat (*Triticum aestivum* L.) is one widely grown staple food crops and provides nearly 20% of daily human calorie intake. Wheat cultivation started about 10,000 years ago, probably in south-eastern part of Turkey and was then spread by humans to other parts of the world. Bread wheat is composed of three distinct subgenomes and its evolutionary history suggests that it originated from two polyploidization events. Landraces of wheat have a higher degree of genetic diversity compared to modern cultivars. Roughly 70% of wheat genome is composed of DNA repeats, but the precise genome size (GS) remains unclear, despite extensive genome sequencing projects and it is not known how much variation there is between landraces and cultivars. Previously, GS measurements of wheat have reported values of 15.4 Gb/1C, 16 Gb/1C and 17.3 Gb/1C, a 1.9 Gb/1C difference, equivalent to about 12 *Arabidopsis thaliana* genomes. In addition, tetraploid and hexaploid wheat have large differences in GS. Such differences can affect their physiology irrespective of their genic content (= nucleotypic effects). For example, in other plant species, GS diversity has been reported to influence where and how a plant can grow. This poster demonstrates GS diversity between wheat landraces and elite cultivars. It also shows how ploidal diversity in wheat affects biomass production and photosynthesis under nutrient limitation.

P.1117 Join the polyploid party! Polyploid sympatry and persistence in an African geophyte

Damian Vaz de Sousa[1], Michelle Greve[1], Kenneth C. Oberlander[1]

1 Department of Plant and Soil Sciences, University of Pretoria, Pretoria, South Africa.

Polyploidy plays a major role in plant speciation and adaptation. A fundamental question is how polyploids can persist when faced with the challenges of minority cytotype exclusion. Multiple abiotic and biotic factors can contribute to polyploid persistence and shape cytotype distribution patterns. The aims of this investigation were to explore and document the distribution of cytotypes of *Oxalis obliquifolia* across Gauteng Province, South Africa, and assess potential mechanisms that may have contributed to polyploid persistence in local populations. *Oxalis obliquifolia* cytogeography was assessed using standard flow cytometry (320 individuals from 25 sites), and chromosome counts determined using meiotic chromosome squashes. Potential abiotic niche differentiation between cytotypes was assessed using GIS data and soil samples. Morphological and phenological differences between cytotypes were assessed in a common garden experiment. Inter-cytotype reproductive isolation was assessed using crossing experiments. The number of potential polyploid origin events were analysed using Internal Transcribed Spacer DNA. Substantial cytotype diversity (six different cytotypes) was identified, with most sites having mixed ploidy populations. Chromosome squashes revealed a monoploid chromosome number of x = 7. Abiotic variables did not predict cytotype distribution. Clear size differences between diploids and polyploids (the Gigas effect) were observed. Larger vegetative and floral structures, and differences in flowering phenology, suggest biotic interactions (both competitive and pollinator interactions) could facilitate polyploid persistence. Crosses between cytotypes do yield (low) seed set, however DNA analysis suggests strong barriers to reproduction in situ. Remarkably, diploids and polyploids are behaving as distinct biological entities across Gauteng Province, despite high levels of sympatry, little observed niche differentiation and non-zero inter-cytotype seed set.

P.1118 Adaptive evolution of intraspecific genome size variation in Roscoea tibetica (Zingbiberacea)

Qing-Song Xiao[1], Wen Guo[1], Wen-Jing Wang[1], Mei-Yuan Huang[1], Qing-Jun Li[1], Li Li[1], Jian-Li Zhao[1]

1 Ministry of Education Key Laboratory for Transboundary Ecosecurity of Southwest China, Yunnan Key Laboratory of Plant Reproductive Adaptation and Evolutionary Ecology and Centre for Invasion Biology, Institute of Biodiversity, School of Ecology and Environmental Science, Yunnan University, Yunnan, China.

Although there are several hypotheses for explanations of adaptive evolution of genome size, their universality is questioned and applicability in intraspecific genome size evolution is unknown. This study aims to test these hypotheses through variations of the intraspecific genome size. Intraspecific genome sizes were collected from 53 *Rosocea tibetica* populations using flow cytometric approach. Stomatal size and density were measured from individuals in the field and common garden. Quantitative indicators of local adaptation and niche suitability were extracted from previous researches. Associations between intraspecific genome size and environmental factors, local adaptation and niche suitability were explored thoroughly though multiple statistical data analysis including (partial) Mantel tests. Large variations of intraspecific genome size of *R. tibetica* significantly positively correlated with altitude, latitude, precipitation, average temperature and water vapor pressure, but negatively correlated with solar radiation of growth season of *R. tibetica*. There was no correlation between genome size and oil nutrients. Mantel tests indicated environments controlled the variations of intraspecific genome size rather than the geography. Average temperature has the most contribution to variations of intraspecific genome size. Stomatal size and density from the field present significant correlation with genome size, while these two stomatal traits from the common garden have no clear correlation with genome size. Moreover, intraspecific genome size showed positive association with local adaptation. Our findings violate prevalent hypothesis about adaptive evolution of genome size, nucleotypic hypothesis and the nucleoskeletal hypothesis, that stomatal size should not be the predictor of genome size. This study refreshed our knowledge about evolution of genome

size that close relationship between stomatal traits and genome size was likely the casual result mediated by environmental factors, and the large genome size may be detrimental for survival in future climate changes.

S.129. PLANT RESPONSES TO STRESSES AND CLIMATE CHANGE

P.1119 Allelopathic activity of Euphorbia hirta against Avena fatua and Rumex dentatus and identification of potential allelochemicals

Muhammad Akbar[1], Taqdees[1], Tayyaba Khalil[1]

1 Department of Botany, University of Gujrat, Gujrat, Pakistan.

Phenomenon of allelopathy can be utilized to develop eco-friendly herbicides and there are number of reports of allelopathic effects of many weeds against other weeds but no reports are available that show the allelopathic effects of *Euphorbia hirta* against *Avena fatua* and *Rumex dentatus*. In the present research, allelopathic activity of *Euphorbia hirta* was investigated against *Rumex dentatus* and *Avena fatua*. *E. hirta* extract was prepared in dH_2O (10g:100mL w/v) as 100% extract concentration. Lower concentration (50%) was prepared by adding dH_2O to 100% extract. The allelopathic activity of *E. hirta* was evaluated by growing *R. dentatus* and *A. fatua* either alone or grown side by side with wheat plants in pots. The experiments were repeated twice. There were 5 treatments viz., dH_2O, half dose herbicide, full dose herbicide, 50% plant extract, and 100% plant extract. In *in vivo* bioassays, the effect of 50% and 100% plant extract of *E. hirta* on shoot dry biomass of *A. fatua* and wheat was non-significant in general, while there was 50% and 67% significant decline in shoot dry biomass of *R. dentatus,* respectively, when grown alone. Moreover, when *R. dentatus* was grown side by side with wheat, there was 71% and 86% decrease in shoot dry weight of *R. dentatus* at 50% and 100% extract concentrations of *E. hirta,* respectively. The reference herbicides, Sulfosulfuron, at full dose, significantly inhibited shoot dry weight of *A. fatua* by 14%, while, Fluroxypyr Meptyl + Florasulam + MCPA Isooctyl, completely eradicated *R. dentatus,* when grown side by side with wheat. The Gas Chromatography Mass Spectrometry (GCMS) analysis of *E. hirta* extract depicted the presence of potent allelochemicals, the major ones including quercetin, hexadecanoic acid, methyl ester, β-sitosterol, afzelin, gallic acid, neophytadiene, stigmasterol, trans, trans-2, 6-Dimethyl-2, 6-Octadiene-1, 8-Diol, and 2,3,5-trimethyl-1H-pyrrole.

P.1120 Citric acid amendment reshapes willow metabolism under cadmium stress

Danijela Arsenov[1], Milan Župunski[1], Dejan Orčić[2], Milan Borišev[1], Nataša Nikolić[1], Marko Kebert[3], Slobodanka Pajević[1]

1 University of Novi Sad Faculty of Sciences, Department of Biology and Ecology, Novi Sad, Serbia. 2 University of Novi Sad Faculty of Science, Department of Chemistry, Biochemistry and Environmental Protection, Novi Sad, Serbia. 3 University of Novi Sad, Institute of Lowland Forestry and Environment, Novi Sad, Serbia.

The ongoing rise of heavy metals in the environment underscores the urgent need to discover effective solutions for removing pollutants. A promising approach for phytoremediation of heavy-metal-contaminated soil involves the use of safe chelating agents in combination with the cultivation of tolerant trees. To address the impact of citric acid (CA) on the cadmium (Cd) tolerance of willows (*Salix viminalis*, *S. matsudana*, and *S. alba*), we conducted a potted soil experiment involving Cd (3 and 6 mg/kg) and CA (20 mmol/kg soil) treatments. The study delved into plant growth, Cd accumulation, antioxidant systems, and metabolic pathways in leaves and roots. The results underscored that exogenous CA alleviates Cd stress by enhancing the activity of antioxidant enzymes and non-enzymatic compounds, boosting the levels of osmotic metabolites like proline, and the amount of cysteine, ultimately resulting in the promotion of stress tolerance. However, the observed changes showed dose and plant-species-dependent manner and were more prominent in *S. viminalis* and *S. matsudana*, while *S. alba* can be distinguished as a less tolerant species regardless of the CA application. Metabolomic findings indicated that CA application alters the activity of the tricarboxylic acid (TCA) cycle by providing the necessary energy under adverse conditions, ultimately contributing to a notable enhancement of Cd resistance. The overall findings support the notion that CA lessens Cd-induced stress in willows and can help elucidate mechanisms governing Cd-induced stress.

P.1121 Genes-at-Extremes: An ecological multi-omics approach to uncover climate change relevant stress resilience genes

Lauren Audi[1,2], Tim Jeffers[1], Gil Eshel[1,3], Viviana Araus[4], Dennis Stevenson[2], Manpreet Katari[1], Samantha Frangos[1], Veronica M. Sondervan[1,2], Richard W. McCombie[5], Rodrigo A. Gutiérrez[4], Gloria M. Coruzzi[1]

1 Center for Genomics and Systems Biology, Department of Biology, New York University, New York, USA. 2 New York Botanical Garden, Bronx, USA. 3 Cytoreason, Azrieli Round Tower Begin, Israel. 4 Center for Genome Regulation, Santiago, Chile. Inst. for Integrative Biology (iBio), Institute of Ecology and Biodiversity, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile. 5 Cold Spring Harbor Laboratory, Cold Spring Harbor, USA.

Climate change is projected to threaten global food systems with a projected 17% increase in global desertification of the total land surface. Currently, over 50% of major crop yields are lost due to exposure to drought, salinity, and extreme temperatures. The genes of plants adapted to extreme environments can reveal underlying mechanisms involved in stress resilience that may otherwise remain hidden in model organisms. Chile's Atacama Desert is an ideal system, characterized by hyper-arid conditions, high UV irradiance, and extremely low soil nitrogen content, yet plants across diverse Angiosperm families have adapted to these conditions. We use comparative phylogenomics to identify genes under convergent positive selection for low nitrogen and drought tolerance in five major plant lineages. Transcriptome sequences from 28 Atacama species were compared to closely-related triplet sister species from other Mediterranean ecosystems— California Xeric, (drought tolerant, not nitrogen deficient) and California Mesic (not drought-adapted). Within the agriculturally-relevant Lamiid clade (tomato), we identified 67 Positively Selected Ortholog Groups (PSOGs) for specific adaptation to the Atacama, while 276 PSOGs were globally adapted to drought (Atacama *and* CA Xeric). Some of these PSOGs are orthologs to Arabidopsis genes with functional relevance to stress tolerance, including transcription factors (TFs). GO enrichment analysis, Protein Family (P-Fam) selection analysis and network analysis provide additional support for functional relevance of the PSOGs. Validation of the regulated targets of 3 TFs under positive selection was performed via the plant cell-based TF perturbation assay, TARGET (Transient Assay Reporting Genome-wide Effects of Transcription factor). In planta testing via agrobacterium mediated plant transformation will provide functional validation of TFs roles in drought and low nutrient tolerance. Identification and validation of these Atacama genes could improve the bioengineering of crop cultivars that are resilient to changing temperatures, water scarcity and nutrient limitation, improving the sustainability of our agricultural systems.

P.1122 Leaf pattern variation in vegetation according to pluviometric gradient in the Caribbean of Colombia

Mary Lee Berdugo-Lattke [1,2], J. Orlando Rangel-Ch [2]

1 Grupo de investigación de agua y desarrollo sostenible, Semillero Tygua, Programa de Biología, Facultad de Ingeniería y Ciencias Básicas, Universidad Central, Bogotá, Colombia. 2 Grupo de investigación de biodiversidad y conservación, Instituto de Ciencias Naturales, Universidad Nacional de Colombia, Bogotá, Colombia.

The leaf pattern was characterized in the vegetation (37 surveys) of localities of the pluviometric gradient of the Colombian Caribbean, defined such as the average annual rainfall in dry (600 – 1,000 mm), semi-humid (1,000 – 1,400 mm), humid (1,400 – 1,800 mm), very humid (1,800 – 2,200 mm), super humid (2,200 – 3,000 mm) and pluvial humid (> 3,000 mm). Between 5 to 20 leaves and one branch fragment were collected per survey to estimate leaf area (cm^2), specific weight (gr/dm^2), succulence (gr/dm^2), dry mass (%), thickness (mm) and wood density (gr/ml). A total of 1699 leaf samples were processed, belonging to 67 families, 213 genera and 562 species. The biotypological pattern found corresponds to simple, mesophyll leaves (45.01 - 182.2 cm^2), elongated shape, with entire margins, pointed apex, with acute or obtuse base, membranous consistency, unprotected, thickness type A (P.05 - 0.15 mm) and B (0.16-0.35 mm). In the pluviometric gradient, a linear trend was detected with the increase in specific weight values (gr/dm^2), succulence (gr/dm^2), dry mass (%), leaf thickness (mm) as precipitation increases; in drier areas, wood density and leaf area are smaller. In the most humid sites, a prevalence of coriaceous/sub-coriaceous consistency, pointed apex and irregular margins (serrulate and wavy) related to the effective drainage of water on the leaf lamina; the predominant shape is elongated and the thickness is greater (> 0.35 mm). In sites with less precipitation, microphyll leaves (2.26 - 20.25 cm^2), angled apex, A-type thickness, and protection on both sides of the leaf blade prevail. A novel pattern is documented with the prevalence of coriaceous/sub-coriaceous conditions in humid environments, contrary to the association that considered membranous characteristics indicative of high humidity in Colombia.

P.1124 Trade-offs between leaf traits and wood density in secondary forests in the Eastern Amazon

Botelho, Luane G.[1], Silva, Karoline C.[2], Barbosa, Beatriz V.[3], Negrão-Rodrigues, Vanessa[2], Elias, Fernando[4], Ferreira, Joice N. [4]; Barlow, Jos[5]; Teodoro, Grazielle S.[3]

1 Universidade Federal de Lavras, Lavras, Brazil. 2 Museu Paraense Emílio Goeldi, Belém, Brazil. 3 Universidade Federal do Pará, Belém, Brazil. 4 Embrapa Amazônia Oriental, Belém, Brazil. 5 Lancaster Environment Centre, Lancaster, UK.

Secondary forests are crucial for forest recovery, playing a key role in global warming mitigation, carbon storage, and biodiversity conservation. Covering around 234,795 km^2 in the Amazon, they represent about 4.1% of the total forest cover, making them crucial for large-scale climate change mitigation in the biome. Despite this, there is limited understanding of species' demands for establishment and survival in these forests, especially regarding trade-offs between different functions highlighted by leaf economics and wood economics spectra. Here we model the relationships between leaf area (LA), specific leaf area (SLA), leaf dry matter content (LDMC), and wood density (WD) in five secondary forests across different recovery stages (ages 9 to 60 years) in the Bragantina region, Pará, Brazil. The age of the secondary forests was defined by the Sustainable Amazon Network (RAS; rasnetwork.org) team through interviews with the owners during the installation of the permanent plots. In addition, confirmation of these ages was performed using high-resolution Landsat temporal images. The results revealed significant relationship patterns between leaf traits and wood density ($p<0,005$). All traits measured showed a positive relationship with WD, indicating a dissociation from the expected leaf and wood economics spectra, at least concerning SLA. Understanding these trade-offs is crucial for the sustainable management of secondary forests as it directly influences ecosystem dynamics, biodiversity, and carbon sequestration capacity. The observed variations in leaf traits and WD are attributed to ecological succession processes, revealing distinct adaptive strategies across different recovery stages. This complexity underscores the importance of considering temporal dynamics and diverse adaptive strategies in secondary forests. Our results offer valuable insights for forest management and restoration practices, emphasizing the need for a nuanced approach that aligns with specific characteristics of each recovery stage.

P.1125 Variation in adaptive leaf anatomical traits influencing photosynthesis in Taxus baccata L. clones from contrasting environments

Marc Carriquí[1,2], Maria Mayol[3,4], Miquel Riba[3,4]

1 Universitat de les Illes Balears, Institut d'Investigacions Agroambientals i d'Economia de l'Aigua, Palma, Spain. 2 Instituto de Ciencias Forestales, CSIC, Madrid, Spain 3 CREAF, Cerdanyola del Vallès, *Spain. 4 Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Spain.*

Leaf anatomy is a key determinant of CO_2 diffusion through leaves, hence influencing photosynthesis. Traits such as mesophyll surface area exposed to intercellular airspaces (S_m/S), cell wall thickness (T_{cw}), and chloroplast thickness (T_{chl}) significantly affect the effective CO_2 pathway length inside the leaf. Identifying the genetic basis of such traits is of great interest to uncover how they can influence tree ability to adapt, particularly in the current context of climate change. Exploring the effects of natural intraspecific genetic variability in the leaf anatomy of species with broad climatic distribution gradients in common garden experiments holds promise in addressing this objective. In this study, we investigated the variability of leaf morphoanatomical traits potentially related to local adaptation in *Taxus baccata* L., a non-model dioecious gymnosperm tree exhibiting high phenotypic variation. We sampled 65 mature male and female clones from 19 natural populations with diverse climates and altitudes that are growing in a common garden (Valsaín Clonal Bank) since 1992. Morphoanatomical traits were measured in 1-year-old leaves, and mesophyll conductance to CO_2 diffusion (g_m) was modelled from leaf anatomy. *Taxus baccata* exhibited the highest T_{cw} ever reported for a vascular plant, and particularly high S_m/S. The variability observed in traits such as leaf thickness, tissue proportions, leaf dry mass per unit area, or S_m/S was correlated with the climate of origin, while other key traits like T_{cw} and T_{chl} showed no significant correlations with climate. This might explain the limited impact of climate of origin on g_m. The results suggest that trees can respond to the needs of local conditions by modifyingS_m/S, but not T_{cw}.

P.1126 Limonium vulgare: high frequency micropropagation, shoot neoformation from leaf explants and biological activities

Gilbert Charles[1], Christian Magné[1], Xavier Dauvergne[1], Clément Lemoine[2]

1 Geoarchitecture Laboratory, Brest University (UBO), France. 2 Evonik Advanced Botanicals, Parçay-Melay, France.

Halophytes are submitted to high stress in their natural habitat characterized by severe abiotic conditions, including salinity, high light intensity and temperature, drought and mechanical stress in windy areas. The control of plant micropropagation, successfully achieved in relatively few halophytic species, is a prerequisite for many purposes. Thus, tissue culture of halophytes may be used for fundamental studies of their resistance to salt stress but also for applied objectives such as saline agriculture, salinized site rehabilitation, endangered plant preservation or production of bioactive secondary metabolites extracted from selected genotypes, in the respect of natural resources. The genus *Limonium* comprises over 350 species highly represented in the Mediterranean area. Previous *in vitro* studies focus on various ornamental or endangered species, but only few concern *L. vulgare* Mill. (*Plumbaginaceae*). In this study, a large-scale propagation system of *L. vulgare* was developed using two tissue culture processes: (i) from leafy shoot fragments (side shoots cuttings) from stock plants with a x30 multiplication rate every 6 weeks and (ii) *via* an original efficient neoformation process from leaf explants, producing 50 new buds per leaf. The plants were successfully acclimatized in greenhouse for biomass production, metabolite extraction and analysis. Strong antioxidant activities were identified in the crude extract of *L. vulgare*, as active as the commercial extract of rosemary. The methanolic fractions Fr20 and Fr60 present anti-radical activities equivalent to those of BHT (butylated hydroxytoluene) or resveratrol and are rich in phenolic compounds. Anti-tyrosinase activity was also described for the first time in this species.

P.1127 Transcriptomic analysis reveals an effect of the scion on rootstock gene expression in maritime pine (Pinus pinaster Ait.)

Irene Cobo-Simón[1], Laura Piccoli[2], Daniel Ramírez[3], Nuria de María[1], María Ángeles Guevara[1], María Dolores Vélez[1], José Antonio Cabezas[1], Paula Ramos[1], José Antonio Mancha[1], Alberto Pizarro[4], Miriam López-Hinojosa[1], Lorenzo Federico Manjarrez[1], Carmen Díaz-Sala[4], María Teresa Cervera[1]

1 Institute of Forest Science - National Institute for Agricultural and Food Research and Technology, Spanish National Research Council (ICIFOR-INIA, CSIC), Madrid, Spain, 2 University San Pablo CEU, Madrid, Spain, 3 Complutense University of Madrid, Spain, 4 University of Alcalá, Alcalá de Henares, Spain

Climate change is threatening the adaptive capacity of several forest tree species due to increasing drought and rising temperatures. Especially in the Mediterranean region, subjected to recurrent droughts which, according to future predictions, will progressively increase. Therefore, understanding the molecular and functional mechanisms that control the adaptation of trees to drought is highly valuable for conserving Mediterranean forests. Maritime pine (*Pinus pinaster* Ait.) is one of the conifers with the greatest socioeconomic and ecological importance in southwestern Europe. It is the main source of softwood in this region and shows a remarkable ability to adapt to different environments. In a previous study using a full-sib family design, and two *P. pinaster* individuals, from contrasting precipitation regions, as progenitors, we found transcriptional activity on drought stress-related genes, even without water deprivation, in tolerant genotypes. Here, we aim to improve our knowledge between above- and below-ground organ communication on maritime pine by analyzing four graft-type constructions. To this end, we used two siblings with contrasting response to drought (tolerant and sensitive), from the previous pedigreed design, as rootstocks, and their progenitors as scions. Then, we study the effect of the scion origin in the rootstock's gene expression by analyzing the transcriptional profile of the roots. The results showed that the gene expression of both tolerant and sensitive rootstocks was modified by the scion origin, regardless the existence of water deprivation. They also showed activation of genes involved in tolerance to abiotic stress. This study sheds light on the effects of grafting in the gene expression and tolerance to abiotic stress on conifers, as well as on their organ-organ molecular and functional communication. This information can be also useful to design conservation and management programs, since trees, as long-lived sessile organisms, would greatly benefit from drought tolerance improvement by grafting.

P.1128 A flammable desiccation-tolerant seeder drives fire across vegetation islands on rock outcrops

Abel A. Conceição[1], Soraia, C. Dias[1], Jamine M. Rocha[1], Pedro, M. Villa[1], Thiago F. Araújo[2]

1 Universidade Estadual de Feira de Santana- UEFS, Feira de Santana, Bahia, Brazil. 2. Instituto Federal de Educação, Ciência e Tecnologia da Bahia- IFBA, campus Irecê, Bahia, Brazil.

Rock outcrop vegetation present in grasslands and savannas are often regarded as "fire-free habitats". However, a recent study in Brazilian campo rupestre showed that islands of vegetation burn and regenerate after fire on rock outcrop vegetation, where the desiccation-tolerant seeder post-fire strategy was described, mainly represented by a dominant *Vellozia punctulata* Seub. Here, we evaluated the flammability of *V. punctulata* to assess the proneness of fire spreads across the vegetation islands on rock outcrops. We collected branches of 15 individuals of *V. punctulata* in three campo rupestre areas in the Chapada Diamantina, Bahia, Brazil, and measured flammability components using a device for a standard measurement of shoot flammability (metallic structure with, grill, burners, and a blowtorch, constructed to simulate a forthcoming fire). We put the branches on grill for two minutes at a150 °C and then ignited them with a blowtorch. We measured the time to burn (ignitability), the burning time (sustainability and combustibility), the maximum temperature (combustibility) and the proportion of fuel consumed (consumability). The branches of 13 individuals ignited immediately, while two delayed one second. The fire reached mean maximum temperatures of 532°C, 554°C and 685°C in each population and burned for 45, 49 and 121 seconds. All fuel was consumed in one population, and 92% and 96% in others. The high ignitability of *V. punctulata* indicates high proneness of fire occurrence, and the high sustainability, combustibility and consumability suggest high capacity to fire spread and release heat sufficient to flame the neighboring vegetation island. Considering the high flammability and dominance of *V. punctulata* in vegetation islands, our results highlight the key role of desiccation-tolerant seeder *V. punctulata* driving wildfires on rock outcrops in the campos rupestres of Chapada Diamantina.

P.1129 Plant diversity and forest structure: a comparison between reforestations and mature forests in the central Iberian Peninsula

Estrella Conde[1], Ana I. García-Cervigón[1], Jesús López-Angulo[1], David S. Pescador[1,2], Adrián Escudero[1]

1 Biodiversity and Conservation Area, ESCET, Rey Juan Carlos University, Móstoles, Spain. 2 Department of Pharmacology, Pharmacognosy and Botanic, Faculty of Pharmacy, Complutense University of Madrid, Madrid, Spain.

Forest conservation represents one of the most effective tools to mitigate biodiversity loss resulting from Global Change. Given the extensive degradation and widespread destruction of forested areas worldwide, substantial and effective reforestation efforts are needed. Despite the historical implementation of reforestations in Spain, the extent of their success in improving biodiversity remains unknown. Plants are an essential component of the forest and support the entire trophic structure of the community. However, we do not know whether historical reforestations have been successful in recovering the structure and diversity of forests. We expect that reforestations with a structure similar to reference mature forests will exhibit higher diversity indices. To approach this question, we compared the diversity of vascular plants and forest structure among reforestations and reference mature forests. Based on a perennial plant inventory conducted in 30 mature forests and in 33 reforestation plots with ages up to 75 years in Castilla-La Mancha and Madrid regions, we calculated taxonomic and phylogenetic diversity metrics. In addition, heights and diameters of tree species were measured in each plot. A comparative analysis was carried out to classify diversities based on forest type and their relationship with plot structure. We found that mature forests had higher levels of biodiversity, and although species composition of vascular plants varies more with geology and climatology, it also varied between mature and reforested forests. However, there are no significant changes in phylogenetic diversity between mature and reforested forests. These promising results will be highly valuable in adapting forest management to address the impacts of Global Change and biodiversity loss.

P.1130 Biotic and abiotic protection of colleters in Rubiaceae species within the Amazonian Savanna and Atlantic Forest

Maura Da Cunha[1*], Lucas L. Reis[1], Ana L.C. Silva[1], Laís A. Bezerra[1], Saulo Pireda[1], Renata P. Amélia, Marcos J.G. Pessoa[2], Fabio L. Olivares[1], Valdirene M. Gomes[1]

1 Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brazil. 2 Univesidade do Estado do Mato Grosso, Alta Floresta, MT, Brazil. *maura@uenf.br.

This study focuses on the characterization of stipular colleters in Rubiaceae species from Amazonian savannas and the Atlantic Forest, specifically examining *Ladenbergia amazonensis* Ducke, *Ferdinandusa chlorantha* (Wedd.) Standl., *Ferdinandusa elliptica* (Pohl) Pohl, *Bathysa mendoncaei* K.Schum and *Palicourea tetraphylla* Cham. & Schltdl. Colleters, specialized secretory structures, were found to exude a mixture of mucilage, lipophilic substances, and proteins, playing a crucial biological role in protecting meristematic tissues and organs from desiccation, herbivory, and pathogens. Additionally, the study revealed the interaction between colleters and microorganisms in their surroundings influenced by the exudates. The colleters exhibited standard and reduced types, with a distinctive translucent hue at the first nodule and a brownish-brown appearance from the second nodule onward. The first node displayed active exudate synthesis and secretion, while the second node exhibited cellular disarray and the onset of senescence. Histochemical analyses identified phenolic compounds, crystals, mucilage, proteins, lipids, and alkaloids within the colleters. Moreover, the outer cell wall of the colleter developed a reticulated network of polysaccharides in its cuticular layer, displaying arborescent, reticulated, and cuticle-proper divisions. The extraplasmic space between the plasma membrane and the cell wall contained secretory material with fibrillar structures, housing microorganisms embedded within the secretion. While the ultrastructure of secretory cells adhered to the norm, the unique behavior of the outer cell wall suggested an active role in the secretion process. The study concluded that colleters in Rubiaceae species retained taxonomical structural attributes, suggesting two main functions: combating fungi and creating an environment conducive to beneficial organisms. These roles align with the additional function of averting desiccation, emphasizing the ecological and taxonomic significance of colleters in these plant species from diverse habitats.

P.1131 Mitigating role of silicon nanoparticles in soybean under cadmium contamination

Jaqueline Santos[1], Salete Gaziola[1], Ricardo Azevedo[1]

1 University of Sao Paulo, Sao Paulo, Brazil.

Soybean, one of the most economically important crops in the world, may be subject to cadmium (Cd) contamination from different sources, including fertilizers containing trace metals. SiO_2 nanoparticles (SiO_2-NPs) are described as mitigating various types of stress in plants. Therefore, we investigated spherical SiO_2-NPs, 5-20 nm (Sigma-Aldrich®) in mitigating Cd oxidative stress in a Non-transgenic soybean (Non-TS) and another transgenic (Roundup Ready®) (TS). The soybeans in the V1 stage received the treatments, each one with 25 specimens. The experiment was carried out in a greenhouse for two months. The TS treated with SiO_2-NPs 200 mg/kg wet substrate had a 20% reduction in SOD activity compared to the control (without SiO_2-NPs and Cd), in contrast, Non-TS increased 5% in SOD activity. For the same treatment, CAT increased 30% for TS and by 12% for Non-TS. For TS, treatments with 4, 8, and 32 Cd mg/kg substrate when compared to plants treated with SiO_2-NPs had a reduction in SOD activity of 47%, 54%, and 63%, and for CAT 27%, 34 %, and 55%, respectively. In Non-TS exposed to 4, 8, and 32 mg of Cd there was a reduction in SOD of 16%, 21%, and 24%, respectively, while CAT had a 28% reduction for 32 mg of Cd. For TS, treatments with Cd and SiO_2-NPs combined (Cd 4, 8, and 32 + SiO_2-NPs 200 mg/kg substrate), compared to treatments with Cd alone, showed an increase for SOD of 157%, 73%, and 91%, respectively. Furthermore, CAT for TS increased 36% and 29%, and SOD for Non-TS increased by 15% and 21% for 4 and 8 mg Cd with SiO_2-NPs. Therefore, SiO_2-NPs attenuated Cd toxicity.

P.1132 Street trees of Rome and their relationship with the changes of urban climatic parameters

D'Amato Luca[1], Flavia Bartoli[1,2*], Valentina Savo[3], Giulia Caneva[1,4]

*1 Department of Science, University of Roma Tre, Rome, Italy. 2 Institute of Heritage Science, National Research Center, Rome, Italy. 3 Department of Education Science, University of Roma Tre, Rome, Italy. 4 National Biodiversity Future Center, Università di Palermo, Palermo, Italy. *Corresponding Author. flavia.bartoli@cnr.it.*

Natural ecosystems nowadays are being damaged by the increasing urbanization and environmental quality of cities. The purpose of this work is to understand What relationship exists between plant chorotypes (as indicators of adaptation to different conditions) found in different municipalities and local climatic conditions. We elaborated on both meteorological data and ecological data. Meteorological data were processed between 2008 and 2013 and from 2019 and 2022. Rivas-Martinez thermicity and ombrothermicity bioclimatic indices on which it was possible to define the bioclimatic context of the different areas identified by the stations. Our data show a heat island effect in the stations in the center, belonging to the upper Thermomediterranean thermotype. These data bring to light not only a certain ombrothermal variability but also a transitional situation toward a less xeric bioclimatic region in the western area, closer to the coast and thus more subject to maritime influence, toward the eastern area (Nimis, 1989). For ecological data, we performed an analysis of species chorotype based on a previous dataset (D'Amato et al. 2023, Bartoli et al 2021, Caneva et al 2020). As for the most represented chorotypes, considering the distribution for the whole city, we find the most significant presence of E-Asiat (24.35%), N-Amer (19.09 %), Eurimedit (15.14 %), Silv-cult (14.03 %) and Steno-Medit (11.01 %). Regarding alien species, we can see that they exceed 60% in all *municipia*. We believe that it would be interesting to be able to favour species more adapted to warm climates in more critical bioclimatic zones highlighted than others. Therefore, this preliminary analysis could lead to greater attention in the planting and design of roadside tree plantings.

P.1133 Germination dynamics of Neoglaziovia variegata: impact of thermal and saline limits on the ecology of the species

Raquel A. Gomes[1], Williane A.S. Oliveira[2], Marcos V.C. Freitas[3], Maria A.R. Ferreira[1], Jamille C. Silva[1], Jailton J. Silva[4], Bárbara F. Dantas[4]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Instituto Federal de Educação, Ciência e Tecnologia, Petrolina, Brazil. 3 Universidade Federal do Vale do São Francisco, Petrolina, Brazil. 4 Embrapa Semiárido, Petrolina, Brazil.

Global warming significantly impacts the environment, constantly altering weather patterns and inducing more frequently extreme events. Temperature, water availability, as well as nutrients and salts in the soil are some factors that directly affect germination, development and growth of plants. *Neoglaziovia variegata* (Arruda) Mez is a Bromeliaceae endemic to the Caatinga Domain that has highly resistant fibers that are used to generate income for several families, in addition to having landscaping and medicinal potential. Therefore, the objective was to identify the thermal and saline limits that influence the germination response of this species. To simulate thermal stress, the seeds were allowed to germinate at constant temperatures between 15 and 40°C. Salt stress was evaluated using a NaCl solution from 0 (distilled water) to 14 dS/m-1. The experiments were set up in a completely randomized experimental design, with four replications of 25 seeds in each trial, for 28 days, with germination being considered by the emission of 2mm from the main root. The germination data were analyzed according to the thermal and halo (saline) time models and then the limits for germination were established. The results showed that the estimated base and ceiling temperatures for N. variegata germination are 14.3 and 41.7 °C, respectively. The optimum temperature for germination of *N. variegata* seeds was 31.1 °C. The estimated germination limit in saline media is 16.2 dS.m^{-1}. The wide range of temperatures observed, as well as the high germination limit in saline environments, demonstrate that *N. variegata* is a species that can maintain its survival in the most pessimistic scenario of climate change for brazilian semiarid region, such as +3.5°C in air temperature and reduction in 50% of rainfall and more saline soils.

P.1134 Harnessing beet's biochemistry: betalains and catecholamines in plant defense

Saswata Dey[1], Alfonso Timoneda[2], Jiafu Tan[1], Hana Azuma[1], Sebastian Eves-van den Akker[1], John P.Carr[1], Samuel F. Brockington[1]

1 University of Cambridge, Cambridge, UK. 2 Virginia Tech, Hampton, USA.

L-DOPA (L-3,4-dihydroxyphenylalanine), dopamine, norepinephrine, and epinephrine belong to a group of compounds known as Catecholamines that are commonly studied in the context of animal biology. They are universally present in all animal groups and their functions are well understood in mammalian systems as neurotransmitters. It is often underappreciated that plants also synthesize and accumulate these compounds in low to high amounts. The biosynthetic pathway of these compounds begins with the amino acid L-tyrosine, as in animal systems. The plant order Caryophyllales is one lineage that excels at specialised tyrosine metabolism, owing to the relaxed regulation of tyrosine in this clade, making them an attractive model system to study these compounds *in planta.* Additionally, this group harbours a unique pigment class, Betalains (the characteristic colour of beetroot), that has replaced the otherwise ubiquitous anthocyanins. Interestingly, these betalains and catecholamines share the same precursors at multiple points. The synthesis of L-DOPA with its genes and enzymes is quite well understood in the model plant *Beta vulgaris* in the context of betalain biosynthesis. In this present study, we express betalain and catecholamine metabolites in the model plant species *Arabidopsis thaliana* to test their potential against biotic stressors. These transgenic lines expressing betalains (RUBY) and catecholamines were challenged with *Heterodera schachtii* (parasitic nematodes) and *Myzus persicae* (green peach aphids). Our results reveal interesting differences in the responses of these pests to betalains and catecholamines. The *Heterodera* pathosystem in conjunction with transgenic lines expressing betalains also revealed interesting observations such as asynchronous pulse-feeding phenotype in cyst nematodes and syncytia-specific differential metabolic pattern of betalains. This reinstates that betalains are much more than just a special colour.

P.1135 Resistance mechanisms of three moss species to lead and copper soil pollution

Isabel Domarco Sagra[1], Diego Sánchez Sánchez[1], Belén Estébanez Pérez[1]

1 Faculty of Science, Universidad Autónoma de Madrid, Madrid, Spain.

Mosses are widely used in biomonitoring programs to estimate the deposition of heavy metals. However, certain species exhibit resistance mechanisms distorting the estimations of heavy metals in the environment. Here we study these resistance mechanisms to copper and lead soil pollution in three common Mediterranean moss species. We conducted an experimental study involving artificial soil pollution in seedbeds grown in a greenhouse, using *Tortella squarrosa*, *Homalothecium aureum*, and *Ptychostomum capillare*. We used different doses of lead, copper, and a combination of both. To detect the presence of lead and copper in the plant tissues, and explore possible resistance mechanisms, we performed some histochemical tests, and scanning electron microscopy with energy-dispersive X-ray spectroscopy (SEM-EDX) analyses. After 8 weeks, all three species survived in high concentrations of heavy metals. We confirmed the presence of resistance mechanisms depending on the moss species and the specific heavy metal used. Two potential strategies were identified: metal exclusion through barriers (such as mucilage or waxes), and metal accumulation in senescent regions of the mosses. The exclusion strategy was observed in all three species when exposed to lead. In contrast, at least *T. squarrosa* and *P. capillare* exhibited a dual strategy—metal exclusion in apical parts and accumulation in basal parts—when exposed to copper. We confirmed the existence of distortion mechanisms in all three species, which may impact heavy metal estimates using them in environmental biomonitoring programs.

P.1136 Response to drought along a climatic gradient through an analysis of wood anatomy and leaf traits in two gypsum shrubs

Sara Escada[1], Ana I. García-Cervigón[1], Silvia M[1].

1 Universidad Rey Juan Carlos, Madrid, Spain.

Gypsum soils tend to be associated with arid and semi-arid climatic conditions and harbor a rich flora adapted to these conditions. However, plants growing in these soils are vulnerable to the expected increase of drought intensity and frequency, triggered by ongoing climate change. The chamaephytes *Helianthemum squamatum* and *Ononis tridentata* are two endemic species that grow in gypsum soils of the Iberian Peninsula. We studied four populations along a latitudinal gradient (northeast, center and southeast), varying in temperature and rainfall. We aim to determine how leaf and wood traits vary in response to environmental conditions along this gradient, and whether there is a coordination between these groups of traits. We collected wood samples from the root collar and leaves from 15 individuals of both species at each of the four locations. We measured four leaf functional traits: specific leaf area (SLA), leaf dry matter content (LDMC) and ^{13}C and ^{15}N isotopes, chemical traits associated with acquisitive resource strategies. Using images of anatomical cross-sections of the last growth ring of each individual, we measured several wood anatomical traits related to hydraulic function, such as vessel density, vessel lumen area and diameter, vessel grouping, percentage of conductive area and an estimation of hydraulic We expect that individuals that inhabit the driest area will show more efficient water strategies, having smaller and thicker leaves as well as smaller and more abundant vessels. Independency of group traits allows plants to develop a more efficient allocation of resources; therefore, we expect to find a lower leaf:stem trait coordination in the location with the most stressful, driest climatic conditions.

P.1137 Adult plants of the moss Tortella squarrosa accumulate calcium as a response to heavy metal soil pollution

Isabel Domarco Sagra[1], Belén Estébanez Pérez[1]

1 Faculty of Science, Universidad Autónoma de Madrid, Madrid, Spain.

Recent research has shown that mosses possess diverse resistance mechanisms enabling them to tolerate relatively high concentrations of heavy metals in terrestrial environments. To further expand our understanding in this field, we conducted an analysis of the presence and distribution of various chemical elements in the tissues of the terrestrial moss species *Tortella squarrosa* growing on soil contaminated with lead and copper. We compared samples of *T. squarrosa* cultivated in a greenhouse on decalcified soil artificially contaminated with different doses of lead, copper, and both in synergy, with uncultivated, wild samples from locations not contaminated with heavy metals. In one location the moss was growing on soil rich in calcium carbonate, while in the other it was collected from calcium carbonate-poor soil. We conducted semi-quantitative analyses on the presence and distribution of elements in the tissues of these plant samples using scanning electron microscopy coupled with energy-dispersive X-ray spectroscopy (SEM-EDX). In the analysis of all samples from soils treated with heavy metals, significant amounts of various elements were recorded, including silicon and potassium, but especially calcium. This contrasts with the control samples (without heavy metals) and the wild samples, where the presence of calcium and other elements apart from carbon and nitrogen, remained consistently low, with no influence of the calcium content in the soil. Additionally, in the case of samples cultivated with copper, we observed the formation of mineral accumulations rich in copper and calcium, apparently excreted by the moss, adhered to the surface of the leaves. Considering that calcium has been described as partially neutralizing the toxic effects of lead and copper, our results suggest that calcium accumulation represents a new resistance mechanism against heavy metal contamination, previously undescribed in mosses.

P.1138 Variability in leaf minimum conductance (g_{min}) in vascular plant species across different island habitats

Antoni Josep Far[1], Miquel Capó[2], Carles Cardona[3,4], Jaume Company[1,5], Jaume Flexas[1], Luis Flor[1], Llorenç Gibanel[1], Javier Gulías[1], Rosana López[2], Pere M. Mir-Rosselló[1], Joan Pons[1], Faustino Rubio[6], Guillermo Toro[6], Marc Carriquí[1,7]

1 Departament de Biologia, Universitat de les Illes Balears, Institut d'Investigacions Agroambientals i d'Economia de l'Aigua, Palma, Spain. 2 Departamento de Sistemas y Recursos Naturales, Universidad Politécnica de Madrid, Madrid, Spain. 3 Centre Forestal de les Illes Balears, Institut Balear de la Natura, Palma, Spain. 4 Department of Biology, University of the Balearic Islands, Palma, Spain. 5 Departament de Geografia, Universitat de les Illes Balears, Palma. 6 Centro de Estudios Avanzados en Fruticultura, Rancagua, Chile. 7 Instituto de Ciencias Forestales (ICIFOR-INIA), CSIC, Madrid, Spain.

Habitat location is significantly influenced by climatic stability. In Mediterranean environments where dry periods coincide with warm seasons, aridity profoundly impacts habitat area and consequently, species distribution. The xylem cavitation threshold and the dehydration rate of a plant determine species survival during acute droughts. While the cavitation threshold correlates with climate, the relationship with dehydration rates remains unclear. Leaf minimum conductance (g_{min}), a critical trait defining dehydration rates after stomatal closure, may provide insights into habitat vulnerability to climate change, especially as longer and more intense drought events are anticipated. This issue is particularly critical for islands, where habitat migration is limited. Here we characterized the g_{min} in over 100 species, including, gymnosperms and angiosperms, ranging from herbs to trees across 18 habitats from Mallorca Island (Balearic Islands, Spain) were annual mean temperature ranges from 13.2 to 16.8 °C, and precipitation from 413 to 792 mm. Data were collected during June and July of 2023, focusing on sun-exposed leaves. Additionally, anatomical leaf mesures where taken. This comprehensive sampling facilitated an in-depth exploration of the variability in g_{min} across patchy habitats, commonly found in islands with complex orography, and its potential correlation with climate. Preliminary results revealed variability in g_{min} throughout different habitats for different life forms (herbs, vines, shrubs and trees) but surprisingly we did not find the expected trend of decreasing g_{min} with increasing habitat aridity. However, we observed that g_{min} was closely related to lifeform. Herbaceous plants exhibited the highest g_{min} followed by vines and shrubs, whereas trees showed the lowest g_{min}. This observed trend could be explained by lifeform-specific adaptations. The increase in complexity of hydraulic segmentation and cuticle investment may explain the observed trend in *gmin* and its link to dehydration rates.

P.1139 Climate change-induced decrease of photosynthetic pigments in Iberian conifer forests

Cristopher Fernández-Blas[1], Miguel A. Zavala[1], Elena Granda[1], Marina Rodes-Blanco[1], Eva Samblás-Vives[1], César Morales-Molino[1], Pedro Rebollo-Orozco[1,3], María J. López-Caro[1], Julián Tijerín-Triviño[1], Mariano García Alonso[1], Inmaculada Aguado[1], J. J. Camarero[3], Antonio Gazol Burgos[3], Mercedes Uscola-Fernández[1,4], Paloma Ruiz-Benito[1]

1 Universidad de Alcalá (UAH), Alcalá de Henares, Spain. 2 Universidad Complutense de Madrid (UCM), Madrid, Spain. 3 Instituto Pirenaico de Ecología, (CSIC), Zaragoza, Spain. 4 Universidad Rey Juan Carlos, Móstoles, Spain.

Climate change is affecting ecosystem dynamics at different biological levels, from individual trees to mixed communities. In the Mediterranean basin, and especially in Spain, climate change is expected to increase drought severity, frequency, and length. Although Mediterranean vegetation is generally adapted to withstand significant long and intense dry periods, this shift in the climatic conditions may affect Mediterranean ecosystems. The increase in evapotranspiration caused by climate change is putting plants under a more severe water stress that can condition their growth and response to perturbations. Reduced vigor can be appreciated when quantifying the concentration of photosynthetic pigments in the leaves, as a reduction in these is pigments is commonly correlated with a higher crown transparency. In this work, we sampled paired healthy and damaged conifer forests due to drought in the Iberian Peninsula (four sites of *Pinus sylvestris*, one site of *P. pinea*, and two of *Abies alba*). To assess differences between paired sites we measured radial growth rates, specific leaf area (SLA), leaf nutrient concentrations and photosynthetic pigments (chlorophylls a and b, and xanthophylls and carotenes), leaf water content and water use efficiency in 462 target trees. We obtained higher growth rates, SLA, photosynthetic pigments, and nutrient concentration in trees from healthy forests than in damaged ones. The reduced concentration of photosynthetic pigments is related to a decrease in overall tree growth and, probably, in ecosystem function. Thus, these parameters might serve as an early warning of tree mortality induced by drought and climate change.

P.1140 Methods for drought-resistance screening in lentils

Andrea Fernández-Gutiérrez[1], Juan J. Gutiérrez-González[1]

1 Department of Molecular Biology-Genetics, University of León, León, Spain.

Lentil (*Lens culinaris* Medik.) ranks the fifth in legume production worldwide being a principal source of protein in developing countries. Nevertheless, predictions on the forthcoming increase in frequency and intensification of drought periods endanger its production. Lentil is considered moderately drought-resistant, however, marked differences between accessions have been observed. The multifaced character of drought resistance hinders accurate phenotyping. Traditional drought-resistance phenotyping involves plants growing until maturity to check yield loss under drought-stress. However, these techniques represent big inputs of work, time, and material. Consequently, the actual trend is to develop early selection methods. In this study, we carried out two different approaches employing the same six lentil accessions to check whether seedling selection in lentil accession is achievable. In the first approach, drought was imposed at seedling stage by adding 15% polyethylene-glycol 6000 to the hydroponic medium for a week; relative water content (RWC), root length, stomatal density and stomatal aperture were measured at the end of the experiment. In the second approach, at reproductive stage, accessions were submitted to 40% soil moisture field capacity for two weeks. After the treatment, RWC, photosynthesis rate, stomatal conductance, water use efficiency, root biomass and water potential were measured. Watering was restored until the end of the life cycle, where seeds were harvested and weighted. Correlations among all the parameters were established. RWC at reproductive stage was the most highly correlated with yield loss (R=-0.92). At seedling stage, correlation between yield loss and RWC was also significant (R=-0.80), implying that an early screening is achievable for lentils. We also found that the 100-seed weight is severely affected by drought stress, and the magnitude of the effect is genotype-dependent. Interestingly, seed weight reduction appears to be more correlated with seedling parameters that reproductive ones. Our findings provide valuable information for drought-resistance studies.

P.1141 Conservation and vulnerability of seagrass communities on the coast of the Gulf of Mexico.

Margarita E. Gallegos Martìnez[1], Sergio A. Fuentes Agueda[1], Gabriela Márquez Labastida[1], Francisco J. Ordoñez Gasca[1], Iliana Pérez Espinosa[2]

1 Universidad Autónoma Metropolitana-Iztapalapa México City, Mexico. 2 Comisión Nacional para el Conocimiento y Uso de la Biodiversidad México City, Mexico.

Seagrass communities are relevant for protecting the coastline and are important carbon sinks. Nowadays, they are experiencing a strong decline globally, due to global warming and anthropogenic changes. However, the current state and ecosystem services they provide in both tropical and temperate zones are unknown. The objective was to analyze the vulnerability of seagrasses with biotic and abiotic variables in the Gulf of Mexico. In 7 areas along 63 stations of The Gulf of Mexico, with an ecosounder BioSonics model DT-X, the relative coverage of Submerged Aquatic Vegetation was registered. Also, environmental parameters (temperature pH, depth, dissolved oxygen, salinity, nutrients in the water column, interstitial water, type of sediment, and organic carbon) and biotic parameters (Distribution and abundance (g/m2) of Submerged Aquatic Vegetation, phytoplankton, and epiphyte biomass) were registered at each site, the years 2016 and 2019 for each of the four months. The areas have significant differences in depth, salinity, and dissolved oxygen, which are related to the composition and abundance of the SAV. Area 4 (Dzilam de Bravo) has the highest biomass in SAV and the lowest is Area 2 (Champotón). Phytoplankton biomass was higher in Area 1 (Laguna de Terminos) and epiphyte biomass was higher in Area 2. Vulnerable seagrass communities are the ones that are less protected and have high anthropogenic activities like Area 2. The most abundant are communities in Area 3 (Petenes) and 4, which are related to conserved areas and have less anthropogenic impacts.

P.1142 Desiccation tolerance in the family Gesneriaceae

Nora Larrañaga[1], Miren I. Arzac[1], Beatriz Fernández-Marín[1], Antonio Hernández[1], Usue Pérez López[1], Daniel Ballesteros[2], José I. García Plazaola[1]

1 Department of Plant Biology and Ecology, University of the Basque Country, Leioa, Spain. 2 Department of Botany and Geology, University of Valencia, Valencia, Spain.

Desiccation tolerance (DT) is defined as the capacity of some plant species to almost fully dehydrate and recover all physiological functions after rehydration. Widespread among terrestrial algae or bryophytes, this is an extremely unusual trait in angiosperms. Desiccation tolerant species, also called resurrection plants, are grouped in a few families. One of the families for which more resurrection species have been characterised is Gesneriaceae. All resurrection gesneriads described so far belong to the tribe Trichosporeae, being mostly distributed in Africa, SE Asia and southern Europe. In the present survey we aim to describe the extent of DT among gesneriads, and specifically whether this trait is a constitutive character of the family and it is present in species belonging to the other tribes of the family or not. We have used a standard protocol for quantitative determination of the degree of desiccation tolerance in leaves from a large collection of plants collected in the field or cultivated in our Campus or in several Botanical Gardens. Despite the tropical origin of the family, some species can be found in temperate/cold climates (such as those of the mountains of central Europe and Asia). Since, we speculate that the primary ability these species have to tolerate desiccation permits them to tolerate freezing too, in parallel to DT we also tested freezing tolerance.

P.1143 Cold and freezing tolerance of photosynthetic apparatus in Balkan resurrection plants of the genus Ramonda

Bekim Gashi[1], Fitim Kastrati[1], Gergana Mihailova[2], Katya Georgieva[2], Erza Çoçaj[1]

1 Department of Biology, Faculty of Mathematical and Natural Sciences, University of Prishtina "Hasan Prishtina", Prishtinë, Kosovo. 2 Institute of Plant Physiology and Genetics, Bulgarian Academy of Sciences, Sofia, Bulgaria.

In the Balkan Peninsula, the genus Ramonda is represented by two species*, R. serbica* and *R. nathaliae*, known as resurrection plants due to their remarkable ability to tolerate both drought and freezing stress. In contrast to desiccation tolerance, the mechanisms of freezing tolerance of these resurrection plants are scarcely investigated. Only a few resurrection species are exposed to subzero temperatures in their natural environments, making them interesting models for studying the photosynthetic mechanisms of freezing tolerances. In this study, we analyze the influence of cold and freezing temperatures on photosynthetic activity and chlorophyll fluorescence parameters in the leaves of both Ramonda species under natural conditions during autumn and winter periods Based on the results for both Ramonda species, it appears that the net CO_2 assimilation (*A*) and stomatal conductance (*gs*) slightly decreased during cold acclimation, but freezing stress significantly reduced the CO_2 assimilation, reaching values to about 1 μmol CO_2 m^{-2} s^{-1}. Moreover, the maximum quantum efficiency of photosystem II (*Fv/Fm*) and the quantum yield of PSII (*PhiPSII*) were not affected during cold acclimation, but strongly declined when temperatures dropped to freezing, especially in *R. nathaliae* leaves. The results indicate that these plant species have evolved physiological and biochemical adaptations that improve their ability to maintain photosynthetic processes in cold conditions. This resilience to low temperatures underscores Ramonda species as promising subjects for further research into the mechanisms of cold tolerance. Unraveling these adaptations may have broader implications, including identifying strategies to boost cold resistance in other plants or informing agricultural practices in cold-prone regions.

P.1144 Explaining altitude adaptation of Toniniopsis separabilis and its apparent association with symbiotic cyanobacteria

Julia Gerasimova[1,2], Andreas Beck[2,3], Ulla Kaasalainen[4], Jouko Rikkinen[4,5]

1 Senckenberg Research Institute and Natural History Museum Frankfurt, Frankfurt am Main, Germany. 2 Ludwig-Maximilians-Universität München, Germany. 3 Botanische Staatssammlung München, München, Germany. 4 Finnish Museum of Natural History, University of Helsinki, Finland. 5 Organismal and Evolutionary Biology Research Programme, University of Helsinki, Finland.

Ramalinaceae is the fourth largest family of lichen-forming fungi with a worldwide distribution, containing 39 genera and more than 900 species (Lücking et al., 2017; Kistenich et al., 2018), including genera of various growth forms. For our study, we have collected specimens in the Alpine area (Europe) and Caucasian mountains (Asia) for comparison and found that *Toniniopsis subincompta* (previously *Bacidia subincompta*) is one of the most common species in these regions. Based on microscopical analyses and phylogenetic data, we demonstrated that this traditionally circumscribed taxon represents two distinct species, *Toniniopsis separabilis* and *Toniniopsis dissimilis* (the name *T. subincompta* was a synonym of a different species, and this epithet could no longer be used). Our research revealed that *T. separabilis* is the more prevalent species found at various elevations, ranging from sea level to high altitudes, although we only examined a limited number of specimens. On the other hand, *T. dissimilis* is less common and is limited to higher elevations above 1000 m or in colder climates such as Sweden. Additionally, we have observed that *T. Separabilis* exhibits a symbiotic relationship with free-living cyanobacteria, which may help explain its wider distribution, whereas *T. dissimilis*does not show this association. Based on these results, we formulated the following three hypotheses: 1) *Toniniopsis separabilis*is warm-adapted and occurs in various habitats from sea level to moderate elevations (<1000 m a.s.l), 2) the presence of cyanobacteria is somehow linked to warm adaptation in *T. separabilis*, and therefore, the frequency of cyanobacterial associations will increase with decreasing altitude, 3) *Toniniopsis dissimilis*is more cold-adapted and restricted to higher elevations (>1000 m a.s.l)

or high latitudes. To address these hypotheses, we examined extensive herbarium collections (over 500 specimens) from the last three centuries and applied more advanced metagenomic and metatranscriptomic approaches.

P.1145 Effect of environmental variables on bromeliads in a lower montane cloud forest in Panama

Diana C. Gómez González[1], Henry Velásquez[1], Darielis Lezcano[1], René Araúz[1], Omar Galán[1]

1 Universidad Autónoma de Chiriquí. Instituto Interdisciplinario de Investigación e Innovación, Chiriquí, Panamá.

Since the '60s, it was mentioned that slight changes in the composition of the atmosphere could cause climatic variations, in the 90´s it was suggested for the first time that changes in atmospheric carbon dioxide levels could modify the temperature of the surface. Currently, it is known that these climate changes cause the greatest damage to biodiversity, both for animals and plants. Epiphytic plants, depend on the atmosphere to obtain nutrients and water and for this reason, have been called sensitive to these changes. However, some epiphytes have developed structures that serve to adapt, this is the case for some bromeliads. The purpose of this study was to evaluate the sensitivity of epiphytic bromeliads from a lower montane cloud forest to environmental variations and to identify species that can be used as indicators of climate change. Two types of experiments were carried out, in the field and the laboratory with two species of bromeliads, one atmospheric *Guzmania stenostachya* and one tank bromeliad *Werauhia macrochlamys* were collected at 1200 m a.s.l. and they have placed again at that elevation (control) and 900 and 500 m a.s.l. variables such as light, temperature, and relative humidity were monitored in each site to evaluate whether the species adapt to climate change or to establish. The plants at the laboratory were placed at different temperatures 23 °C as in the control site and 26 and 29 °C and with different water supplies, simulating climate changes. The dynamics of the response mechanisms of plants were evaluated, quantifying the morphological changes in plants and studying if they suffer from the change. Leaves in plants at 900 at 500 were withered in atmospheric plants, but tanks were adapting. Also, atmospheric plants at 26 and 29 °C were withered, but plants at 23 °C were in a good state.

P.1146 Response to extreme conditions of drought and salinity of the invasive species Carpobrotus sp.pl. from different genetic clusters

Sara González Orenga[1,2,3], Sara Rodríguez-Arias[2], David López González[2,3], Fabrizio Araniti[4], Luís González[2], Adela M. Sánchez Moreiras[2,3]

1 Universitat Politècnica de València, Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Valencia, Spain. 2 Universidade de Vigo, Departamento de Bioloxía Vexetal e Ciencias do Solo, Facultade de Bioloxía, Vigo, Spain. 3 Universidade de Vigo, Instituto de Agroecoloxía e Alimentación, Ourense, Spain. 4 Università Statale di Milano, Dipartimento di Scienze Agrarie e Ambientali, Produzione, Territorio, Agroenergia, Milano, Italia.

Carpobrotus is one of the most dangerous genera in the world due to their rapid propagation, low resource requirements and high tolerance to stress factors such as drought and salinity. Native from South Africa, it was introduced for dune stabilisations and as an ornamental plant worldwide. Presently, high-value coastal habitats are invaded by *Carpobrotus* species with the associated ecosystem damage. Many studies demonstrated their influence in the germination and survival of native studies as well as the alteration of soil characteristics. Developing successful conservation efforts requires an understanding of the invasion mechanisms and ecological repercussions. In this study, seedlings from two genetic clusters of *Carpobrotus* sp.pl. – cluster A (Cádiz and A Lanzada) and cluster B (La Marina and Samil) – from different climatic regions (Mediterranean and Atlantic) were subjected to high-level of salinity, 800 mM of NaCl, to drought and their combination over 50 days. Tolerance mechanisms were evaluated using morphological parameters and various biomarkers associated to abiotic stress such as photosynthetic pigments and malondialdehyde. In addition, metabolomic profile and root plasticity at the microscopic level was include in the study to a better understanding of the adaptability process to salinity soil conditions. Morphological differences were found between populations in reference to the climatic region of origin. Plants from the Atlantic region were more affected by salinity than Mediterranean plants. The effect of the treatments was also evident in the accumulation of metabolites and in the anatomy of the roots. Metabolomics could simplify future analysis in *Carpobrotus* sp.pl., focusing on the compounds that have significant results between populations and treatments. The results underline how crucial genetic variety is to the invasion process, how important acclimatization is, and how important it is to take genetic variation and adaptability into account when managing invasive species.

P.1147 From friend to foe: the negative effect of Azolla filiculoides in rice (Oryza sativa) co-cultivation in the presence of cadmium

Giorgia Guardigli[1], Gabriella Pellino[1], Diego Comparini[2], Stefania Caparrotta[2], Camilla Pandolfi[2], Stefano Mancuso[2], Ilaria Colzi[1], Nadia Bazihizina[1], Cristina Gonnelli[1]

1 Department of Biology, University of Florence, Florence, Italy. 2 Department of Agriculture, Food, Environment and Forestry, University of Florence, Florence, Italy.

High concentrations of Cadmium (Cd) in paddy soils and its uptake and accumulation in rice are considered an important and widespread problem in agriculture. In this study we evaluated how intercropping rice with the floating pteridophyte *Azolla filiculoides*, a practice commonly used to sustainably improve rice yields, alters rice responses to Cd. For this purpose, experiments were conducted by co-cultivating rice with azolla in a hydroponic system under control conditions and increasing Cd concentrations (up to 1 μM). Our results indicate a synergistic negative interaction between *A. filiculoides* and Cd, with Cd-induced growth reductions in rice substantially greater when in presence of the fern, both at the shoot and root level. Additional results indicated that *A. filiculoides* boosts Cd translocation in shoots. Confirming this, the analysis of the Cd concentration in rice shoots revealed that, in Cd treated plants, the presence of *A. filiculoides* raised the concentration of this heavy metal in rice shoot tissues. Overall, our results suggested a complex interaction between *A. filiculoides* intercropping and Cd responses in rice. It can be concluded that the beneficial association between *A. filiculoides* and rice in non-polluted paddy soils transforms into a detrimental relationship in Cd-polluted soils.

P.1148 Spectral imaging for root phenotyping in common bean and avocado under diverse stresses

Tatiana Rondon[1], Manuel Guzman[1], John Diaz[1], Maria C. Torres[2], Maria Casamitjana[1,3]

1 Corporación Colombiana de Investigación Agropecuaria (Agrosavia), Rionegro, Colombia. 2 Instituto Tecnológico Metropolitano de Medellín, Medellin, Colombia. 3 Universidad de Girona, Girona, Spain.

In recent decades, scientific interest in plant root systems has grown. However, quantifying these systems is still highly time-consuming and often does not meet the throughput requirements for comparative structural-functional root system analysis. Currently, technological advances in root measurement methods are linked to imaging analysis. High-throughput imaging, based on common 2D RGB allows a simple dissection between roots and background. The objective of this study is to validate the use of spectral images for the quantification of traits of the root system, under the effect of different stresses. Greenhouse experiments were conducted in 2022 in Rionegro, Colombia. Three experiments involved plants from a nursery of avocado cv. Hass grafted on two rootstocks and stressed by: (E1) avocado red mite, *Oligonychus yothersi*, (E2) water-regulated, and (E3) nutrient-regulated. A fourth experiment was conducted on (E4) five common bean genotypes infested with *Thrips palmi*. Each experiment included a control treatment. In all cases, roots were manually extracted and photographed using a RGA digital camera. The REST v.1 software processed the root images, determining up to 15 traits. Previous experiments have validated a high correlation between image analysis using this software and manual measurements for all traits. The software differentiated between the roots of different genotypes and under various stresses in each experiment. Statistical differences (p<P.5) were observed among genotypes and treatments for total opening, left and right root angle opening, total root length, and depth with maximum root density in all experiments. The total root area was statistically significant in each experiment, with an exception in E4. Our results demonstrate the efficiency of the REST software for rapid root phenotyping in different crops and under various stresses. This approach could be utilized in plant physiological and breeding programs across different phenological stages to study root changes induced by stress.

P.1149 Paradigm shift in forest tree resistance research: embracing epigenetic and microbiome approaches

Hans Hoenicka[1]

1 Thünen Institute of Forest Genetics, Grosshansdorf, Germany.

Forests face an array of pressing challenges due to climate change and the introduction of invasive pathogenic fungi and pests. Conventional breeding methods, which rely on long generation times, are inadequate for addressing these urgent issues. Genetic engineering and genome editing, while offering promising solutions, are often restricted by regulatory constraints. A paradigm shift in forest tree resistance research is essential to expedite the development of resilient tree populations. Epigenetic modifications, which alter gene expression without altering DNA sequence, offer a rapid and viable alternative. However, their stability is a critical consideration. The microbiome, comprising the community of microorganisms that reside on and within plants, plays a crucial role in plant health and resilience. Neglecting microbiome research in resistance induction is detrimental as this interface can be harnessed for rapid resistance enhancement. Our research focuses on developing innovative methods for epigenetic and microbiome modification to induce resistance in forest trees. Comparative molecular analyses of resistant and susceptible tree species provide insights into the molecular basis of resistance and guide our research. Field trials are underway to evaluate the efficacy of our strategies and assess their potential for practical application. By embracing epigenetic and microbiome approaches, we can accelerate the development of resistant forest tree populations, ensuring their long-term survival and contributing to a resilient and sustainable forest ecosystem.

P.1150 Ectopic expression of a bacterial thiamin monophosphate kinase enhances vitamin B1 biosynthesis in plants

Yi-Hsin Chung[1], Ting-Chieh Chen[1], Wen-Ju Yang[1], Soon-Ziet Chen[1], Jia-Ming Chang[1], Wei-Yu Hsieh[1], Ming-Hsiun Hsieh[1]

1 Institute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan.

Plants and bacteria have distinct pathways to synthesize the bioactive vitamin B1 thiamin diphosphate (TDP). In plants, thiamin monophosphate (TMP) synthesized in the TDP biosynthetic pathway is first converted to thiamin by a phosphatase, which is then pyrophosphorylated to TDP. In contrast, bacteria use a TMP kinase encoded by *ThiL* to phosphorylate TMP to TDP directly. The Arabidopsis *THIAMIN REQUIRING2*(*TH2*)-encoded phosphatase is involved in TDP biosynthesis. The chlorotic *th2* mutants have high TMP and low thiamin and TDP. Ectopic expression of *Escherichia coli ThiL* and *ThiL-GFP* rescued the *th2-3* mutant, suggesting that the bacterial TMP kinase could directly convert TMP into TDP in Arabidopsis. These results provide direct evidence that the chlorotic phenotype of*th2-3* is caused by TDP rather than thiamin deficiency. Transgenic Arabidopsis harboring engineered ThiL-GFP targeting to the cytosol, chloroplast, mitochondrion, or nucleus accumulated higher TDP than the wild type (WT). Ectopic expression of *E. coli ThiL* driven by the *UBIQUITIN*(*UBI*) promoter or an endosperm-specific*GLUTELIN1*(*GT1*) promoter also enhanced TDP biosynthesis in rice. The *pUBI:ThiL* transgenic rice accumulated more TDP and total vitamin B1 in the leaves, and the *pGT1:ThiL* transgenic lines had higher TDP and total vitamin B1 in the seeds than the WT. Total vitamin B1 only increased by approximately 25–30% in the polished and unpolished seeds of the *pGT1:ThiL* transgenic rice compared to the WT. Nevertheless, these results suggest that genetic engineering of a bacterial vitamin B1 biosynthetic gene downstream of TMP can enhance vitamin B1 production in rice.

P.1151 Characterizing roles of Ethylene Response Factors (ERFs) in regulating submergence tolerance of cabbage

Yun-Rou Chou[1], Chi-Hsuan Lu[1], Fu-Chiun Hsu[1]

1 Department of Horticulture and Landscape Architecture, National Taiwan University, Taipei, Taiwan.

As the global climate continues to change, extreme rainfall and floods wreck crop production, resulting in issues of food security and economic losses. Ethylene has long been known to mediate multiple flooding-adaptive traits. However, such knowledge is limited to studies for model plant systems, such as Arabidopsis, Rumex, and rice, but not to studies on vegetables or applications of farming practices. In this study, we carried out a translational agriculture study on major vegetables and cultivation recommendations to strengthen climate resilience. We found that 5 $mg \cdot L^{-1}$ ethephon spray, an ethylene-releasing compound, at 2 hours prior to 48 hours of submergence, increased the submergence tolerance of '228' intolerant cabbage. A group of ethylene response factors (ERFs) were responsive to submergence, and some ERFs were induced higher in the tolerant cabbage variety. The N-degron-mediated ERF protein destabilization, considered an oxygen-sensing mechanism in plants, is also observed in cabbage in response to oxygen levels. The reconstruction of ERF regulatory machinery in cabbage derived from this study will not only provide insights into tolerance mechanisms in cabbage but also have potential applications to accelerate the breeding of submergence-tolerant Brassica. The ethylene-related plant growth regulator strategy being developed from this study has the potential to become a farming practice to improve the submergence tolerance of Brassica.

P.1152 Prairie grass ecotypes across the rainfall gradient of the US great plains shows decadal evidence of local adaptation

Jack Sytsma,[1] Matthew Galliart,[2] Trevor Heffley[5], Sara G. Baer,[3] Nora Bishop[1], Helen Winters[1], Eli Hartung,[1] David Gibson,[4] Adam B. Smith[6], Hannah Tetreault[7], Loretta Johnson[1] Jack Sytsma,[1] Matthew Galliart,[2] Trevor Heffley[5], Sara G. Baer,[3] Nora Bishop[1], Helen Winters[1], Eli Hartung,[1] David Gibson,[4] Adam B. Smith[6], Hannah Tetreault[7], Loretta Johnson[1]

1 Division of Biology, Kansas State University, USA. 2 Department of Biological Sciences, Fort Hays State University, Kansas, USA. 3 Ecology and Evolutionary Biology, University of Kansas, USA. 4 School of Biological Sciences, Southern Illinois University Carbondale, USA 5 Department of Statistics, Kansas State University, USA. 6 Missouri Botanical Garden, Fort Collins, USA.

Understanding ecotypic variation is critical for ecosystem restoration and conservation, especially across ecosystems that span vast climatic gradients, such as the US Great Plains. Big bluestem (*Andropogon gerardii*) is a dominant grass growing across a steep rainfall gradient spanning ~500-1,200 mm yr^{-1} across 723 km. We used reciprocal gardens with natural communities to test for local adaptation of *A. gerardii* to precipitation. Reciprocal gardens were established in 2010 and canopy cover and aboveground biomass were measured through 2022. Our objectives were to characterize climatic ecotypes that were reciprocally transplanted into four sites (dry to wet; Colby, Hays and Manhattan, KS, Carbondale IL, USA). To examine performance of ecotypes under drought, rainout shelters reduced rainfall. Finally, we determined the impact of local adaptation on the surrounding plant community. First, we expected to detect local adaptation in response to rainfall. Second, we predicted the wet ecotype would be most poorly affected by the drought imposed by the rainouts. Finally, strong adaptation of the local ecotype would result in competitive dominance over the surrounding community. The study supports several lines of evidence documenting strong local adaptation to climate. Local adaptation of wet and dry ecotypes became stronger over time, and in some sites, detected as much as three years into the experiment. Under rainouts, the dry ecotype in the wet site had higher performance compared to the other ecotypes, independently demonstrating adaptation to reduced rainfall. Local ecotypes suppressed neighboring plants compared to non-local ecotypes, also corroborating strength of local adaptation. This decadal study is amongst the longest running tests of local adaptation in communities. Long-term reciprocal gardens are necessary to draw proper conclusions in long-lived perennial grasses on relevant time scales for ecological communities. Ecosystem restorations should consider using ecotypes that would be favored under future climate scenarios.

P.1153 Identification of Orobanche crenata variants using ISSR-DNA molecular markers

Mahmoud Ahmed Khater[1]

1 Botany Dept. National Research Centre, Giza, Egypt.

The study aimed to detect, identify and characterize the genetic similarity and genetic variability in *Orobanche crenata* collected from naturally infested fields in Sharkia Governorate, Egypt. Five different ISSR primers were used in this study. Obtained results showed that in general, significant genetic variation was detected by these ISSR primers; moreover, there was a clear relationship/genetic similarity between and within all collected *O. crenata* parasite plants. However, the results revealed that there were high relationships where similarity matrix ranged from 0.837 (the highest) between R4 and R17 followed by 0.831 for R4/R25 and at the end the lowest one was R1/R29 which similarity matrix scored 0.655. It was observed that the relationship and similarity didn't reach 100% but the maximum was 83.7% (there were no identical plants). Therefore, each *Orobanche* plant in this study considered as different genotype than neighboring plant within location.

P.1154 Production of Datura stramonium L. alkaloids via cell suspension culture

Mahmoud Ahmed Khater[1]

1 Botany Dept. National Research Centre, Giza, Egypt.

This study aimed to in vitro production of tropane alkaloids from cell suspensions of Datura stramonium L. There were markedly increases in the growth of cells in cell suspension. Putrescine, as alkaloids stimulate, caused a markedly increases in the growth of cells (packed cell values, cell fresh weight and cell density) by increasing putrescine concentration until 2.0 mg/l. The same effect of potassium nitrate concentrations was recorded, increasing of cell fresh weight (gm) and packed cell volume (ml) by increasing Potassium nitrate concentration until 2.0 mg/l. compared with basal media. There were also, a markedly increases in both Hyoscyamine and Hyoscine concentrations by increasing putrescine concentrations until 2.0 mg/l. Hyoscyamine value in suspension cultures, that containing putrescine, was increased than basal media as a control, about three times. In addition, hyoscine value with 2 mg/l putrescine treatment possessed approximately two times and half than basal media. There were more increase in Hyoscyamine and Hyoscine concentrations by adding putrescine up to 2.0 mg/l, due to that polyamines (Putrescine) consider as the main source in alkaloid (Hyoscyamine) biothynsis pathway.

P.1155 Recent climate change and reproduction patterns of mediterranean plant communities.

María Landa Barrio[1], Arne Saatkamp[1]

1 Institut Méditerranéen de la Biodiversité et d'écologie, Avignon, France

Recent global warming, caused by human activity, is one of the main threats to biodiversity today. These climate variations are not homogeneous and can vary greatly at regional level. In Mediterranean France, warming has already exceeded 1.7°C and is beginning to affect plant species' phenology. In this study, we test the links between the reproductive patterns of Mediterranean vascular flora and recent warming, taken into account by meteorological observations and species' thermal and humidity niches. We show that species reproducing in the region are significantly more thermo-xero-philic than those who weren't observed in a reproductive phase. This phenomenon in amplified around the meteorological stations where there has been a greater increase in temperature over the last 12 years.

In addition, factors such as altitude, mean temperature and shade influence reproduction, with it being more frequent at lower altitudes and in warmer locations. Forest environments appear to buffer the effects of aridification, and species with hygrophytic tendencies continue to be able to reproduce under the canopy. These results may point towards a possible turning over of plant communities composition, with only the thermo-xerophytic species managing to reproduce in the region. Despite the study's temporal limitations, these results are promising and add a new observation of the traces of climate change on plant phenology and raise some concerns about the conservation of mediterranean flora. Nevertheless, the program needs to be continued in order to calculate temporal trends and reach more robust conclusions.

P.1156 Spatial and temporal response of leaf traits to climate change and ecosystem implications

Yaoqi Li[1,2], Zhiheng Wang[1]

1 Institute of Ecology and Key Laboratory for Earth Surface Processes of the Ministry of Education, College of Urban and Environmental Sciences, Peking University, Beijing, China 2 Department of Health and Environmental Sciences, Xi'an Jiaotong-Liverpool University, Suzhou, China.

Leaves as the important functional organs for carbon fixation in plants are diverse in morphological, ecophysiological and biochemical characteristics. Botanists have sought to explore the biological significance of leaf traits and their environmental drivers. However, large-scale studies on leaf trait variation across China have been limited by data quality. Based on online databases, herbarium specimens, published floras and additional literature, we obtained leaf morphological traits for 11,405 Chinese woody plants and extracted data from over 6,000 leaf sampling of 7 species spanning approximately 100 years. By integrating species distribution maps, environment data (i.e. climate, soil and terrain) and dated phylogenies, we mapped the spatial patterns of leaf traits, explored their environmental drivers, discussed the influence of plant life-forms and evolutionary history, and evaluated their potential to predict ecosystem productivity. Our findings indicate that leaf trait variations are driven by both temperature and water available, and we further confirmed a strong link between ecosystem primary productivity and leaf size variation across species with different life-forms and evolutionary history. Additionally, we revealed spatiotemporal variation of leaf size and shape in response to climate change, with temporal variation of leaf size significantly positively correlated with precipitation, while leaf shape variation primarily responded to temperature. We also emphasized the importance of herbarium specimens in studying plant responses to climate change.

P.1157 Carbon nanosol promote plant growth by regulating the content of endogenous hormones in plants

Taibo Liang[1], Huaxin Dai[1], Yadi Guo[1], Yanling Zhang[1]

1 Zhengzhou Tobacco Research Institute of CNTC, Zhengzou, China.

In the hydroponic conditions, the effects of carbon nanosol on endogenous hormone content and plant growth were studied using model plant tobacco. Carbon nanosol can promote the synthesis of endogenous hormones such as auxin and cytokinin in tobacco. After 8 days of carbon nanosol treatment, the IAA content in tobacco leaves increased by 150%, and the CTK content increased by 120%. Carbon nanosol can negatively regulate the synthesis of endogenous hormones such as ABA, ACC, SA, and JA, reducing their content in tobacco plants. After 8 days of carbon nanosol treatment, the ACC content decreased by 75%, and the SA content decreased by 44%. Carbon nanosol can significantly promote the growth of tobacco roots and the biomass accumulation of both aboveground and underground parts of the plant. After 8 days of treatment, the fresh weight of the aboveground part and root of tobacco plants increased by 45% and 80% respectively compared to the control. The regulation of endogenous hormones in tobacco by carbon nanosol is an important reason for its promotion of plant growth, but its underlying mechanism still needs further research.

P.1158 The response of savanna juvenile Dichrostachys cinerea and Terminalia sericea to single cutting

Maanda Hadzhi Ligavha-Mbelengwa[1], Ochanda Ogola[2], Peter Milingoni Tshisikhawe[1], Aphonce Bere[3]

1 Department of Biological Sciences, University of Venda, Faculty of Sciences, Agriculture and Engineering, Thohoyandou, South Africa. 2 Department of Crop Sciences, 3 Department of Statistics and Mathematical Sciences. University of Venda, Faculty of Sciences, Agriculture and Engineering, Thohoyandou, South Africa.

The objective of this study was to investigate how the resprouts heights and number of leaves of woody tree juveniles depend on season of cutting and tree species. The investigation was conducted at Nylsvley Nature Reserve, Limpopo Province, South Africa. The study site is a savanna ecosystem. The study focused at two species, namely *Dichrostachys cinerea* and *Terminalia sericea*. For each species, 11 random samples of 35 juveniles were selected. One of the 11 samples was cut in each of the months from March to November and then January and February of the following year. The resprout height of each plant was then measured one year after cutting. It was found that these plants regrew following cutting at any month of the year and that their average resprout heights varied by season and species. In all seasons except autumn the average regrowth height of *T. sericea* exceeded that of *D. cinerea*. Across the species, plants cut in winter (79.9 cm) had the highest resprout height followed by autumn (56.3 cm). Plants cut in summer (18.3 cm) had the smallest average resprout height. The winter cut plants also had the highest average number of sprout leaves followed by autumn. The least number of sprout leaves was for juveniles cut in summer. The winter season therefore proved to be the most favourable season to cut savanna woody plants, whilst summer showed to be least favourable season to cut these plants. These results are useful to communities who want to cut and utilize these tree species in a conservative manner.

P.1159 Amaranth´s face to face with climate change: Deciphering its flood-adaptation strategies

Andrea C. López-Díaz[1], NormaMartínez-Gallardo,[1] John F. Délano-Frier[1]

1 Department of Biotechnology and Biochemistry, Center for Research and Advanced Studies of the IPN (CINVESTAV), Guanajuato, Mexico.

Climate change is causing drastic changes in the precipitation patterns worldwide, resulting in severe floods, damaged crops and significant economic losses. Grain amaranths, i.e., *Amaranthus hypochondriacus*, *A. caudatus* and *A. cruentus*, are known for their high nutritional value and ability to tolerate various stress conditions, including flooding. The latter was found to induce species-specific morphological changes known to improve gas exchange under hypoxic conditions, such as root autophagy and adventitious roots formation. However, the mechanisms behind the activation of these adaptations remain unknown. Microscopy assays showed divergent alterations in the cellular structure and organization of two contrasting flood-tolerant grain amaranths: *A. cruentus*, resistant, and *A. caudatus*, susceptible. Additionally, the expression levels of genes associated with root degradation and adventitious root formation were strikingly different in the two grain amaranth species tested. These findings suggest that root morphological adaptations, in addition to the induction of genes involved in autophagy, ethylene signaling, reactive oxygen species generation and fermentation metabolism, play a crucial role in grain amaranth's flood-stress resistance. The present study led to a further understanding of the adaptive responses to flooding stress in grain amaranths. This knowledge could be employed to improve the performance of other economically important crops under adverse ambient conditions, including flooding, ultimately strengthening the World´s food security in the face of the looming climate crisis.

P.1160 When things happen belowground. Shifts in root strategy reflects better than leaf function the health status of Fagus sylvatica

Rosana López[1*], Marta Pastor-García[1], Martin Venturas[1], Juan Piñeiro[1], Gonzalo Monteoliva[2], Álvaro Rubio-Cuadrado[1], Jesús Rodríguez-Calcerrada[1], Clara Martínez-Arias[2], Juan Sobrino-Plata[1, 3], Roberto Salomón[1], Juan Antonio Martín[1]

*1 Grupo de Investigación FORESCENT, Departamento de Sistemas y Recursos Naturales, Universidad Politécnica de Madrid, Madrid, Spain. 2 Centro de Biotecnología y Genómica de Plantas, Universidad Politécnica de Madrid, Madrid, Spain. 3 Departamento de Genética, Fisiología y Microbiología. Facultad de CC. Biológicas. Universidad Complutense de Madrid, Madrid, Spain. * contact: rosana.lopez@upm.es*

Concerns about mortality of beech (*Fagus sylvatica*) forests have risen in the last decade as a result of the stalemate of growth and long-term increase in atmospheric vapor pressure deficit. Beech sensitivity to drought and climate change may jeopardize beech populations inhabiting marginal sites or the driest limits of its distribution range. We selected centennial trees with different health status, decaying vs. vigorous, in one of the southern-most beech populations in Europe, Montejo de la Sierra (Madrid, Spain), characterized by a sub-Mediterranean climate. Annual secondary growth of the last 100 years was measured from tree-ring cores. We characterized aboveground processes regulating tree photosynthesis and water utilization during a growing season. Water relations, gas exchange and chlorophyll fluorescence were measured at the beginning of summer and at the end, coinciding with the least and the most stressful periods. Xylem vulnerability curves and the relationship between transpiring and conductive tissues at the branch level were measured at the beginning of summer. Additionally, we compared fine root morphology, production and turnover during two consecutive years. While annual growth was lower in decaying trees than in vigorous trees during the last decades, changes in leaf and branch physiology followed a common trend throughout the season in trees with contrasted health status. Contrary to our expectations, neither xylem vulnerability to embolism or the safety margin differed among groups. However, our results showed a shift in roots strategy from conservative to acquisitive in decaying trees. Vigorous trees showed thicker roots, with longer lifespan at the expense of absorptive capacity, whereas decaying trees showed higher root turnover rates and higher specific root length. Overall, the understudied belowground processes in tree dieback processes seem to be crucial in determining plant health and play a critical role in connecting tree physiology and soil functioning.

P.1161 Root anatomical features of the sunflower seedlings for prediction of drought tolerance

Jadranka Luković[1], Aleksandra Radanović[2], Sandra Cvejić[2], Anna Galinski[3], Jelena Jocković[2], Kerstin Nagel[3], Dunja Karanović[1], Dragana Miladinović[2], Lana Zorić[1]

1 University of Novi Sad, Faculty of Sciences, Novi Sad, Serbia. 2 Institute of Field and Vegetable Crops, Novi Sad, Serbia. 3 IBG-2: Plant Sciences, Forschungszentrum Jülich GmbH, Jülich, Germany.

To improve crop's vitality and productivity, due to the constant climate changes, plants need to cope with instantly fluctuating conditions of the environment. Sunflower is characterized as a moderate drought-tolerant crop. However, its yield is significantly affected by water deficit. The aim of this research is to determine whether selected sunflower genotypes with higher yields in a range of conditions with limited water availability have differences in root morpho-anatomical features. The phenotyping tools included the digital root morphology and root anatomical characterization on fourteen days old seedlings grown in rhizotrons. For the detailed root anatomical characterization, we analyzed inbred lines that differ in maturity: early, medium early and late maturing. Along with the root seedlings maturity, three sections per root were made to prepare cross-sections using cryotechnic procedure. The proportion of tissues along maturity gradient were estimated by point-counting method. The obtained results of the classical and stereological root anatomy revealed significant phenotypic variability among genotypes. The theoretical hydraulic conductance (kh), the volume density (Vv) of xylem and vessel diameter, increase along the maturity gradient for all genotypes. According to the results obtained by an application of the Discriminant Analysis of the main components, characteristics: Vv of cortex, number of cell layers cortex parenchyma, Vv of xylem, and % of vessels with lumen <1000 µm2 contributed to the discrimination among the genotypes. For breeders, it is important to find connections between variation in root anatomy, especially division of vascular cambium initials within and among genotypes, and adaptive and physiological traits that determine how they respond to environmental variation. Considering that sunflower root anatomical characteristics have not been directly used in breeding programs, these findings open the way for new breeding strategies.

P.1163 Nutrient resorption efficiency in Quercus ilex along a north-south gradient and its relation with climate

Esteban Manrique[1], Mohamed Alifriqui[2], Christian Kindler[3], Francisco I. Pugnaire[3]

1 Real Jardín Botánico, Madrid, Spain. 2 Biology Department, Cadi Ayyad University, Marrakech, Morocco. 3 Estación Experimental de Zonas Áridas, La Cañada, Almería, Spain.

Plants in nutrient-limited environments have developed strategies to maximize nutrient efficiency; for instance, by avoiding losses through nutrient resorption from senescent leaves. There seems to be no relationship between resorption efficiency and nutrient availability in soils and, therefore, other factors should control the process. Experimental manipulations have evidenced impacts of temperature and rainfall changes on nutrient resorption efficiency. We addressed the effects of these two climate factors on nutrient resorption efficiency in holm oak (*Quercus ilex* L.) forests, an evergreen species that dominates wide areas of the western Mediterranean Basin along with *Q. rotundifolia* Lam. Our objective is to analyze the importance of nutrient resorption efficiency (NRE) in *Q. ilex* along a latitudinal gradient from Bordeaux (France) in the north to Ain Asmama (Morocco) in the south, with several points in the Iberian Peninsula that differed in mean annual temperature and rainfall. Our results show that nutrient resorption efficiency (NRE) differed across sites and nutrients. NRE of N, P and K is linked to the nutrient pool in the green leaf and to N-S gradient, suggesting a water-controlled resorption mechanism.

P.1164 Role of gibberellic acid biosynthesis in growth and metabolic content of in vitro grown catmint (Nepeta nuda L.)

Anna Zaharieva[1], Georgi Ivanov[1], Ioanna Ivanova[1], Margarita Popova[1], Ivanka Malincheva[1], Velina Chingarova[1], Mila Rusanova[2], Krasimir Rusanov[2], Desislava Mantovska[1], Miroslava Zhiponova[1]

1 Faculty of Biology, Sofia University "St. Kliment Ohridski", Sofia, Bulgaria 2 Agrobioinstitute, Agricultural Academy of Sciences, Sofia, Bulgaria.

Plant hormones play a crucial role in modulating various facets of plant growth and development. A recent study on the medicinal plant *Nepeta nuda* L., commonly known as "catmint", revealed different endogenous hormonal levels in plants cultivated *in vitro* and in nature. Namely, the *in vitro* plants had increased gibberellins (GA) level, and the wild-grown plants had a much higher abscisic acid (ABA) content. In this work, we aimed to study *in vitro N. nuda* to assess the growth and metabolic impact of exogenously applied (4-6 µM) GA, paclobutrazol (PBZ) which is a GA biosynthesis inhibitor, and ABA acting as a GA antagonist. The application of GA notably changed plant architecture by heightening *N. nuda* stem but decreasing leaf area. On the other hand, PBZ and ABA caused a compact plant stature with lower water content. All the phytoeffectors reduced plant biomass compared to the untreated control indicating growth retardation at high concentrations. Conversely, the three regulators enhanced the levels of reducing sugars known to be involved in growth, acting as free radicals-scavengers, and increasing the solutes during dehydration. Both PBZ and ABA significantly raised the phenolic antioxidants. In line with the evidence for role of GA biosynthesis in the plant drought response, a differential pattern in the accumulation of volatile metabolites was observed. The specific *for N. nuda* iridoid nepetalactone was higher in control and GA-treated plants, while it was reduced by PBZ, and not affected by ABA. Other species-specific iridoids as eucalyptol, caryophyllene, and germacrene D, reported to accumulate in dry environments, were stimulated by PBZ. These findings indicate that a decline in GA biosynthesis may contribute to *N. nuda* adaptation to harsh environmental conditions and provide valuable insights for enhancing the respective production of bioactive compounds.

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P.1165 A global synthesis of climate change effects on plant reproductive traits and plant-pollinator interactions

Silvana Martén-Rodríguez[1],Martín Hesajim de Santiago-Hernández[1,3], Lucero Clemente-Martínez[1], Gary Krupnick[2], Orley Taylor[4], Martha E. Lopezaraiza-Mikel[5], Estrella E. Paramo-Ortiz[1], Guillermo Huerta-Ramos[1], Eugenia M. Sentíes-Aguilar[1], Sergio Díaz-Infante[1], Armando Aguirre Jaimes[6], Samuel Novais[6], Edson Jacob Cristobal-Pérez[1], Jorge Cortés-Flores[7], Francisco Javier Balvino-Olvera[1], Karen D. Pérez-Arroyo[1], Oliverio Delgado-Carrillo[1], Jorge Lobo-Segura[8], Ilse Ruiz-Mercado, María J. Aguilar-Aguilar[1], Roberto Sáyago-Lorenzana[5] , Yvonne Herrerías-Diego[1,3], Mauricio Quesada[1]

1 Laboratorio Nacional de Análisis y Síntesis Ecológica, Escuela Nacional de Estudios Superiores, Unidad Morelia, Morelia, Michoacán, Mexico. 2 National Museum of Natural History, Smithsonian Institution, USA. 3 Laboratorio de Vida Silvestre, Facultad de Biología, Universidad Michoacana de San Nicolás de Hidalgo, Morelia Michoacán, Mexico. 4 Department of Ecology and Evolutionary Biology, University of Kansas, USA. 5 Escuela Superior de Desarrollo Sustentable, Universidad Autónoma de Guerrero, Técpan de Galeana, Guerrero, Mexico. 6 Red de Interacciones Multitróficas, Instituto de Ecología, México. 7 Jardín Botánico, Instituto de Biología, Sede Tlaxcala, Universidad Nacional Autónoma de México, Santa Cruz Tlaxcala, Mexico. 8 Universidad de Costa Rica, Escuela de Biología, San Pedro, Costa Rica.

Climate change is expected to affect the ecological, physiological, morphological, and life history traits of plants and animal pollinators. We surveyed the published literature on the effects of climate change on plant reproductive traits and plant-pollinator interactions at a global scale. We recorded impact directions and patterns of change across different plant and animal traits, latitudes, and world ecosystems. We found ample evidence that warming temperatures are associated with reduced geographic ranges of plant and pollinator species worldwide and with advanced flowering and pollinator phenologies in temperate regions (75% of plant and pollinator species); in contrast, there is a paucity of studies that directly evaluate the effects of climate change on flowering or pollinator phenologies in tropical regions. Results also suggest that floral rewards mainly experience adverse effects under warming and drought but scent emissions either increased or changed in composition. Flower production, plant reproductive success, and pollinator abundance exhibited diverse responses under different warming and water availability levels. In contrast, pollinator physiologies and life history traits mostly showed negative responses under warming temperatures. Drought, extreme weather events, and synergistic effects with land-use change had predominantly adverse effects on plant and pollinator traits. In conclusion, global warming is having significant consequences for plant reproduction across the globe, although the effects are not always negative. Few cases of spatial or temporal plant-pollinator mismatches have been confirmed; however, the widespread occurrence of geographic and phenological displacements suggests that mismatches will probably be frequent in our warming world. The review underscores the urgent need for further research in tropical and subtropical regions and underrepresented plant and pollinator groups worldwide.

P.1166 Towards a more efficient Montreal Protocol: simulating “ozone holes” in Antarctica for a better evaluation of ultraviolet-B damage

Javier Martínez-Abaigar[1], Laura Monforte[1], Rafael Tomás-Las-Heras[1], Mª Ángeles Del-Castillo-Alonso[1], Gonzalo Soriano-Sancha[1], Encarnación Núñez-Olivera[1]

1 Faculty of Science and Technology, University of La Rioja, Logroño, Spain.

Ultraviolet-B (UV-B, 280-315 nm) represents only about 0.33% of the solar photosynthetic radiation, but has strongly determined the evolution of life on Earth. The discovery of the anthropogenic strato-

spheric ozone degradation ("ozone hole") and the consequent UV-B increase in the biosphere greatly stimulated the research on its effects on the environment, which was strengthened by the signing of the Montreal Protocol in 1987. However, despite the Montreal Protocol is being the most efficient international agreement signed to date and has also contributed to mitigate global warming, the current interactions between "ozone hole" and climate change will probably cause a further UV-B increase at the ground level. Thus, the Montreal Protocol parties need new and realistic information to assess how organisms and ecosystems will respond to the ongoing changes in UV-B radiation and climate, and to implement the most adequate measures to minimize risks. This can be particularly referred to Antarctica, where "ozone holes" have recently (2020 and 2021 austral springs) been much more severe than expected. Given this background, we simulated "ozone hole" episodes on 12 Antarctic species (10 mosses, one lichen and the only two native flowering plants) under field conditions and analysed their effects in terms of both damage (through the measurement of the maximum quantum yield of photosystem II, F_v/F_m) and protection (evaluating the bulk amount of potentially protecting UV-absorbing compounds). Our study was performed in the vicinity of the Spanish Antarctic Station "Juan Carlos I" (Livingston Island, 62° 40′ S, 60° 23′ W) during the XXXV Spanish Antarctic Campaign (February-March 2022). Clearly, the responses strongly depended on the species considered, and thus the implementation of conservation measures should contemplate these differences.

P.1167 Bridging past and present: a methodology for interpreting flowering time from herbarium specimens

Andrew E. McDougall[1], Steven Delean[1], Michelle Waycott[1,2]

1 Faculty of Sciences, Engineering and Technology, The University of Adelaide, Australia. 2 The State Herbarium of South Australia.

Understanding the timing of plant flowering is crucial for gaining insights into climate responses, particularly in the face of global climate change. Utilizing herbarium records presents a promising avenue for studying phenology, yet their interpretation has been hindered by the diverse phenological phases and collection sites of specimens. We introduce a novel method for interpreting flowering timing from herbarium specimens, focusing on the species *Arthropodium strictum* R.Br. This method determines the difference between the collection date and the date of a chosen earlier flowering phase, basing the difference on the timing, (in days), of the transition of one flowering phase to the next observed on living plants. Using this difference to place herbarium observations onto an intra-annual timeline enables true comparison among specimens. We coupled the timeline placed observations with temporally and spatially appropriate climatic and elevation data for pheno-climatic assessment. The climatic and elevation variables were modelled against the timeline placed flowering dates. At the few sites where repeat sampling has occurred, we detected changes in flowering timing. However, the spatial heterogeneity among the remaining collections prevents direct detection of change elsewhere. Higher spring temperatures were associated with earlier flowering timing. Most late-year flowering occurred at higher elevations compared to early-year flowering. Our methodology provides a clearer understanding of historical flowering timing and facilitates comparison with contemporary observations. This method establishes a framework for phenological data collection that could be applied to other species and will have defined, meaningful and interpretable results, because it enables realistic estimates of the timing of the individual phases of historic flowering events. Furthermore, it allows revisiting sites corresponding to the herbarium collection to collect contemporary observations for comparison with a single visit.

P.1168 Photosynthetic response of Quercus suber. L seedlings

Zaineb MHALHLI[1], Issam TOUHAMI[1], Hammadi Achour[2], Zouhair NASAR[1], Touhami RZIGUI[1,2]

1: National Research Institute of Rural Engineering, Water and Forests (INRGREF), LR16INRGREF01 Laboratory of Management and Valorization of Forest Resources, Carthage University, Ariana, Tunisia 2: Institute Sylvo-Pastoral of Tabarka, University of Jendouba, Tabarka, Tunisia.

Photosynthetic traits of four years *Quercus Suber. L* greenhouse seedlings coming from seven different Tunisian provenances were investigated: JES: Djebal

Essarej, SZD: Sidi Zid, KER: Kef Errand, DCH: Djebal Chahid, MEJ: Majel Essaf, FEJ: Feija, BEL: Bellif. JES, SZD, KER and DCH are the provenances originated from the driest sites meanwhile MEJ, FEJ and BEL are the ones originated from the wettest sites. Using the Farquhar analysis model Farquhar et al., (1980), we reported a change in the maximum rate of carboxylation, *Vcmax*, from 63µmol m^{-2} s^{-1} for JES provenance to 82 µmol m^{-2} s^{-1} for MEJ provenance. Also, a shift in the maximum rate of electron transport, *Jmax,* was observed from 119 µmol m^{-2} s^{-1} for JES provenance to 155 µmol m^{-2} s^{-1} for MEJ provenance as well. A strong correlation between *Vcmax* and *Jmax* was recorded. However Specific leaf area (SLA) and relative stomatal limitation (Ls) did not show any differences between the seven provenances. Additionally, MEJ and JES provenances had shown the highest and lowest CO2 assimilation rates at both natural ambient (A_n) and saturated CO2 (A_{sat}), respectively. These results indicate that provenances-specific differences in the CO2 uptake are due to the differences of the biochemical reactions capacities that regulate the gas-exchange process.

P.1169 The abiotic stress factors and the genetic changes generated in grassland plants belonging to the Fabaceae and Poaceae families

Ciprian Valentin Mihali[1], Neculai Dragomir[1], Dana Elena Ilie[1], Radu Ionel Neamț[1], Alexandru Eugeniu Mizeranschi[1], Rareș Dumea[2], Gheorghiță Anghelus Olenici[2], Monica Alexandrina Tod[2]

1 Research and Development Station for Bovine-Arad, Romania. 2 Research-Development Institute for Grassland Brașov, Romania.

Abiotic stress in plants refers to environmental factors that can negatively impact plant growth and development. These stressors are non-living factors, and they include extreme temperatures, drought, salinity, heavy metals, and other conditions that can affect plant health. When plants are exposed to abiotic stress, they often undergo physiological and molecular changes as part of their adaptive responses. The genes nad1/2-3, coxI, rbcLa, rpoC1, psbA-trnH, trnL-trn play crucial roles in various cellular processes, including energy production, photosynthesis, and transcription. In relation of abiotic stress and genes, plants often respond to environmental stress by altering the expression of specific genes. The expression of genes involved in energy metabolism, photosynthesis, and stress response pathways may be upregulated or downregulated in response to various stressors. In the present study, we evaluate changes induced by abiotic stress factors at the SNP`s level in genes (nad1/2-3, coxI, rbcLa, rpoC1, psbA-trnH, trnL-trn) which could be involved in stress response pathways in plants species (together with genes already known to be involved in abiotic stress as NAC, DREB1/2) in the spontaneous pastoral flora belonging to the Fabaceae and Poaceae families. During the study we evaluated the existing differences between spontaneous species compared with the same species from different plant breeding programs and their genetic evaluation in different environmental conditions (altitude, water regime, photo-period, temperature, soil, etc.). The statistical component is made with reference to the genes sequences similarity by similarity matrices to highlight the genetic distance or proximity between the species from our study. An association analysis of two matrices (Mantel test) between the SNPs profiles (from analyzed genes) correlated with the geoclimatic parameters from the places where the samples were collected. Concluding, this study output can be valuable for developing improved pastoral perennial stress-tolerant plant species and improving agricultural practices, also.

P.1170 Investigating the impact of environmental stress on pollen development in Cakile maritima

Diana-Maria Mircea[1], Ricardo Mir[1], Monica Boscaiu[2], Oscar Vicente[1]

1 Institute for Conservation and Improvement of Valencian Agrodiversity, Universitat Politècnica de València, València, Spain 2 Mediterranean Agroforestry Institute, Universitat Politècnica de València, València, Spain.

Environmental stresses like salinity, drought or increasing temperatures, exacerbated under the current climate change scenario, present a growing threat to *Cakile maritima*, a halophytic species that thrives in coastal habitats (Arbelet-Bonnin *et al.* 2019). This prospective study aims to clarify how abiotic stress, particularly salt and water stress, affects *C. maritima*'s reproductive biology, emphasising pollen formation and gametophytic function. To address this question, *C. maritima* plants are being exposed to different stress levels and their reproductive responses monitored over time. The complex interactions between abiotic stressors and plant reproduction represent an active field of study in plant biology, and the general negative effects of stress on pollen function and other reproductive traits are well-known for many crop species. However, similar studies are lagging far behind in halophytes. Therefore, it is likely that environmental stress also disturbs the reproductive phenology of *C. maritima*, potentially affecting flowering time and the number of flowers formed. A detailed study of microspore and pollen development within anthers will be conducted to detect possible stress-induced changes in morphology, pollen viability and germination capacity *in vitro* and *in vivo*, which are critical for efficient pollen reproductive competence. This study aims to provide valuable insights into the link between environmental stress and *C. maritima* reproductive biology and may be relevant for predicting how resilient coastal plant communities will be to environmental disturbances.

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P.1171 A step toward understanding heavy metal tolerance in violets based on metabolome analysis

R. Miszczak[1,2*], B. Slazak[3,4,**], K. Sychta[2,***], U. Göransson[4,****], A. Słomka[2,*****]

1 Doctoral School of Exact and Natural Sciences, Jagiellonian University in Kraków, Cracow, Poland, *rebecca.miszczak@doctoral.uj.ed u.pl. 2 Department of Plant Cytology and Embryology, Faculty of Biology, Jagiellonian University in Kraków, Cracow, Poland, ***klaudia.sychta@uj.edu.pl, *****aneta.slomka@uj.edu.pl. 3 W. Szafer Institute of Botany, Polish Academy of Science, Kraków, Poland, **b.slazak@botany.com. 4 Department of Pharmaceutical Biosciences, Uppsala University, Uppsala, Sweden, ****ulf.goransson@uu.se.

Viola genus (violets) includes species known as obligate metallophytes or pseudometallophytes displaying different levels of tolerance to heavy metals (HMs). Because of onlya few studies, the specific tolerance mechanisms rendering the violets tolerant to metalsremain unclear. It remains an open question whether violets use universal metal tolerance mechanisms (metallothioneins, phytochelatins, organic acids) and/or have specific tolerance mechanisms, e.g. the production of low-molecular-weight peptides – cyclotides. In the current experiment, sterile seedlings were obtained from seeds of *V. tricolor* from metallicolous (Bukowno mine heap; M) and nonmetallicolous populations (Botanical Garden in Cracow; NM). The following treatments were applied: 0 (control), 100 or 1000 ppm of $Zn(NO_3)_2$ or $Pb(NO_3)_2$ for 3 or 7 days. The content of heavy metals in the treated seedlings was measured using Atomic Absorption Spectroscopy (AAS). Metabolite contents in methanolic extracts were analyzed using LC-MS and compared between samples. The statistical analysis of results included PCA and univariate analyses performed using RStudio. Under the treatment 1000 ppm (3 days), lead content was very high, both in roots and leaves, twice as much in M as in NM. Zn's content in both concentrations (100 ppm, 1000 ppm), genotypes (M, NM), and organs (roots, leaves) was comparable between all samples except M root treated with 1000 ppm. The pool of identified metabolites mainly consisted of flavonoids, lignans, and sterols. High Pb concentrations accumulated within plant organs had the most cytotoxic effect on metabolite content. Some substances did not occur in leaves. Further in-depth bioinformatics analyses will identify key compounds involved in Zn and Pb tolerance in violets. Acknowledgements: This work was funded by National Science Centre (grant no. 2021/41/B/NZ8/01737).

P.1172 Genomic structure and diversity of Quercus suber across its complete latitudinal distribution

Melissa Viveiros Moniz[1], ÁngelaSánchez-Miranda[2], A. Jesús Muñoz Pajares[1], Mohamed Abdelaziz[1], Luis Matías[2]

1 Departamento de Genética, Universidad de Granada, Granada, Spain. 2 Departamento de Biología Vegetal y Ecología, Facultad de Biología, Universidad de Sevilla, Sevilla, Spain.

Drought conditions caused by climate change pose a threat to many plant species across the world. This global trend is prompting scientists to look at the potential involvement of local adaptations through intraspecific differences in functional traits, which could improve conservation methods by increasing plant resilience to the decreasing availability of water. Cork oak (*Quercus suber* L.) is an economically and ecologically valuable woody species that is endemic to the Mediterranean region. For the last 80 years, the entire surface area of cork oak woodlands has been reduced from 140,000 ha to 70,000 ha. In recent years, there has been considerable research on the decline of *Q. suber* to understand how climate change impacts the distribution and viability of cork oak populations. Studies have shown that *Quercus suber* populations exhibit latitudinal variation in their response to different environmental stressors, including drought, which is possibly attributed to adaptations to specific environmental conditions. This evidence suggests that certain populations may have developed genetic variants that enable resistance to drought conditions prevalent in their specific latitudinal range. Hence, this study aimed to characterize the genetic diversity of natural populations of cork oak and to compare genomic patterns across populations in a latitudinal transect covering the complete latitudinal distribution of the species. Particularly, we have sequenced the genomic DNA of a total of 97 individuals from seven populations to evaluate the genetic structure of the entire transect as well as the genetic diversity of every population. Our sequencing strategy also allows us to explore the genetic mechanisms involved in the different tolerance to drought conditions of the studied natural populations.

P.1173 Current and future prospects of ethnomedicinal potential of Mistletoe, an ‘intriguing and mystic all-purpose herb’

Maeleletse G. Mopai[1], Semakaleng Mpai[1], Ashwell R. Ndhlala[1]

1 Department of Plant Production, Soil Sciences and Agricultural Engineering, University of Limpopo, Limpopo Province, South Africa.

Mistletoe is a common name for parasitic plant species that belong to the families Loranthaceae and Viscaceae, which are both taxonomically related. The most common Viscaceae genera is Viscum, which comprise of approximately 120 species and an estimate of 100 species under Loranthaceae. Mistletoe plants are known for their ethnomedicinal purpose for treatment of various ailments including cancer, diabetes, epilepsy, asthma, hypertension, headaches, menopausal symptoms, infertility, dermatitis, arthritis, and rheumatism. Mistletoe is abundant in forest regions and orchards as a hemiparasite and has long been used. The aim of this study is to comprehensively generate documentation of the dispersal and establishment mechanism on a host, nutritional and phytochemical composition and ethnomedicinal potential of some Mistletoe species in a consensus. Researchers have reported on the effect of tissue culture on nutritional composition of the most *Viscum* species, in comparison with mistletoe plants and hosts. Moreover, the major phytochemical constituents of some extensively exploited mistletoe plants that have been reported previously include gastric-irritating alkaloids, cardiac toxins (viscotoxins, phoratoxins), saponins, and lectins as well as tannins, flavonoids and phenolic compounds. The morphology, ecosystem and economic impact, and mistletoe-host relationship of some mistletoe species has been intensively studied and documented. Therefore, this review will briefly show up research gaps in relation to the objectives herein.

P.1174 Phyto-nutrient profiling of two amaranth species grown under the organic medium enclosed trough system

Maeleletse G. Mopai[1], Semakaleng Mpai[1], Ashwell R. Ndhlala[1]

1 University of Limpopo, Limpopo Province, South Africa.

P.1175 Phenotypic differences in presence and absence of drought stress across different populations of Solanum chilense

Sidra Tul Muntaha[1], Aurelien Tellier[1]

1 Dept. of Life Science Systems, School of Life Sciences, Technical University of Munich, Population Genetics, Freising, Germany.

Drought stress presents a significant challenge to agriculture globally due to its limiting effects on crop yields, which will be reinforced by climate change. Wild tomatoes (Solanum section Lycopersicon), and *Solanum chilense* in particular, are good model systems for studying plant demography and local adaptation to abiotic stresses. *Solanum chilense* has colonized habitats around the Atacama Desert, and thus this species is considered one of the most promising genetic resource for tomato selection of tolerance to abiotic (drought) stresses. In this study, we compared the effect of normal watering versus drought under controlled climatic conditions on the physiology of different populations of *S. chilense*, each characterized by a distinct local habitat. We use seven accessions of parental populations LA4107, LA3111, LA1963, LA4330, LA4117A, LA2932, LA2755 from coastal up to highland habitats. Five individuals from each accession and three replicates per individual are studied and grown in climatic chambers, with measures of plant physiology taken from 4 to 6-week-old cuttings (from mother plants). Plant growth parameters (Shoot length, shoot diameter), physiological responses (Seed germination, stomatal conductance, transpiration rate), and morphological characters of leaves, shoot and leaves fresh and dry biomass are observed and analyzed. Our results demonstrate strong variability between populations (accessions), with central plant generally showing vigorous growth as compared to all other populations. We also observe nonetheless a large variation within the population reflecting the known intra-population genetic diversity. Overall, our findings indicate that the tolerance of *S. chilense* to water stress and adaptability to local habitat is not based on one individual trait but a combination of several polygenic loci governing plant growth, morphological and physiological traits.

P.1176 Change in coastal dune vegetation invaded by invasive tall grass over 17 years in northern Japan

Yoko Nishikawa[1], Takashi Shimamura[1]

1 Hokkaido Research Organization, Sapporo, Japan.

Coastal dune vegetation has changed drastically worldwide due to the stabilization of dune systems and rapid replacement of species growing there. In recent years, *Miscanthus sinensis*, a tall inland grass, has invaded and expanded its distribution on the dunes at Ishikari Beach, Hokkaido of Northern Japan. To clarify the temporal changes in the community structure with reference to the invasion of inland plants, we investigated species composition and abundance of individual plant species within a 10 m square plot over a 17-year period since 2000. *M. sinensis* increased the abundance from year to year by 2006 and replaced coastal species, such as *Lathyrus mollis*. Additionally, the distribution of invasive grasses, *Carex microtricha* and *Poa pratensis*, also expanded at the understory of *M. sinensis*. A total percent cover of these inland species exceeded 70% by 2017. The NMDS ordination analysis revealed that coastal vegetation in this area has changed to inland-plant dominated community with homogeneous species composition during the 17 years. On the other hand, many coastal species continued to survive, although their abundance was decreasing. The temporal patterns of these coastal plants varied depending on the growth characteristics of individual species. Coastal plants with creeping belowground rhizomes or aboveground stems were able to survive against the invasion of inland grasses owing to the ability of flexible mobility. However, continuous impacts of invaded plants may make it difficult for coastal plant populations to survive. For the conservation of coastal vegetation, trials of vegetation management, such as artificial control of invasive plants, are urgent.

P.1177 Assessing the contribution of deterministic vs. stochastic processes to local species assembly: a field experiment with annual-plant dominated communities

Laura Ortiz[1], Arantzazu L. Luzuriaga[1], Pablo Ferrandis[2]

1 Departamento de Biología, Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos, Móstoles, Spain. 2 Instituto Botánico de la Universidad de Castilla-La Mancha, Jardín Botánico de Castilla- La Mancha, Albacete, Spain.

Understanding the processes involved in the formation of communities is still a hot topic with many unresolved questions. Assembly of plant communities is generally approached within the frame of a conceptual gradient defined by two opposing postulates: the deterministic (Clements, 1916) *versus* the stochastic views (Gleason, 1926). Although both approaches have received much attention, species assembly theory has grown mainly based on observational studies due to the difficulty of manipulating entire communities. In this study, we designed a novel field experiment in a semi-arid Iberian gypsum system lasting four consecutive years, to evaluate the relative contribution of both stochastic events (here represented by the arrival of seeds) and biotic (represented by the presence of *Macrochloa tenacissima* perennial tussocks and biological soil crust) and abiotic (yearly rainfall) environmental filtering to the assembly of the annual-plant dominated communities. Our field experiment was performed on paired plots (i.e., seed free soil *vs.* homogenised natural soil with the complete seed bank) testing the effects of tussocks *vs.* BSC *vs.* open areas on plant assemblages. Results demonstrated that, in years without water stress, stochastic processes were more active than deterministic processes. Although the latter affected cover and taxonomic diversity in assemblages, they did not clearly select for species on the basis of their functional traits. Furthermore, the role played by the presence of BSCs in the community assembly should be highlighted, as their presence substantially accelerated the reconstitution of major plant community features.

P.1178 Tracing 30 years of genetic diversity changes along pollution gradients in brown algae: A pool-sequencing approach

Carme Pacín[1,2], M. Teresa Boquete[1], Jesús R. Aboal[1], J. Ángel Fernández[1], Bodil Cronholm[3], Thomas Wernberg[4], Samuel Starko[4]

1 CRETUS, Universidade de Santiago de Compostela, Santiago de Compostela, Spain. 2 CIQUS, Universidade de Santiago de Compostela, Santiago de Compostela, Spain. 3 Department of Bioinformatics and Genetics, Swedish museum of Natural History, Stockholm, Sweden. 4 UWA Oceans Institute and School of Biological Sciences, University of Western Australia, Crawley, Australia.

Studying the temporal evolution of genetic diversity is crucial for predicting adaptative potential and mitigating future ecological changes, particularly in ecosystem engineer species like the brown algae *Fucus vesiculosus*. This alga serves as a foundational species in the North Atlantic coastal environments, making its genetic health vital for the entire ecosystem. In this study we analyzed samples of *F. vesiculosus* from an environmental specimen bank to investigate changes in genetic diversity over a 30-year period across a pollution gradient. Specifically, we examined samples from five populations of *F. vesiculosus* (~50 thalli per population) collected in 1990, 2005 and 2021 in the North Atlantic Ocean (Galicia, NW Spain), assessing genetic variation and their pollutant concentrations. Levels of the latter in *F. vesiculosus* tissues ranged from 0.31 to 2.4 to mg kg^{-1} for Cd, from 0.22 to 6.5 mg kg^{-1} for Pb and from 7.2 to 372.5 ug $kg^{-1}$for Hg during the 30-year period. We hypothesize that populations in polluted areas have could experienced a loss in genetic diversity as a result of chronic pollutant exposure, and that populations from areas that varied from polluted to unpolluted have not recovered genetic variability yet. The ongoing pool-sequencing analysis will allow us evaluate the impact of anthropogenic activities on genetic variability. Loss of genetic diversity can limit adaptative potential, which is particularly relevant in the context of global change and in this specie given its essential roles in coastal ecosystems. By elucidating temporal patterns of genetic diversity, we gain valuable insights into the mechanisms driving evolutionary processes. This study highlights the broader implications of utilizing environmental specimen banks to understand genetic temporal patterns to offer valuable contributions to ecological and evolutionary research under a reliable and cost-effective method.

P.1179 Mercury concentration declines in brown algae along the North Eastern Atlantic Coast: Three decades of observations

Carme Pacín[1,2], Zulema Varela[1], Inés G. Viana[3], Rita García-Seoane[3], Carlos Real[4], Rubén Villares[4], J. Ángel Fernández[1], Jesús R. Aboal[1]

1 CRETUS, Universidade de Santiago de Compostela, Santiago de Compostela, Spain. 2 CIQUS, Universidade de Santiago de Compostela, Santiago de Compostela, Spain. 3 Instituto Español de Oceanografía (IEO-CSIC), Centro Oceanográfico de A Coruña, A Coruña, Spain. 4 Escola Politécnica Superior de Enxeñaría, Universidade de Santiago de Compostela, Lugo, Spain.

Mercury pollution poses a significant threat for the marine ecosystem due to its toxicity and persistence in the environment. This study investigates temporal trends in mercury (Hg) concentrations within over 450 samples of brown algae (*Fucus vesiculosus*, *Fucus ceranoides*, and *Fucus spiralis*) collected from the Northeastern Atlantic coast (Galicia, NW Spain) from 1990 to 2021 at consistent sampling sites, providing high resolution data. The results indicate substantial decreases in Hg concentrations across most sampling locations, with a median reduction of ~50% over time and total median values ranging from 17.78 µg kg^{-1} in 2021 to 60.75 µg kg^{-1} in 1990. The observed decline is likely attributed to reductions in metal concentrations within marine environments because of the emergence of environmental policies such as the Minamata Convention or the Regulation (EU) 2017/852. However, factors associated with global change, such as declining pH, increasing sea surface temperature, and heat content, might also have a role in these declines. In addition, the emergence of adaptations in the algae could also be explaining a decrease in the uptake of metals by the algae. In any case, the reduction in Hg concentrations in brown algae is significant itself given their key role as ecosystem engineers and their potential trophic transfer of these contaminants to consumers. Due to the scarcity of studies on the temporal trends in metal contamination in coastal ecosystems, this data provides valuable insights for future environmental conservation strategies and environmental policy assessment.

P.1180 Better soon than never: climate change induces strong phenological reassembly in the flowering of a Mediterranean shrub community

Daniel Pareja-Bonilla[1], Montserrat Arista[1*], Leonor Patricia Cerdeira Morellato[2], Pedro L. Ortiz-Ballesteros[1]

1 Departamento de Biología Vegetal y Ecología, Universidad de Sevilla, Sevilla, Spain. 2 Instituto de Biociencias, Universidade Estadual Paulista "Júlio de Mesquita Filho", Rio Claro, Brazil.

Flowering is a key process in the life cycle of a plant. Climate change is shifting flowering phenologies in the northern hemisphere, but studies with long data series at community level are scarce, and even more so those regarding the consequences of phenological changes for emerging ecological interactions. In the Mediterranean region, the effects of climate change are stronger than the global average and there is an urgent need to understand how biodiversity will be affected in this area. In this study we investigated how the entire flowering phenology of a community comprising 51 perennial species from the south of the Iberian Peninsula changed from the decade of the 1980s to the 2020s. Furthermore, we have analysed the consequences of these changes for flowering order and co-flowering patterns. We have found that the flowering phenology of the community has advanced by about 20 days, and was coherent with the increasing temperatures related to climate change. Individual species have generally advanced their entire flowering phenology (start and end) and increased their flowering duration. The early flowering has resulted in a re-organisation of the flowering order of the community and generated a new co-flowering assemblages of species, with a slight trend towards an increase of shared flowering time among species. The advanced flowering phenology and changes on flower duration reported here were of unprecedented magnitude, showcasing the extreme effects of climate change on Mediterranean ecosystems. Furthermore, the effects were not similar among species, which could be attributed to differences in sensitivities of environmental cues for flowering. One consequence of these changes in flowering times is the ecological mismatches indicated by the changes in flower order and co-flowering between decades. The novel scenario may lead to new competition or facilitation interactions and to the loss or gain of pollinators.

P.1181 Biased retention of environment-responsive genes following genome fractionation

Rimjhim Roy Choudhury[1], Marc Beringer[1], Terezie Mandáková[2], Sandra Grünig[1], Ilia J. Leitch[3], Martin A. Lysak[2], Christian Parisod[1]

1 Department of Biology, University of Fribourg, Fribourg, Switzerland. 2 Central European Institute of Technology, Masaryk University, Brno, Czech Republic. 3 Royal Botanic Gardens, Kew, Surrey, United Kingdom.

The molecular underpinnings and consequences of whole-genome duplication (WGD) cycles and subsequent gene loss through subgenome fractionation remain largely mysterious. Endogenous drivers, such as transposable elements, are well-studied as they shape genome-wide dominance and expectedly result in a conserved least-fractionated (LF) and a degenerated most-fractionated (MF) subgenome (biased fractionation). However, the role of exogenous factors, such as those induced by environmental stresses, continues to be overlooked. A chromosome-scale assembly of the alpine Buckler Mustard (*Biscutella laevigata*; Brassicaceae) that underwent a WGD event about 11 million years ago, coupled with transcriptional responses to heat, cold, drought and herbivory, show that both endogenous and exogenous drivers of gene expression have led to differential gene retention across the MF and LF subgenomes. Apart from the impact of transposable elements in reducing the expression and retention of nearby genes across the MF subgenome, transcriptional changes among 3,334 pairs of duplicated genes highlight the endogenous stoichiometry of gene products under purifying selection (dosage balance) as the chief driver of duplicate retention. About one third of the retained duplicates exhibit novel expression patterns, indicating that genes that respond to the environment have turned "their hobby into a job" and typically show one constitutively-expressed supporting the increased gene dosage after WGD, whereas the other copy remains conditionally-expressed. This mesopolyploid genome shows uneven patterns of fractionation, with some regions remaining unbiased whereas others are highly biased and significantly enriched in environment-responsive genes. The specialization of the MF subgenome in response to drought supports the link between stress tolerance and WGD.

P.1182 New records of vascular flora from wild coastal areas of the Mediterranean-temperate phytogeographic belt in Chile.

Jimmy M. Pincheira-Ulbrich[1,3,4], Ulises R. Zambrano[2], Fernando A. Peña-Cortés F[3]

1 Departamento de Ciencias Ambientales, Universidad Católica de Temuco, Temuco, Chile. 2 Universidad Católica de Temuco, Geografía, Temuco, Chile. 3 Laboratorio de Planificación Territorial, Universidad Católica de Temuco, Chile. 4 Núcleo de Estudios Ambientales, facultad de Recursos Naturales, Universidad Católica de Temuco, Temuco, Chile.

The study of floristic diversity is key to understanding the spatial and temporal dynamics of plant communities, especially in the context of climate change. The lack of systematic and updated inventories has hindered the assessment of these changes in diversity. This study focused on the diversity of climbing plants, vascular epiphytes and associated species in five wild areas of the Mediterranean temperate coastal phytogeographic belt of Chile, areas that had not been surveyed for more than 25 years. Our hypothesis was a possible reduction in species richness over time, influenced by a north-south latitudinal gradient, due to the potential effects of climate change. The sampling design was based on transects, with 100 circular quadrats of 3 m diameter created for analysis. Results showed that, contrary to hypothesis, the data revealed unexpectedly high species richness, with 34 previously undocumented records. This may be due to a combination of factors, including differences in sampling methods between studies, advances in taxonomic knowledge, and variations in microhabitats that may have favoured the presence of new species. Although climate change remains a critical factor in species distributions, these results question the validity of direct comparisons between inventories, both in time and space. They also highlight the need for more systematic botanical studies using standardised methods to monitor vascular plant biodiversity.

P.1183 Phenotypic plasticity is predicted from plant life history and traits of the economics spectrum

Javier Puy[1], Mónica Medrano[1], Carlos Herrera[1], Conchita Alonso[1]

1 Estacion Biológica de Doñana- CSIC, Sevilla, Spain.

Phenotypic plasticity is a key mechanism by which plants respond to changing or heterogeneous conditions. Knowing functional plasticity of the species allows understanding their adaptive capacity, predict population responses to changing drivers and guide preventive conservation measures. Efforts to predict phenotypic plasticity across plant species have mainly focused on computing their environmental niche range. However, within sites, trait and magnitude of plasticity of the species might greatly differ. because of their different selective pressures. For example, plants with different life-history or on distant in the resource-use strategy are thought to differ in their plasticity. In order to test whether functional traits values might be associated with phenotypic plasticity, we conducted an experiment where nine different species of similar distribution but contrasting traits from the *Erodium* and *Geranium* genus (*Geraniaceae*), experienced two opposing environments (extreme drought stress or not) to quantify their maximum phenotypic plasticity. We found that acquisitive traits (e.g. higher SLA) was associated with increased phenotypic plasticity in biomass allocation, leaf morphology and physiology, although dependent of the life-history of the species. Our results show the potential of building predictive frameworks for phenotypic plasticity based on easily measured plant functional characteristics.

P.1184 Anthropogenic land-use changes negatively affect pollination and decrease male and female fitness in angiosperms

Mauricio Quesada[1,2,3], Ramiro Aguilar[1,4,5], E. Jacob Cristóbal-Pérez[1,2,6], Victoria Marquez[4], Lucas M. Carbone[4], Isis Paglia[7], Leandro Freitas[7], Lorena Ashworth[1,4], Silvana Martén-Rodríguez[1,2], Geraldo Wilson Fernandes[1,5], Jorge Lobo[1,2,6], Eric J. Fuchs[1,2,6]

1 Laboratorio Nacional de Análisis y Síntesis Ecológica, Escuela Nacional de Estudios Superiores Unidad Morelia, Universidad Nacional Autónoma de México, Morelia, Mexico. 2 Laboratorio Binacional de Análisis y Síntesis Ecológica, México-Costa Rica. 3 Instituto de Investigaciones en Ecosistemas y Sustentabilidad, Universidad Nacional Autónoma de México, Morelia, Mexico. 4 Instituto Multidisciplinario de Biología Vegetal, Universidad Nacional de Córdoba–CONICET, Córdoba, Argentina. 5 Departamento de Genética, Ecologia e Evolução, Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazil. 6 Escuela de Biología, Universidad de Costa Rica, San Pedro, Costa Rica. 7 Instituto de Pesquisa Jardim Botânico do Rio de Janeiro, Jardim Botânico, Brazil.

Today, most of the planet has been modified and occupied by humans. Measuring how angiosperms reproduce in these pervasive environments is essential for predicting the evolutionary potential of plant populations and their ability to adapt to changing environments. In this study, we conducted hierarchical and phylogenetically independent meta-analyses to assess the overall effects of anthropogenic land-use changes on pollination, and male and female fitness in terrestrial angiosperms. Our results found negative global effects of land use change, mainly associated with habitat loss and fragmentation, on pollination and female and male fitness of terrestrial flowering plants. Negative effects were stronger in plants with self-incompatibility (SI) systems and pollinated by invertebrates, regardless of life form and sexual expression. Pollination and female fitness of pollination generalist and specialist plants were similarly negatively affected by land-use change, whereas male fitness of specialist plants showed no effects. Our findings indicate that angiosperm populations remaining in fragmented habitats produce on average lower quantity and quality of progeny as both female and male fitness are significantly depleted, which is likely to reduce the recruitment, survival, and long-term viability of plant populations remaining in fragmented landscapes. We underline the main current gaps of knowledge for future research agendas and call out not only for a decrease in the current rates of land-use changes across the world but also to embark on active restoration efforts to increase the area and connectivity of remaining natural habitats.

P.1185 Landscape-level vegetation dynamics in fire-affected zones of the Santa Monica Mountains using synergistic remote sensing methods

Kamal Humagain[1], Dylan Stephens[2], Zach Raposo[1,3], Samuel Ericksen[1,3], Kyle Nessen[1,3], Mark Mendelsohn[4]

1 Althouse and Meade, Inc., Paso Robles, USA. 2 University of Lausanne, Lausanne, Switzerland. 3 California Polytechnic State University, San Luis Obispo, USA. 4 National Park Service, Thousand Oaks, USA.

Chaparral landscapes in Southern California, vital for biodiversity and ecosystem services, face challenges from disturbances such as more frequent fires and prolonged droughts. To comprehensively study land cover dynamics in these landscapes, we implemented data acquired from a multitude of remote sensing platforms. Employing multispectral imagery captured by UAV-mounted sensors in conjunction with NAIP imagery within the Santa Monica Mountains (SAMO) region, we utilized a Normalized Difference Vegetation Index (NDVI) threshold value of 0.3 for woody cover estimation. This approach facilitated the creation of a second-degree polynomial regression model ($R^2 = 0.51$) for estimating woody cover percentages using NDVI generated from NAIP imagery. Our analysis of woody cover changes in the SAMO Ecological Monitoring zone and areas affected by fire between 2012 and 2022 indicated a decreasing trend of the high woody cover areas even multiple years after the fire. Additionally, we leveraged a random forest classifier, integrating field data and Landsat 8 imagery within NPS vegetation monitoring sites from 2014 to 2022 (overall accuracy = 0.77). An examination of woody vegetation in relation to grasslands and other vegetation types indicates a notable decline in woody vegetation. In a changing world characterized by increased fires and droughts, these models and analyses provide valuable landscape-level insight that can be repeatedly applied. This valuable information guides land managers and policymakers in proactive planning and the implementation of necessary mitigation measures to protect and effectively manage ecologically significant landscapes vulnerable to these challenges.

P.1187 Stem and root anatomical traits of 24 young tree species of Cerrado Legumes in relation to fire.

Aline R. Martins[1], Tainah Eduarda B. Carneiro[1], Liliane S. Camargos[1], Wesller S. Paiva[1]

1 Departamento de Biologia e Zootecnia, Faculdade de Engenharia de Ilha Solteira, UNESP, Ilha Solteira-SP, Brazil.

Plant communities in flammable environments present morphological adaptations that allowed them to survive and resprout after fire. The present study aimed to anatomically investigate 24 young tree species from the Cerrado that were submitted to a fire experiment under controlled conditions. Plants from fire experiment were anatomically analyzed and the stem and underground structures were sectioned using a sliding microtome and stained with safranin and alcian blue. The obtained cross sections were photographed in a light microscope with an attached camera. The underground structure observed in the 24 species studied was characterized by roots. For some analyzed species, such as *E. contortisiliquum*, an increase in root bark thickness was observed in plants from fire experiment, while for other species, such as *P. parviflora*, a decrease in bark thickness was observed in seedlings after fire. Regarding vessel elements in the secondary xylem, almost all species, except for *E. mulungu* and *S. alata*, presented changes in the quantity and size of these structures after fire experiment. For the stem anatomical characteristics, it was observed well developed buds with variable degrees of bark protection. The root crown cross sections, of 12-month-old plants after fire experiment, presented self-grafting anatomy. Thus, it was concluded that Fabaceae species exhibited some plasticity traits related to fire, including changes in bark thickness and the density and diameter of vessels in the xylem for some species and the bud bank of young leguminous species from the Cerrado was located in the root-crown region in 23 of the studied species.

P.1188 Characterization of the flammability of woody species in a pine-oak forest in Michoacán, Mexico

Esthela Rodríguez[1], Moisés Méndez[1,2]

1 Bajío Regional Center, Ecology Institute (INECOL A.C.), Michoacán, Mexico. 2 National Council of Humanities, Sciences, and Technologies, Mexico City, Mexico.

Flammability can be defined as the ability of a fuel to ignite and sustain a flame. The intensity, spread and impact of fires depend in part on how susceptible plants are to fire: more flammable plants benefit fire and its spread. The flammability of thirty-nine woody plants in the pine-oak forest of the Protected Natural Area "Parque Nacional Barranca del Cupatitzio" in the state of Michoacán, Mexico, was evaluated and compared. Portions of plants measuring 50 cm in length were preheated and burned in a standardised manner. Measurements of maximum temperature, burning rate and percentage of biomass consumed were taken to calculate overall flammability values ranging from 0 (no flammability) to ~3 (maximum flammability). Ignition time and flame sustainability variables were also used to assess their susceptibility to ignition and heat transfer and/or flame. Fifty-nine percent of the total woody species assessed in this forest have a moderate to high degree of flammability (1.01-2.83), while the remaining 41% are slightly flammable (1<). The highest flammability is observed in five species of the genus Pinus , which are dominant in this vegetation type, with Pinus lawsonii being the most flammable and having the shortest ignition time (P.1 seconds). The longest sustainability time was recorded by Arbutus xalapensis with 870.74 seconds (14.5 minutes). The species Clusia salvinii showed no ignitability. Our results provide valuable information that will contribute to improve the efficiency of prevention activities and evaluation of fire behaviour and management in the area, identifying the most vulnerable sites according to their plant composition.

Note: This abstract was translated with AI.

P.1189 Seawater acidification affects nutritional value of Skeletonema tropicum from coastal upwelling

Zuoxi Ruan[1], Yi Wang[1]

1 STU-UNIVPM Joint Algal Research Center, Marine Biology Institute, Shantou University, Shantou, China.

Upwelling areas play a critical role as fishing grounds and are also among the regions most severely impacted by seawater acidification (SA). By the end of this century, the H^+ concentration in these areas is predicted to be twice that of other waters. We thus hypothesize that SA may potentially alter the macromolecular composition of phytoplankton, consequently influencing nutritional value—a key factor governing the efficiency of nutrient and energy transfer between trophic levels. In experiments where the pH dropped from 8.2 to 7.9, macromolecule contents, such as proteins and carbohydrates, of *Skeletonema tropicum* from coastal upwelling, decreased, while the lipid pool size increased by 71%. Concomitantly, key genes related to photosynthesis (including light reactions and the Calvin cycle), glycolysis, and fatty acid synthesis were significantly upregulated. Various fatty acids, such as linoleic acid and hexadecane, also exhibited an increase, indicating enhanced photosynthesis and glycolysis to support lipid accumulation. As the pH further decreased to 7.6, lipid content increased by an additional 59%, while protein and carbohydrate content remained constant. These changes can be elucidated by the upregulation of key enzymes in glycolysis and fatty acid synthesis (e.g., acetolactate synthase). Our findings revealed that *S. tropicum* tended to accumulate lipids at the expense of proteins and carbohydrates, while containing less toxic polyphenols and Si, implying an improvement in nutritional value under seawater acidification conditions.

P.1191 Evaluation of nitrogen compounds in Canavalia ensiformis (L.) DC and Cajanus cajan (L.) Millsp. cultivated under different doses of manganese

Thalita F. S. Mendes[1], Nayane Cristina P. Bomfim[1], Jailson V. Aguilar[1], Liliane S. Camargos[1]

1 Department of Biology and Zootechny, São Paulo State University, Ilha Solteira, São Paulo, Brazil.

Mn is considered an essential trace element, as it plays an important metabolic role in the life of plants, however, when present in high concentrations in the soil, it generates symptoms of toxicity. With regard to the regulation of ion transport and radical mitigation, total soluble amino acids operate as signaling molecules, including in stress situations. Therefore, the objective of the present study was to evaluate the metabolism of nitrogenous compounds and the production of biomass of *Canavalia ensiformis* (L.) DC and *Cajanus cajan* (L.) Millsp., identifying possible non-enzymatic defense mechanisms linked to nitrogen metabolism, under concentrations of 80, 100, 120, 140 and 160 mg kg^{-1} of Mn applied to the soil. The metabolic response when analyzing nitrogen compounds between *C. ensiformis* and *C. cajan* was different between the species. The metabolism of nitrogen compounds under excess Mn in the soil was more systematically affected in *Cajanus cajan*, with significant differences in shoot, root and nodules for amino acids, total soluble proteins and ureides and a significant variation in the concentration of biomass in the root system. In *Canavalia ensiformis*, stability in the concentration of compounds was observed, mainly ureides and proteins, as the doses of manganese in the soil increased. These results demonstrate that the metabolism of amino acids in the legumes studied can be a central point for understanding the mechanisms of tolerance to Mn in soil.

P.1192 Tree ring-climate relationship in Atlas cedar and Aleppo pine in Northwestern Algeria

Mohamed Sarmoum[1], Fatiha Abdoun[2], Julio Camarero[3], Frederic Guibal[4], Rafael Navarro-Cerrilo[5]

1 Plant physiology and soilless culture laboratory, FSNV, Ibn Khaldoun University Tiaret, Algeria. 2 Plant ecology and environment laboratory, FSB, University of Science and Technology, Algiers, Algeria. 3 Instituto Pirenaico de Ecología (CSIC), Zaragoza, Spain. 4 Mediterranean Institute of Biodiversity and Marine and Continental Ecology, CNRS-IRD, Aix-Marseille University, Aix-en-Provence, France. 5 Laboratory of Silviculture, Dendrochronology and Climate Change, Department of Forestry Engineering, University of Cordoba, Spain.

In the context of global and climatic changes, forest species are showing changes in their productivity, growth and range distribution. The Aleppo pine is a typically Mediterranean species with a wide geographical distribution. Atlas cedar is an endemic species in Algeria and Morocco. Tree-ring and climate relationships were studied in Atlas cedar and Aleppo pine populations in northwestern Algeria. The aim of this work is to understand the response of each of the two species to climate change marked by persistent drought over the past three decades. Although the two species are exposed to similar ecological conditions, their response to climate is not the same. Atlas cedar show positive relationships with annual and monthly precipitation for several months, especially in winter and spring. This sensitivity is more marked in populations located at low altitude and/or on a sandstone substrate. The Aleppo pine has positive relationships with monthly precipitation in spring and negative relationships with minimum temperatures in its upper altitudinal limit. The two species could therefore show mixed responses to climate change, these responses are modulated by environmental conditions such as substrate and altitude. These results can improve our knowledge of the response and resilience to drought for both species and guide future reforestation and ecological restoration projects.

P.1193 The role of the microsite in reproductive effort of the legume Neltuma chilensis (Molina) C.E. Hughes & G.P. lewis

Maite D. I. Sepúlveda[1], Juan I. Reyes[1], Paulette I. Naulin[1]

1 Laboratorio Biología de Plantas, Universidad de Chile, Santiago, Chile.

Neltuma chilensis is a tree native to Chile and adapted to the Mediterranean climate. The flowering and fruiting season of the species occurs in summer, when the stock of resources is limited. This factor limits the reproductive fitness of the species and the survival fitness of the next generation. This study evaluated the reproductive effort of N. chilensis in three different microsites after the megaseason (2010-2022). Microsites were located 500 m (BS) and 50 m (LA) from a lagoon, and in an irrigated plantation (PL). Thirty fruits were harvested from 6 trees in each microsite. Fruit and seed mass and size were measured, and seed development, seed health, germination and survival were assessed. The percentage of healthy and viable seeds (HVS) was 40% for BS, 86% for LA and 81% for PL, meaning an average of 5, 17 and 18 HSV per fruit in each microsite, respectively. The initial seed stock decreased due to aborted, vain and parasitized seeds. The percentage of germinated HSV was 92% for BS, 90% for LA and 92% for PL, of which 84%, 71% and 76% survived, respectively. Reproductive efficiency of N. chilensis was positively related to the available resources in each microsite, and resource allocation influenced seed characteristics and seed germination and survival ability.

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P.1194 Quantification of the relative expression of a salinity stress-responsive Na+/H+ exchanger (NHX) in Amaranthus dubius

Shakira Shaik[1], Ashiq Haripershad[1], Muhammad Nakhooda[2]

1 School of Life Sciences, University of KwaZulu-Natal, Durban, South Africa. 2 Department of Biotechnology and Consumer Science, Cape Peninsula University of Technology, Cape Town, South Africa.

Amaranthus dubius is an easy-to-grow, annual shrub and a highly nutritious food source. It contains elevated leaf nutrients, and can tolerate salinity, water-deficit and high temperature stresses, rendering it cultivable on marginal land. Despite these advantages, this species is categorized as an orphan (undervalued) crop in South Africa. Moreover, agricultural propagation of *A. dubius* has thus far not been realised due to high hybridisation frequency, leading to unpredictable genotypic and phenotypic variability. To realize its agricultural potential, particularly on high-saline soils, the present study aimed to screen, identify and clonally propagate salinity-tolerant genotypes of *A. dubius,* coupled with elucidating the underlying gene expression of the stress response at the different experimental stages, using degenerately primed Real Time-qPCR. Importantly, a direct organogenesis approach was used in the clonal propagation phases to ensure genetic fidelity in the regenerated populations. Fifty, four-week-old *A. dubius* seedlings were subjected to 100, 200 and 400 mM NaCl treatments to determine their degree of salt tolerance against a control (0 mM NaCl). Fifteen genotypes demonstrating high growth rates and biomasses under the salinity treatments, were clonally propagated through nodal cuttings before being subjected to the same range of salinity treatments as the seedlings. Their vigour, and protein and chlorophyll concentrations matched those of the non-stressed control plants. Quantification of the relative expression of an NHX1-like transcript in the clonal genotypes revealed some with salinity stress tolerance capabilities rivalling established halophytes by regulating the constitutive or inducible expression of an NHX1-like protein. Four of these genotypes were micropropagated through direct organogenesis using nodal explants for which the acclimatised stressed clones maintained the traits of chlorophyll and protein levels, and NHX1-like expression. One stress tolerant genotype also sustained the genetic fidelity in recovered plants after controlled-rate cooling of nodal explants and storage in liquid nitrogen.

P.1195 Mechanism of OsABT gene to improve the salt tolerance of roots at rice seedling

Danni Wen[1], Bo Shen[1,*]

*1 Hangzhou Normal University, Hangzhou, China, *bshen65@hznu.edu.cn.*

Salinity is a major factor that affects rice yield. Proteins containing WD40 repeats play important roles in eukaryotic development and environmental adaptation. Here, we identified *OsABT* and found that its overexpression significantly enhanced salt tolerance in rice seedlings. To identify the functions of OsABT, the roots of *OsABT* overexpressing rice and Nipponbare were used as materials. The root activity, malondialdehyde content, $O_2^{\bullet-}$ production rate, sodium-potassium ion content and ABA content were measured and the expression of related genes were analyzed. Transcriptome analysis, proteomic analysis and yeast two-hybrid experiment were conducted to explore the mechanism of salt tolerance mediated by *OsABT* in root system of rice seedling. Based on our experimental results, *OsABT* can inhibit ROS accumulation, thereby reducing the damage caused by ROS to cells under salt stress. Moreover, *OsABT* maintains the intracellular Na^+ and K^+ balance by enhancing the expression of *OsSOS1* and *OsHAK5* in roots. *OsABT* also inhibits the expression of the ABA synthesis genes *OsNCED3* and *OsNCED4* and promotes the expression of the ABA catabolic gene *OsABA8ox2*, thereby inhibiting the accumulation of ABA. Meanwhile, OsABT interacts with OsPYL4/10 and OsABIL2, and negatively regulates the expression of ABA signal transduction-related genes and ABA responsive genes, resulting in the attenuation of ABA signaling. Furthermore, it was reported the ABA signaling pathway is related to ROS and SOS signaling pathway. Thus, OsABT may affect the ROS levels and Na^+/K^+ balance through the ABA signaling pathway to regulate root salt tolerance in rice seedlings.

P.1196 Multivariate analysis of physiological responses of wild tomato species to moderate salinity under reduced watering conditions

Sofia Spormann[1], Cristiano Soares[1], Manuel Azenha[2], Viviana Martins[3], Fernanda Fidalgo[1]

1 GreenUPorto - Sustainable Agrifood Production Research Centre & INOV4AGRO, Department of Biology, Faculty of Sciences of University of Porto, Porto, Portugal. 2 CIQUP - Research Center in Chemistry, Department of Chemistry and Biochemistry, Faculty of Sciences of University of Porto, Porto, Portugal. 3 CBMA - Centre of Molecular and Environmental Biology, Department of Biology, University of Minho, Campus de Gualtar, Braga, Portugal.

Exploring wild germplasm of crops has emerged as an attractive strategy in the search for abiotic stress tolerance mechanisms. This study investigated the effects of moderate salinity stress under different watering conditions on the ion distribution, redox homeostasis, osmoregulation, and antioxidant defenses in tomato and its wild relatives *Solanum galapagense, Solanum habrochaites*, and *Solanum neorickii*. A principal component analysis (PCA) resulted in five PCs with eigenvalues>1, explaining 84.4% of the total variability. *S. neorickii* and *S. galapagense* formed distinct clusters on the right side of the PCA biplot, showing higher hydrogen peroxide levels and activity of ascorbate peroxidase and catalase enzymes, while *S. habrochaites,* in contrast, showed increased superoxide anionlevels, superoxide dismutase activity and non-enzymatic antioxidant metabolites.PC2 highlighted the higher levels of pigments in *S. galapagense* and *S. lycopersicum*. When plotting PC3, which is influenced by Na^+, K^+ and proline, the ellipses from each genotype (except *S. neorickii*) scattered down the y axis in accordance with salt application. *S. galapagense* sustained growth despite accumulating Na^+in shoots under salinity, which compromised K^+ uptake but correlated positively with enzymatic antioxidants, suggesting an efficient Na^+ compartmentalization. The domestic cultivar reached the highest Na^+ content in roots and the lowest ability to sustain K^+ uptake and K^+/Na^+ ratio under stress, leading to high growth inhibitions and an exaggerated accumulation of proline in leaves. Proline buildup was more notorious in *S. habrochaites,* but in both cases it did not relate to improved antioxidant or growth performances, indicating sensitivity.*S. neorickii* showed an improved antioxidant potential under salt stress and could sustain a higher K^+/Na^+ ratio, but revealed a negative correlation between growth and oxidative stress. These findings unveil distinctive stress responses among wild species.

P.1197 Physiological characterization of selected isolates of microalgae from Lake Tai (Jiangsu province, China)

Dongling Li[1,2], Bastian Steudel[1]*

*1 Xi'an Jiaotong-Liverpool University, Suzhou, China. 2 University of Michigan, Ann Arbor, United States of America. *bastian.steudel@xjtlu.edu.cn.*

Microalgae blooms are a frequent thread to ecosystems. Interestingly, algae mats growing on the water surface consist of different species. These consortia and the interaction of the species involved need to be studied in more detail. One prominent and dangerous species often involved in algae blooms is *Microcystis*. This cyanobacterium is of specific interest as it may produce toxins threatening the whole lake ecosystem and food and drinking water supply. However, the algae floating on the lakes surface are a mixture of different species, probably indicating, that all species need to be faced to their optimal growing conditions to build a bloom. By understanding the physiological properties of microalgae a sound management can be implemented to avoid the blooming of algae. We isolated microalgae strains from Taihu, the third biggest lake of China, in summer 2022. Then we faced them to different growth conditions to identify possible water treatment strategies allowing a management of algae blooms. Further, we determined the optimal growth conditions of selected strains regarding temperature and light intensity.

P.1198 Water stress alters leaf element concentrations in Silene

Janet C. Steven[1], Jenna R. Miladin[1], Katherine E. Ransone[1]

1 Christopher Newport University, Newport News, USA.

Plants across many habitats have plastic responses to drought stress that span morphology, physiology, and biochemistry. Some of these responses, such as reduced leaf size, are also well-studied as adaptations to arid habitats. However, less is known about whether plastic physiological responses to drought are also the physiological mechanisms involved in adaptation to arid habitats. For example, osmotic adjustment through increasing vacuolar concentrations of ions occurs in drought stressed crop plants, suggesting that wild species growing in arid habitats could also have increased concentrations of ions as an adaptation to dry conditions. In this study, we explore whether ion uptake of both essential and non-essential elements is associated with tolerance to drought and aridity in the genus *Silene*. We conducted a drought stress experiment in *Silene latifolia* in a growth chamber, and used herbarium specimens to determine how concentrations vary across a precipitation gradient in North American *Silene* species. We measured leaf elemental composition with a hand-held X-ray fluorometer calibrated for leaf tissue, which reports concentrations of elements heavier than sodium. We found that drought-stressed *Silene latifolia* leaves contained more potassium and chlorine than control leaves. Plants in both treatments also accumulated silicon in their leaves. We found that North American *Silene* species generally contained high concentrations of chlorine, magnesium, and potassium. In addition, we found that most of these species contained aluminum, and concentrations were greater in species growing in more arid habitats. In *Silene*, adaptation to dry conditions potentially involves high ion concentrations and the uptake of non-essential elements. These traits are similar to the plastic response to drought stress seen in *Silene latifolia,* suggesting that responses favored by microevolution may also play a role in lineage evolution.

P.1199 Similar climate-growth couplings but divergent drought resilience strategies in coexisting Mediterranean shrubs

Elisa Tamudo Mínguez[1], Antonio Gazol Burgos[1], Cristina Valeriano Peñas[1], Ester González De Andrés[1], Michele Colangelo[2], Jesús J. Camarero Martínez[1]

1 Instituto Pirenaico de Ecología (CSIC), Zaragoza, Spain. 2 School of Agricultural, Forestry, Food and Environmental Sciences, University of Basilicata, Potenza, Italy.

Anticipating future impacts of climate warming and aridification on drylands requires understanding how coexisting woody plant species respond to climate variability. However, we lack knowledge of the growth resilience capacity of Mediterranean shrubs. Do coexisting trees and shrubs differ in their response to climate? Do coexisting shrub species have comparable post-drought growth resilience? This study was conducted in two Mediterranean shrublands with sparse trees in semi-arid north-eastern Spain. We selected two sites situated in formerly agricultural or grassland areas. We sampled six shrubs' species (*Juniperus phoenicea*, *Juniperus oxycedrus*, *Pistacia lentiscus*, *Pistacia terebinthus*, *Rhamnus lycioides*, *Rhamnus alaternus*) and one tree species (*Pinus halepensis*) to measure their radial growth and to reconstruct their past growth patterns using dendrochronology. We quantified climate-growth couplings of trees and shrubs, as well as the growth resilience capacity after drought events. Growth patterns differed between species but a prevalent trade-off between growth and longevity was found. Growth responses to climate were comparable between species but differed between sites. Most species responded positively to precipitation and negatively to temperature. The most negative correlations of growth with a drought index were found at the driest Valcuerna site. Shrubs differed in their resilience capacity. Across sites, species were more resistant and resilient in Alcubierre, the wettest site. The shrubs *P. terebinthus* and *R. lycioides* were more resistant and resilient than the rest of species, which required longer growth recovery times and accumulated stronger growth reductions, particularly *J. phoenicea*. These results highlight the importance of drought as a driver of growth in Mediterranean scrublands. Growth resilience strategies differed between species with junipers being less resilient to drought than other coexisting angiosperms. Further research should investigate how this difference in post-drought resilience is related to functional traits, particularly those related with water-use strategies.

P.1200 Drought response in Arabidopsis displays synergistic coordination between stems and leaves

Ajaree Thonglim[1], Giovanni Bortolami[1], Sylvain Delzon[2], Maximilian Larter[2], Remko Offringa[3], Joost J.B. Keurentjes[4], Erik Smets[1,5], Salma Balazadeh[6], Frederic Lens[1,5]

1 Naturalis Biodiversity Center, Research Group Functional Traits, Leiden, The Netherlands (ajaree.thonglim@gmail.com, frederic.lens@naturalis.nl). 2 BIOGECO INRA, Université Bordeaux, Pessac, France. 3 Leiden University, Institute of Biology Leiden, Plant Developmental Genetics, Leiden, The Netherlands. 4 Laboratory of Genetics, Wageningen University, Wageningen, The Netherlands. 5 Leiden University, Institute of Biology Leiden, Plant Sciences, Leiden, The Netherlands. 6 Leiden University, Institute of Biology Leiden, Molecular Plant Stress Biology, Leiden, The Netherlands.

The synergy between drought-responsive traits across different organs is crucial in the whole-plant mechanism influencing drought resilience. These organ interactions, however, are poorly understood, limiting our understanding of drought response strategies at the whole-plant level. To address this gap, we investigated inflorescence stems and rosette leaves of eight *Arabidopsis thaliana* genotypes with contrasting drought tolerance and comprehensively analyzed anatomical and hydraulic traits in well-watered and water-deficit conditions. Our study revealed remarkable findings, demonstrating that multiple strategies can be employed to achieve their respective levels of drought tolerance. These strategies primarily involve two key approaches: the development of xylem resistance through specific anatomical traits, and the maintenance of high and stable leaf water potential (Ψ_l) to prevent sap pressure from reaching critical thresholds through precise stomatal regulation. Among the Arabidopsis genotypes studied the *soc1ful* knock-out mutant demonstrates the greatest tolerance to drought based on its synergistic combination of low stomatal conductance (g_s), largest stomatal safety margin (SSM), more stable Ψ_l during non-watering, in combination with the highest embolism resistance, most pronounced lignification, and thickest intervessel pit membranes. In contrast, in the sensitive genotypes, including Col-0, Cvi, Kel-4, and *jub1kd*, we observed the traits that contribute to increased water loss through transpiration, and a rapid decline in Ψ_l during drought, resulting in immediate wilting. Interestingly, unlike the other drought-resistant genotypes, the resilient *JUB1OX* does not possess hydraulic and stem anatomical traits that have been associated with increased drought resilience. Instead, it compensates for those traits by only displaying a stably high Ψ_l with a lower initial g_s that gradually decreases during drought. These distinct drought response strategies within a single annual species highlight the remarkable adaptive capabilities of plants to respond to challenging environmental conditions.

P.1201 Myrosinase isogenes identified in Wasabia japonica Matsum (wasabi) and their putative roles in glucosinolate metabolism

To Quyen Truong[1,2], Yun Ji Park[2], Sang Min Kim[1,2]

1 Division of Bio-Medical Science & Technology, Korea Institute of Science and Technology, University of Science and Technology, Seoul, Republic of Korea. 2 Smart Farm Research Center, KIST Gangneung Institute of Natural Products, Gangneung, Gangwon-do, Republic of Korea.

Wasabia japonica (wasabi), a Brassicaceae member, is well-known for its unique pungent smell and hot flavor derived from glucosinolate (GSL) hydrolysis. Myrosinase (MYR) is a principal enzyme catalyzing the primary conversion of GSLs to GSL hydrolysis products (GHPs) which is responsible for plant defense system and food quality. Given the limited information regarding MYR present in *W. japonica*, this study aimed to identify *MYR* isogenes in wasabi plant and unravel their roles in GSL metabolism. The identification of *MYR* sequences in *W. japonica* was performed using de novo assembly. Expression levels of identified *MYRs*, GSL accumulation, and GHP formation were investigated across vegetative organs of wasabi plants, subjected to various abiotic treatments. Our results revealed three potential isogenes (*WjMYRI-1*, *WjMYRI-2*, and *WjMYRII*) encoding for different MYR isoforms identified in *W. japonica*. Particularly, *WjMYRI-1* was abundantly expressed in all organs, whereas *WjMYRI-2* showed only trace expression levels. *WjMYRII* was highly expressed in the aboveground tissues. Interestingly, *WjMYRII* expression was significantly upregulated by certain abiotic factors, such as methyl jasmonate (more than 40-fold in petioles and 15-fold in leaves) and salt (10-fold in leaves). Young leaves and roots contained 97.89 and 91.17 µmol/g of GSL, whereas less GSL was produced in mature leaves and petioles (38.36 and 44.79 µmol/g, respectively). Notably, despite the non-significant changes in GSL production, abiotic treatments significantly enhanced GHP content in samples. Pearson's correlation analysis revealed a positive correlation among *WjMYRI-1* abundance, and GSL and GHP contents, indicating the primary role of *WjMYRI-1* in GSL hydrolysis. In contrast, *WjMYRII* expression level showed no correlation with either GSL or GHP content, suggesting another physiological role of *WjMYRII* in stress-induced response. In conclusion, *W. japonica* possesses at least three different *MYR* isoforms: *WjMYRI-1* and *WjMYRII* abundantly expressed and markedly responded to abiotic treatments.

P.1202 Deciphering above-treeline vegetation greenness trends: Insights from the Carpathian Mountains

Pavel D. Turtureanu[1], Arthur Bayle[2], Mihai Pușcaș[1], Philippe Choler[2]

1 A. Borza Botanic Garden, Babeș-Bolyai University, Cluj-Napoca, Romania. 2 Laboratoire d'Ecologie Alpine, LECA, Univ. Grenoble Alpes, Univ. Savoie Mont Blanc, Grenoble, France.

The long-term increase in vegetation greenness is a topic of considerable interest in ecology. This study aims to decipher the spatial distribution patterns of greening and their relationships to land cover in the above-treeline ecosystems of the Carpathian Mountains, a range that has been understudied so far in greening studies. We calculated the greenness trends using Landsat imagery dating back to 1984 and employed a large training dataset for high-resolution land cover classification. The land cover types included screes, grasslands, low shrublands (mainly composed of Ericaceae and Juniperus communis), tall shrubs (composed of Pinus mugo) and woodlands dominated by Picea abies. Our analysis revealed widespread greening and high spatial variability associated with land cover types. Overall, the most pronounced greening signal was detected within Ericaceae-rich shrublands, with varying intensity observed across different mountain ranges and other land cover types. Our findings highlight that high-resolution distribution models of land cover types are pivotal to unravel the complexity of greening in mountains.

P.1203 Photosynthesis in sessile oak and common beech provenances under drought in relation to different soil phosphorus concentrations

Antonia Vukmirović[1], Željko Škvorc[1], Saša Bogdan[1], Daniel Krstonošić[1], Marko Bačurin[1], Magdalena Brener[1], Ida Katičić Bogdan[1], Tomislav Karažija[2], Krunoslav Sever[1]

1 University of Zagreb Faculty of Forestry and Wood Technology, Zagreb, Croatia. 2 University of Zagreb Faculty of Agriculture, Zagreb, Croatia.

Inhibition of photosynthesis is the primary physiological consequence of drought stress. This research aimed to examine the response of photosynthesis of common beech and sessile oak saplings from two provenances, Karlovac (KA) and Slavonski Brod (SB) under the impact of drought and phosphorus fertilization (P). During the growing season of 2022, the saplings were treated with regular watering (W) and drought (D). Half of the plants treated with regular watering or drought were fertilized (+P), and the other half were not fertilized with P (-P). Accordingly, the saplings were subjected to four treatments (W/+P, W/-P, D/+P and D/-P). The dry period was interrupted on September 1st by re-watering. Every 10 days during the growing season, the photosynthetic performance index (PI_{abs}) and rate of net photosynthesis (A_{net}) were measured. The significance of the main effects (provenance and treatment) and their interactions on the PI_{abs} and A_{net} in drought and post-drought periods in common beech and sessile oak was tested by factorial ANOVA. In both species, during the drought period, the highest values of A_{net} and PI_{abs} were recorded in W/-P treatment and the lowest in D/+P treatment. During the drought period A_{net} and PI_{abs} in oak, as well as PI_{abs} in beech, were higher in KA compared to SB provenance. During the post-drought period A_{net} and PI_{abs} in both species, regardless of the provenances, were still lower in drought (D/+P and D/-P) compared to regularly watered (W/+P and W/-P) treatments. However, PI_{abs} in both species was higher in the D/-P compared to D/+P treatment in both provenances. Our results indicate that elevated P concentrations did not have a significant effect on photosynthesis in oak and beechsaplings in drought and post-drought periods.

P.1204 Altered trends in spring- and autumn-flowering species in Japan in response to global warming

Ai Nagahama[1], Hitomi Uemura[2], Taro Nikaido[2]

1 Department of Botany, National Museum of Nature and Science, Ibaraki, Japan. 2 Tsukuba Botanical Garden, National Museum of Nature and Science, Ibaraki, Japan.

Recent phenological studies have shown that the onset of flowering is significantly affected by global warming, which causes plant phenological shifts. It has been reported that spring-flowering species bloom earlier and autumn-flowering species bloom later when the temperature increases, but it was unclear whether both trends were prevalent in Japan. In this study, we examined responses to temperature increase and trends in phenological shifts using the flowering records of 350 Japanese native species collected at the Tsukuba Botanical Garden over the past 20 years. We observed that 64 species showed a significant negative correlation with temperature and advanced trends, whereas 17 species showed a significant positive correlation with temperature and delayed trends. The former bloomed mainly in spring (March–June), whereas the latter bloomed mainly in autumn (September–November). The distributions of 57 species that were significantly correlated with temperature increases but did not show any clear advanced/delayed trends were spring-biased, suggesting that spring-flowering phenology should be carefully monitored.

P.1205 High-latitude plants evolve faster in temperature niches than those in low-latitudes

Yin Wen[1,2]

1 Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China. 2 South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, China.

Under the background of global climate change, the rise of land surface temperature and frequent extreme weather events threaten the growth and survival of plants. It's essential to assess the temperature adaptability accurately for predicting their response to climate change in plants. Temperature niches are critical indicators, especially their evolutionary rates, which can be used to indicate temperature adaptability, with high research value. In this study, we selected diverse plant lineages from tropical, temperate, and alpine regions, equipped with comprehensive distribution data and robust phylogenetic trees. We used phylogenetic comparative analysis and macroecology approach, to analyze the global distribution pattern of the evolutionary rate of temperature niche. Our findings reveal a latitudinal trend: evolutionary rates of temperature niches increase from the equator towards the poles, inversely correlated with local environmental temperatures, particularly in niches associated with cold tolerance. This pattern provides new insights into the large-scale adaptive strategies of global plants and contributes significantly to our understanding of latitudinal biodiversity patterns and plant adaptation to environmental changes across latitudes.

P.1206 Screening of lupin (Lupinus spp.) lipases for functional analog of yeast Atg15

Karolina Wleklik[1], Katarzyna Nuc[2], Małgorzata Pietrowska Borek[1], Szymon Stefaniak[1], Sławomir Borek[1]

1 Adam Mickiewicz University, Poznań, Poland. 2 Poznań University of Life Sciences, Poznań, Poland.

Autophagy is a survival-promoting process of eukaryotic organisms, including plants, during which cell components, like organelles or macromolecules, are degraded and recycled. The molecular course of autophagic body degradation, one of the last but crucial step of autophagy, is significantly less known in plants than in other organisms as no enzymes involved in this process are yet identified. However, comparative studies can help fill this knowledge gap about plant autophagy. The early 1990s studies on yeast identified vacuolar putative lipase Atg15 as one of the enzymes involved in autophagic body degradation. Despite ATG (AuTophaGy) genes and proteins being well conserved among eucaryotes, Atg15 homologs are not found outside the fungi. We conducted screening for yeast Atg15 analogs in white lupin (Lupinus albus L.) and Andean lupin (Lupinus mutabilis Sweet) embryonic axes cultured in vitro under various carbon (sugar) and nitrogen (asparagine) conditions. We performed RNA-Seq to identify gene transcripts encoding lipases in lupin embryo axes and bioinformatic analysis to predict the subcellular localization of their protein products. We found 90 and 111 transcripts for white and Andean lupin embryonic axes, respectively, demonstrating probable vacuolar localization. Three transcripts coding potentially vacuolar lipases in lupins represented significant similarities with yeast Atg15, especially at the enzyme active-site motif. References: Wleklik K, Stefaniak S, Nuc K, Pietrowska-Borek M, Borek S 2024. Identification and potential participation of lipases in autophagic body degradation in embryonic axes of lupin (Lupinus spp.) germinating seeds. Int. J. Mol. Sci. 25, 90, doi:10.3390/ijms25010090.

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P.1207 Analysis of the starch synthase gene family reveals that NtGBSS2 positively regulates resistant starch synthesis and enhances drought resistance in tobacco (Nicotiana tabacum L.)

Xin Xu[1,2], Bingyu Li[1,2], Haiying Xiang[3], Zefeng Li[1,2], Zhaopeng Luo[1,2], Zhong Wang[1,2], Mingzhu Wu[1,2], Xiaodong Xie[1,2], Qian Gao[3], Jun Yang[1,2]

1 China Tobacco Gene Research Center, Zhengzhou Tobacco Research Institute of CNTC, Zhengzhou, China. 2 Beijing Life Science Academy, Beijing, China. 3 Yunnan Key Laboratory of Tobacco Chemistry, R&D Center of China Tobacco Yunnan Industrial Co. Ltd., Kunming, China.

Starch synthase is a crucial enzyme in plant starch biosynthesis and has been well-documented in plant development and stress responses. Under the backdrop of global warming, drought and high temperatures severely restrict growth, development, yield, and quality formation of tobacco. This study performed a genome-wide investigation and conducted an integrated analysis of starch synthase in tobacco. A total of 15 putative starch synthase genes unevenly distributed on chromosomes were identified in the tobacco genome, classified into five subfamilies according to the phylogenetic tree. The same subfamily displayed some similarities in gene structure and motif composition, while different subfamily exhibited variations. Gene duplication analysis indicated that segmental duplication was the primary driving force for the expansion of tobacco starch synthase gene family with all segmental duplication gene pairs undergoing purification selection during evolution. The promoter regions of starch synthase genes contained abundant stress- and hormone-related cis-elements. Real-time fluorescence quantitative PCR (RT-qPCR) analysis further revealed the expression patterns of 10 potential candidate genes under several abiotic stresses. *NtGBSS1*, *NtGBSS2*, *NtSS2* and *NtSS12* were upregulated under both stress conditions, while *NtSS4*, *NtSS7* and *NtSS10* were upregulated at certain stress. Gene interaction network analysis revealed that *NtGBSS2* is likely the core gene involved in starch metabolism. Further subcellular localization and genetic transformation experiment showed that the *NtGBSS2* was localized in the chloroplast and stable overexpression *NtGBSS2* enhanced the resistant starch content and improved the drought tolerance of transgenic tobacco plants. These results comprehensively analyze the starch synthase genes in tobacco, and also provide the theoretical basis and provide valuable information for understanding resistant starch metabolism and suggest targets for altering starch quality and drought resistant breeding.

S.130. PLANTS IN FOSSIL LAGERSTÄTTEN

P.1208 Diversity of inclusions of fruits in the Miocene amber of Chiapas, México

Emilio Estrada-Ruiz[1], Naylet K., Centeno-González[2], Leonardo Osvaldo Alvarado-Cárdenas[3]

1 Departamento de Zoología, Escuela Nacional de Ciencias Biológicas, Instituto Politécnico Nacional, México. 2 Facultad de Estudios Superiores Zaragoza, Universidad Nacional Autónoma de México, México. 3 Departamento de Biología Comparada, Facultad de Ciencias, Universidad Nacional Autónoma de México, México.

The outcrops of amber of the Miocene from Simojovel de Allende, Chiapas, Mexico, contain a diversity of plant, fungal, arthropod and vertebrate inclusions that suggest a complex ecosystem. The reconstruction of the past environment, based on the fossil record of the amber, suggest estuarine system, similar to the mangrove formation near the coast of the Gulf of Mexico. Here we present new records of different reproductive structures such as a cypsela and winged fruits from the Los Pocitos, Montecristo, Guadalupe Victoria mines of the Simojovel Formation, located in Simojovel de Allende, Chiapas. Several winged fruits represented by pseudosamaras of *Podopterus* genus (Polygonaceae) characterized by achenes with obovate to elliptical shape, three wings, thin with entire to undulate margin, decurrent towards the pedicel of the fruit, as well as a fruit with longitudinally elliptical to widely elliptical shape, with two wings coriaceous belonging to Combretaceae. While the samara fruits we describe here, are butterfly-shaped with three wings, one is a small dorsal wing, and two well developed thin lateral wings belonging to Malpighiaceae, while that the fourth fruit, is lanceolate-winged samara belonging to Petiveriaceae. The last fruit belongs to Asteraceae and it is characterized by a cypsela with a fusiform obovoid shape, hairy, with phytomelanin layers with persistent radial pappus. The presence of a cypsela and winged fruits, facilitated dispersal to colonized other areas over long distances by the wind. The new records increase the diversity of the proposed sturine environment and underline the paleobotanical importance of the Simojovel site.

P.1209 Lagerstätten of microbial plants: the case of Early Oligocene diatomites

Irena Kaczmarska1, James M. Ehrman[2]

1 Biology Dept., Mount Allison University, Sackville, Canada. 2 Digital Microscopy Facility, Mount Allison University, Sackville, Canada.

Even though featured in every botany textbook, it is sometimes debated whether colored micro-photoautotrophs are in fact plants. This is despite their common global ecological functions: carbon fixation, airing, and feeding the world. Diatoms are one of such primary producers, with an impact on the Earth's ecosystem on par with the terrestrial plants combined. Diatomites are sedimentary rocks made primarily of fossilized diatom cell walls, sometimes with silicified components of other micro-eukaryotes as minor contributors. The Early Oligocene occurs near the end of the Eocene-Oligocene transition, a major stage in a sequence of changes in global paleoceanography. These changes also affected regional land-ocean interactions, occasionally providing conditions for exceptionally good preservation of delicate nanno- and microfossils. In Rupelian (Early Oligocene) diatomites from the Central Paratethys (now in southeastern Poland) we recovered a wide range of microbial siliceous remains in addition to diatoms. In these diatomites, we discovered a new family of parmaleans in only the second record of fossil remains left by this division. We recovered nano-size scales from nucleomyceans and from organisms of unknown affinity. Ours is the first record of silicoflagellates for the Central Paratethys and includes more than a dozen species. We also discovered one of the most diverse assemblages of fossilized archaeomonads, with ~25% of species new to science. Furthermore, we recorded remains of very delicate valves of planktonic diatoms (e.g., *Leptocylindrus*), among 200+ other species, including an unprecedented number of raphid taxa with minute (< 15 µm) valves. Although the work is not yet completed, it is already clear that these exceptionally rich and diverse diatomites will significantly contribute to better understanding of the evolution of many microbial lineages, the Rupelian coastal marine environment, and their communities in the Central Paratethys.

P.1210 The Dibona section (Dolomites, northern Italy) records the transformation of the conifer flora during the Carnian Pluvial Episode

Guido Roghi[1], Piero Gianolla[2], Evelyn Kustatscher[3,4,5], Alexander R. Schmidt[6], Leyla J. Seyfullah[7]

1 Institute of Geosciences and Earth Resources, Padova, Italy. 2 University of Ferrara, Ferrara, Italy. 3 Museum of Nature South Tyrol, Bozen/Bolzano, Italy. 4 Ludwig-Maximilians-Universität, Munich, Germany. 5 Bayerische Staatssammlung für Paläontologie und Geologie, Munich, Germany. 6 University of Göttingen, Göttingen, Germany. 7 University of Vienna, Vienna, Austria.

The Carnian Pluvial Episode (CPE) has been identified as a time of plant radiations and originations of new lineages, likely related to observed rapid changes from xerophytic to more hygrophytic floras. Increasing humidity, causally resulting from LIP (large igneous province) volcanism, is considered the likely trigger for these changes in terrestrial ecosystems. Understanding the cause and effects of the CPE on the plant realm requires study of well-preserved floras that are precisely aligned with the CPE. To understand the floristic compositions within the CPE, we studied the Dibona succession of the Italian Dolomites, which is considered the best age-constrained section within the CPE for the terrestrial to marginal marine environment. This succession also preserved the oldest fossiliferous amber worldwide which delicately preserved palynomorphs and allowed combining palaeobotanical data from sediments and amber inclusions. Our integrated study of palynomorphs and macro-remains related to the conifer families of the fossil resin bearing level revealed a mixture of diverse taxa of predominantly late Palaeozoic (Majonicaceae, Voltziaceae), Mesozoic (Cheirolepidiaceae), and extant (Araucariaceae, Pinaceae, and Podocarpaceae) conifer families. These findings suggest a transformation of the conifer flora during the CPE and underline firmly the effects of the LIP-induced climatic changes on the evolution and radiation of conifers.

P.1211 New data on conifer evolution from the Late Triassic of Poland

Grzegorz Pacyna[1]

1 Institute of Botany, Faculty of Biology, Jagiellonian University, Kraków, Poland.

After the Carboniferous, the Triassic is the second most important period in conifer evolution. Conifers originated in the Carboniferous and were represented by extinct Walchian Voltziales. In the Triassic, more evolutionarily advanced Voltzian Voltziales reached their peak of diversity and gave rise to modern conifer families. New fossil conifer material from the Upper Triassic of southern Poland provides important new data, extending our knowledge of this group's diversity during that time and illuminating evolutionary processes during the origination of modern families. The specimens are compressions with well-preserved cuticle details. They provide new data about scale-bract complex evolution; some specimens allow us to modify Florin's views on Triassic conifer evolution. At least four new types of male cones were found, all atypically very small for the Triassic, and with pollen preserved *in situ* in pollen sacs. Some seeds and ovules with preserved anatomical details have pollen grains in micropylar canals. Additionally, some organs are preserved in organic connection, e.g. with cones attached to shoots, enabling reconstruction of complete plants. Especially interesting are taxa that combine seed scale-bract complex morphology typical for Voltziales, leafy shoots of *Brachyphyllum – Pagiophyllum* type characteristic of younger Mesozoic conifers and modern families, and evolutionarily advanced very small male cones. For taxa with such a mixture of features the new family Patokaeaceae was pro Allchar unveiled: posed. The array of characters of Patokaeaceae shows that during the origination of modern conifer families, many new taxa appeared with different combinations of plesiomorphic and apomorphic features. The presence of Patokaeaceae only in the Late Triassic indicates that some combinations of features did not prove to be evolutionarily effective; such plants became extinct quite quickly. The material also contains one of the oldest members of Cheirolepidiaceae.

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P.1212 Vegetation and climate in the Zanclean (Early Pliocene) at Puerto de la Cadena (SE Spain)

José Mª Postigo-Mijarra[1], Rafael Moreno-Domínguez[2], Ignacio Fierro[3,4], Yul Altolaguirre[5], Manuel Casas-Gallego[6], Eduardo Barrón[7]

1 Complutense University of Madrid, Faculty of Biology, Madrid, Spain. 2 Universidad de Zaragoza, Zaragoza, Spain. 3 Fundación Cidaris, Elche, Spain. 4 GeaLand Patrimonio, Alicante, Spain. 5 Senckenberg Research Institute, Frankfurt am Main, Germany. 6 Complutense University of Madrid, Madrid, Spain. 7 Instituto Geológico y Minero de España, Madrid, Spain.

The palaeontological site of Puerto de La Cadena is located on the northern edge of the Carrascoy mountain range (Murcia Region, SE Spain). It is best known for the abundance and diversity of small and large vertebrates, making it an international reference site for Early Pliocene faunas. A large number of plant macrofossils, mainly cuticle-free impressions in varying degrees of preservation, were also recovered from the so-called level VLP3B during the fieldworks at the site between 2010 and 2011. The recent analysis of these plant remains has allowed us to describe the palaeoflora and also to infer other aspects related to the palaeoenvironment of the site. Most of the remains found correspond to hygrophilous and/or mesohygrophilous taxa, with genera such as *Alnus*, *Populus*, *Salix*, *Ulmus*, *Daphnogene*, *Quercus* or *Acer* being represented. The application of CLAMP analysis to the set of plant macroremains allows us to infer a mean annual temperature of around 12 ºC for the site as a whole, with clear seasonality for temperature and precipitation. From a geological point of view, the set of facies occurring in the outcrop and the characteristics of the rest of the overlying and underlying subunits suggest a formation process that could be related to hyperpycnal flows. In this process, the plant remains, originally deposited in the continental environment, are transported during a period of flooding of the fluvial system and subsequently deposited in the marine aquatic environment. The complete lack in the Iberian Peninsula of site studies with palaeobotanical and climatic information regarding the age of this deposit gives it a special relevance. It is also one of the few fossil records with macroflora for the entire Pliocene of the Iberian Peninsula.

P.1213 Mesozoic fossil woods from the Iberian Peninsula: new research insights

José Mª Postigo-Mijarra[1,*], Manuel Casas-Gallego[2], Rafael P. Lozano Fernández[3], Eduardo Barrón[3]

*1 Complutense University of Madrid, Faculty of Biology, Madrid, Spain. 2 Complutense University of Madrid, Faculty of Geology, Madrid, Spain. 3 Museo Geominero, Instituto Geológico y Minero de España – CN IGME-CSIC, Madrid, Spain. *jpostigo@ucm.es*

Within the broad framework of palaeobotanical and palaeoecological studies of Mesozoic palaeofloras, the study of fossil woods is a field of research with few general studies, especially when compared with other types of research such as pollen analysis. The low level of movement that woods undergo in the sedimentary basins where they are produced allows us to obtain reliable data on the characteristics of the flora at a local scale. In addition, they sometimes allow relatively precise taxonomic ranges to be established at a generic and/or specific level, making them a type of remains of clear scientific interest. In the Iberian Peninsula, as in other parts of the world, studies focusing on wood macroremains are scarce. The Jurassic fossil record is particularly scarce. Two studies stand out, one in the north of the peninsula (Ribadesella, province of Asturias) and another in the west of the peninsula (Guimarota, Portugal). On the other hand, the group of studies on Cretaceous wood is more numerous, although there are less than ten sites. Most of them are of Early Cretaceous age, mainly located in the Iberian system and its foothills, with occasional occurrences in Portugal, around Lisbon and Aveiro. Some of the genera of fossil wood mentioned are *Agathoxylon*, *Protocupressinoxylon*, *Prototaxodioxylon* or *Protopodocarpoxylon*. The work on fossil wood macrofossils, carried out within the framework of the Cretaceous Resin Interval (CREI) research project, allows us to increase our knowledge of this type of palaeoflora in areas far from previous sites, such as the Duero depression, thus completing the taxonomic and ecological spectrum already known from previous studies.

P.1214 From historical roots to a digital future - conserve, digitize and link the herbarium BHUPM at the Museum für Naturkunde Berlin

Sabine von Mering[1], Nora Lentge-Maaß[1], Frederik Berger[1], Ludwig Luthardt[1]

1 Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany.

The Museum für Naturkunde Berlin (MfN) houses a little known historical herbarium collection (herbarium code BHUPM) that comprises about 45.000 specimens and serves as a reference collection for palaeobotanical research. Apart from the herbarium specimens, BHUPM holds a seed and micropreparation collection. The general herbarium originates from a collection gathered by head librarian and botanist (Johann Eduard) Julius Schrader (1808-1898) who worked at the Royal Prussian library, today the Berlin State Library. Even though the herbarium is small, it comprises the majority of vascular plant clades on family level, collected from localities all over the world, with a focus on the Southern Hemisphere flora. Around 5 % of the specimens in the collection are supposed to represent type material, mostly isotypes. As part of the museum's so-called future plan, digitisation of the complete herbarium collection is currently ongoing. Following a curatorial process including restoration and relabelling, all specimens are currently imaged and prepared for online publication in the near future. At the same time the object metadata are transformed and prepared for the import into the collection management system Specify. To increase the accessibility and usability of the collection, all specimens are receiving stable identifiers. The open knowledge base Wikidata is used to connect to relevant entities such as the collectors, the herbarium itself and the archive of the MfN. Once the digitisation process has been completed, all scans of the specimens will be published together with the metadata on the MfN Data Portal and shared with other platforms and aggregators such as the Global Biodiversity Information Facility (GBIF). The poster presents both information on the history and the contents of the herbarium collection as well as the process of digitising and opening it up.

P.1215 Diversity of conifers and their pollen in the Late Triassic of Southern Poland.

Alicja Warzecha[1,2], Grzegorz Pacyna[2]

1 Doctoral School of Exact and Natural Sciences, Jagiellonian University, Kraków, Poland. 2 Institute of Botany, Faculty of Biology, Jagiellonian University, Kraków, Poland.

Southern Poland is rich in Upper Triassic localities where significant amounts of plant and animal fossils are found. At locations such as Poręba, Patoka and Siewierz, material containing pollen and spores can be obtained; those locations are of Norian age and belong to one local palynological zone. The Late Triassic is an especially interesting epoch for research on the evolution and diversity of conifers. Its vast taxonomic diversity includes numerous extinct Voltziales and early members of modern conifer families. Due to climatic changes occurring throughout the Late Triassic, starting from humid climate during the Carnian Pluvial Event and gradually becoming drier during the Norian, conifers were forced to adapt to changing conditions, resulting in a variety of forms observable in their macrofossils and in their abundant, diverse pollen, which includes many bisaccate (e.g. *Tradispores*, *Brachysaccus*), monosaccate (*Enzonalasporites*) and asaccate forms. We analysed the diversity of Norian conifer pollen from several southern Poland outcrops yielding many palynological samples. Previously, pollen of conifers from that area has been studied mostly from borehole material, containing fewer specimens and exhibiting lower species diversity. Borehole material limits the ability to study natural intraspecific variation, which can lead to excessive splitting of pollen species. Here we present the intraspecific variation found in our study of pollen preserved in situ in pollen sacs of male cones from Patoka and Poręba. Acknowledgments: The study was financed by funds from the National Science Centre, Poland (No 2021/43/B/ST10/00941).

S.131. POALES: FROM ADDRESSING GLOBAL SCALE QUESTIONS TO UNRAVELING THE EVOLUTIONARY SECRETS OF NEGLECTED FAMILIES

P.1216 Look for rarity in herbs: A case study of the neotropical genus Actinocephalus (Eriocaulaceae)

Roberto Baptista Pereira Almeida[1], Paulo Takeo Sano[1]

1 Departamento de Botânica, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil.

Why are some species rare, and why are others common? These questions have been pondered throughout the history of science. Notably, Rabinowitz's seven forms of rarity represent the most comprehensive and widely used method to assess species rarity in ecological and systematic studies. Evaluating geographic distribution, local abundance, and habitat specificity enables insights into the ecological niche, evolution, and diversification of common species. In turn, this allows us to hypothesize about morphologically key innovations for those species and identify critical species for conservation. However, while extensive research has been conducted on trees, comparatively less attention has been given to herbs and shrubs. To address this gap, we propose investigating the patterns of rarity in the neotropical genus *Actinocephalus* (Eriocaulaceae) with a center of diversity in *campo rupestre* in Brazil, a unique ecosystem on the eastern mountaintops of South America. This ecosystem is characterized by shrublands in the northern portion and grasslands in its meridional portion, where *Actinocephalus* are predominantly found. Moreover, this ecosystem occupied less than 1% of Brazilian territory but has 15% of all Brazilian angiosperms and ca. 1750 endemic species. We compiled a database of the 54 genus species and used Rabinowitz's seven forms of rarity to classify all species and assess their conservation status. These species are mostly confined to small areas along the eastern mountaintop and face pressures derived from human activities, like fire and mining. Our data also emphasizes the importance of considering taxonomy in ecological analysis. In this scenario, we propose a new species of *Actinocephalus*, exploring its morphological relationship with two commonly studied species. These results not only advance our understanding regarding *Actinocephalus* diversity and distribution, but also highlights the importance of using taxonomically curated data in ecological analyses.

P.1217 Systematics of Juncaceae, phylogenetic relationships inferred from hyb-seq data

Reed J. Kenny[1], Lenka Záveská Drábková[2], Daniel Potter[1]

1 University of California Davis, Davis, USA. 2 Botanica Nova, Mnichovice near Prague, Czech Republic.

This project is focused on resolving the subgeneric clades within the genus*Juncus*as well as the correct placement of genera in the Juncaceae. We used targeted sequence capture methods to amplify and sequence hundreds of nuclear and plastid loci from 81 taxa across Juncaceae, focusing on *Juncus*. We recovered a mean of 196 nuclear loci, as well as a mean of 44 chloroplast coding sequences across all taxa. We used iqtree and ASTRAL III to generate gene trees and species tree respectively, as well as a concatenated chlorplast tree. Previous studies have shown *Juncus* to be paraphyletic (Drabkova et al. 2006, Roalson, 2005). Brožová et al. (2022), recently proposed a new classification to resolve the paraphyletic nature of the genus *Juncus*, naming six new genera. Our study confirms the paraphyly of *Juncus* as currently circumscribed, and generallyconfirms the monophyly of the proposed new genera. Notable exceptions include the polyphyly of *Juncinella*, *Australojunucs* and *Boreojuncus,* caused byone or two taxa each. We believe this reflects a need for more robust morphological study of the clades within *Juncus s.l.,* in order to define robust synapomorphies for the newly proposed gen-

era, as well as continued sampling across the family. References: Roalson, E. H. Phylogenetic Relationships in the Juncaceae Inferred from Nuclear Ribosomal DNA Internal Transcribed Spacer Sequence Data. *International Journal of Plant Sciences* **166**, 397–413 (2005); Drabkova, L., Kirschner, J. & Vlcek, C. Phylogenetic relationships within Luzula DC. and Juncus L. (Juncaceae): A comparison of phylogenetic signals of trnL-trnF intergenic spacer, trnL intron and rbcL plastome sequence data. *Cladistics* **22**, 132–143 (2006); Brožová, V., Proćków, J. & Záveská Drábková, L. Toward finally unraveling the phylogenetic relationships of Juncaceae with respect to another cyperid family, Cyperaceae. *Molecular Phylogenetics and Evolution* **177**, 107588 (2022).

P.1219 Genome size variation in Cape schoenoid sedges (Cyperaceae: Schoeneae) and its ecophysiological consequences

Ruan van Mazijk[1,2], Adam G. West[1], G. Anthony Verboom[1], Tammy L. Elliott[1,3]Petr Bureš[3], A. Muthama Muasya[1]

1 Department of Biological Sciences, University of Cape Town, Cape Town, South Africa. 2 C4 EcoSolutions, Cape Town, South Africa. 3 Masaryk University, Brno, Czechia.

Increases in genome size in plants—often associated with larger, low-density stomata and greater water-use efficiency (WUE)—could affect aspects of plant ecophysiological and hydraulic function. Variation in plant genome size is often due to polyploidy, known to have occurred repeatedly in the austral sedge genus *Schoenus* in the Cape Floristic Region (CFR), while the other major schoenoid genus in the region, *Tetraria*, exhibits smaller genomes. Comparing these genera is useful as they co-occur at the landscape level, under broadly similar bioclimatic conditions. We hypothesise CFR *Schoenus* to exhibit greater WUE, as a function of lower maximum stomatal conductance (gw_{max}) imposed by larger, less dense stomata. We investigate relationships between genome size and stomatal parameters in a phylogenetic context, reconstructing a phylogeny of CFR-occurring Schoeneae. Species' stomatal and functional traits were measured from field-collected and herbarium specimens. Carbon stable isotopes were used as an index of WUE. Genome size was derived from flow-cytometric measurements of leafy shoots. Evolutionary regressions demonstrated that stomatal size and density covary with genome size, positively and negatively, respectively, with genome size explaining 72–75% of the variation in stomatal size. Larger-genomed species had lower gw_{max} and C:N ratios, particularly in culms. We interpret differences in vegetative physiology between the genera to evidence more conservative strategies in CFR *Schoenus* compared to the more acquisitive *Tetraria*. As *Schoenus* exhibit smaller, reduced leaves, they likely rely more on culm photosynthesis than *Tetraria*. Across the CFR Schoeneae, ecophysiology correlates with genome size, but confounding sources of trait variation limit inferences about causal relationships between traits.

P.1218 The evolution of holocentricity in Luzula sylvatica (Huds.) Gaudin (Juncaceae Juss.)

Yennifer Mata-Sucre[1,2,3], Marie Kratka[4,5], Ludmila Oliveira[6], Pavel Neumann[6], Jiri Macas[6], Veit Schubert[7], Andreas Houben[7], Andrea Pedrosa-Harand[2], Gustavo Souza[2], André Marques[1]1 Max Planck Institute for Plant Breeding Research, Cologne, Germany. 2 Federal University of Pernambuco, Recife, Brazil. 3 Genetics, Reproduction and Development Institute, Université Clermont Auvergne, Clermont-Ferrand, France. 4 Institute of Biophysics of the Czech Academy of Sciences, Brno, Czech Republic. 5 Masaryk University, Brno, Czech Republic. 6 Institute of Plant Molecular Biology, České Budějovice, Czech Republic. 7 Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany.

Centromeres are highly specialized chromosome regions that ensure genome stability during cell divisions. Concerning their organization, centromeres may be restricted to one region of the chromosome (monocentromeres) or they may assemble at multiple sites throughout the chromosome (holocentromeres). While most plants possess monocentric chromosomes, Juncaceae Juss. species exhibit either monocentric (*Juncus* L.) or holocentric (*Luzula* DC.) chromosomes, offering the opportunity to investigate the evolutionary transition to holocentricity. To elucidate the evolution and organization of *Luzula sylvatica* (Huds.) Gaudin holocentromeres, we performed genome assembly, repetitive DNA analyses, epigenetic profiling, and comparative genomics analysis with the monocentric *Juncus* sister species. Our findings revealed an irregular distribution of genes, centromeric units, and repetitive elements along the *L. sylvatica* chromosomes. The DNA satellite repeats called *Lusy1* and *Lusy2* (monomeric lengths of 124 bp and 174 bp long, respectively) associate with CENH3-containing nucleosomes, whereas other satellite repeats do not interact with centromeric chromatin. Comparative genomic analysis between the genomes of *L. sylvatica* and *Juncus effusus* revealed that for a chromosome number reduction in *Luzula*, likely multiple fusion events involving *Juncus*-like ancestral chromosomes occurred. We propose that the transition to holocentricity in *Luzula* includes (i) fusion of small chromosomes with extended and atypical monocentromeres, similar to those observed in *J. effusus*; (ii) spreading out of centromeric units toward holocentricity; and (iii) subsequentcolonization of satellite DNA for the stabilization of centromeric regions.

P.1220 Neotropical Eriocaulaceae: advances in past decades and insights for the future

Caroline Oliveira Andrino[1], Fabiane Nepomuceno Costa[2], Paulo Takeo Sano[3]

1 Departamento de Botânica, Universidade de Brasília, Brasília, Brazil. 2 Departamento de Ciências Biológicas, Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, Brazil. 3 Departamento de Botânica, Universidade de São Paulo, São Paulo, Brazil.

Eriocaulaceae in Neotropics exhibit remarkable diversity, constituting around 70% of their richness, making them a focal point for botanical research. Recent decades witnessed significant advancements in understanding their taxonomy, evolution, reproductive biology, and ecology. Here, we present an overview of Eriocaulaceae in the Americas, highlighting recent progress and future exploration prospects. Intensive floristic investigations in ecosystems of South America from the 1980s onwards revealed high richness and a notable degree of endemism. Since then, numerous new species have been described. Many morphological studies have shown cohesion among geographically isolated groups, and with the advent of molecular data, phylogenetic hypotheses regarding the family's evolution have become consolidated. As these data were tested, the need for taxonomic realignment to reflect lineage evolution and adhere to phylogenetic systematics became apparent. *Paepalanthus* Mart., previously challenging, was recognized as a non-natural group and recircumscribed, with the monophyletic lineages comprising the genus being split into new genera. The family underwent classifications containing 2 genera in the 19th century, passing through 12, 10 genera in recent years, and now comprises 18 genera, all monophyletic: *Actinocephalus* (Körn.) Sano, *Comanthera* L.B.Sm., *Coracoralina* Andrino & Sano, *Cryptanthella* (Suess.) Andrino, *Eriocaulon* L., *Floralia* Andrino & F.N.Costa, *Giuliettia* Andrino & Sano, *Gnomus* Andrino & Sano, *Hydriade* Andrino, *Lachnocaulon* Kunth, *Leiothrix* Ruhland, *Mesanthemum* Körn., *Monosperma* (Hensold) Andrino, *Nisius* Andrino, *Paepalanthus* Mart., *Rondonanthus* Herzog, *Syngonanthus* Ruhland, and *Tonina* Aubl. Major taxonomic changes were facilitated by expanding our focus to include morphological, reproductive, ecological, and biogeographic aspects. This shift led to a greater emphasis on inflorescence structure and seed morphology. In reproductive biology, insect pollination has supplanted wind pollination hypotheses. Regarding biogeography, Eriocaulaceae emerge as a promising group for elucidating Neotropical open area dynamics, particularly due to their association with areas referred to as “cradles” and “museums” of lineages.

P.1221 Disentangling the Juncus bufonius L. complex

Billy Williams Marland[1], Raúl Sánchez Garcia[2], Andy J. Green[2], Jennifer Rowntree[3], Karin Tremetsberger [4], Casper van Leeuwen[5], M. Ángeles Ortiz[1]

1 Universidad de Sevilla, Seville, Spain. 2 Estación Biológica de Doñana CSIC, Seville, Spain. 3 University of Plymouth, Plymouth, UK. 4 Universität für Bodenkultur Wien, Vienna, Austria. 5 Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, Netherlands.

The systematics of the toad rush *Juncus bufonius* L. polyploid species complex of section *Tenageia* has remained unclear for decades. Toad rushes have a highly variable morphology with overlapping characteristics, apparent hybridisation, and seemingly holocentric chromosomes. Thus, classification and identification of specimens is hard and controversial. Toad rushes are often considered weeds and are widespread in wet or temporarily inundated soils (often saline), with a variety of dispersal mechanisms including endozoochory by waterbirds. Most previous studies of the complex have centred on Central and Western European specimens, and few on Mediterranean ones. However, the Mediterranean region is a hotspot for the complex, especially the Iberian Peninsula where almost all its members can be found. The objective of the present study was to ascertain whether the different taxa of the *J. bufonius* complex can be segregated based on morphological and genetic information. For this purpose, qualitative and quantitative characteristics were measured from specimens from Andalusia (Spain) and other parts of Europe including the United Kingdom and the Netherlands. Specifically, characteristics of the habitat, such as the pH and the salinity of the soil, in addition the height, colour, length and width of the inner and outer tepals, and capsules, from the specimens were measured. The ploidy level was also obtained as well as the sequences of two plastid and one nuclear markers from individuals of the different collected populations.

S.133. POLYPLOIDY AND HOMOPLOID HYBRIDIZATION AS EVOLUTIONARY DRIVERS IN MEDITERRANEAN PLANTS

P.1222 Biosystematics of wlid wheat (Aegilops) from Algeria

Nourdine Baik[1,2], Houda Bandou[2], Miriam Gonzalez Garcia[3], Elena Benavente[4], Juan Manuel Vega[3]

1 University of Akli Mohand, Bouira, Algeria. 2 Université des Sciences et de la Technologie Houari Boumediene, Alger, Algérie. 3 Universidad Complutense, Madrid, Spain. 4 Escuela Técnica Superior de Ingenieros Agronomos, Universidad Politécnica, Madrid, Spain.

The genus Aegilops L, belonging to family Poaceae, represent the main genetic reserve for the improvement of cultivated wheat. In this work, morphological and genetic study of 53 populations of four *Aegilops* species (A. *geniculata*, A. *triuncialis,* A. *ventricosa* and A. *neglecta*) sampled in different eco-geographical site in the north of Algeria was carried. The multivariate analysis allowed the separation of the vegetative and inflorescence characters in two groups and the individuals are grouped into two mainly clusters. Chromosome counting showed that the three species, A. *geniculata*, A. *triuncialis* and A. *ventricosa* were tetraploid (2n = 4x = 28), whereas A. *neglecta* is hexaploid (2n = 6x = 42). Karyo-morphometric analysis of somatic metaphase chromosomes revealed four cytotypes in A. *geniculata* and two cytotypes in A. *triuncialis*, A. *ventricosa* and A. *neglecta*. Chromosomes pairings in diakinesis, metaphase I and anaphase I, revealed a less regular meiosis of tetraploid and hexaploid samples, with univalent, chromosomes lagging and chromatin bridges anomalies. However, the in situ hybridization "FISH" showed a large genetic polymorphism of the sequences of two rDNA loci (5S and 45S) correlated to bioclimatic conditions, reflected by a variation in the hybridization patterns which differentiate populations by deletion and/or duplication of some loci. This analysis allowed us to identify the new loci of ribosomal RNAs genes in each of the four *Aegilops* species sampled in northern Algeria. Finally, the results show the high genetic diversity of Aegilops populations from Algeria, suggesting that environmental factors and geographical location might have an effect on the genetic structure and evolution of chromosomes and interest for the cytogenetic in the identification and characterization of populations, to assess and enhance plant genetic resources.

P.1223 Interspecific hybridization and polyploidy: major factors in the diversification of Juniperus

Perla Farhat [1,2,3], Sonja Siljak-Yakovlev [2], Thierry Robert [2,5], Magda Bou Dagher Kharrat [1,5*]

1 Laboratoire Biodiversité et Génomique Fonctionnelle, Faculté des Sciences, Université Saint-Joseph, Campus Sciences et Technologies, Mar Roukos, Mkalles, Beirut, Lebanon. 2 Ecologie Systématique Evolution, Univ. Paris-Sud, CNRS, AgroParisTech, Université Paris-Saclay, Gif-sur-Yvette, France. 3 Sorbonne Université, CNRS, Integrative Biology of Marine Models, Station Biologique de Roscoff, Roscoff, France. 4 Biology Department, Sorbonne Université, Jussieu, Paris, France. 5 European Forest Institute, Mediterranean, Sant Pau Art Nouveau Site, Barcelona, Spain.

Polyploidy has long been recognized as a significant driver in the evolution of Angiosperms. Although the study of this phenomenon is limited in Gymnosperms, recent research has revealed that *Juniperus* is the only genus within this group that exhibits a high frequency of polyploidy. Here we aimed to assess the potential origin of five polyploid *Juniperus* taxa, including the only hexaploid taxon (*J. foetidissima*), using AFLP markers. Additionally, we aimed to evaluate gene flow between two *Juniperus* taxa that were suggested to be involved in the origin of the tetraploid *J. sabina* var. *balkanensis*. We utilized four chloroplasts and nrDNA markers, along with flow cytometry measurements for ploidy level determination on samples from three populations in France and Spain where these two taxa are present in sympatry. Bayesian analysis of admixture based on AFLP data suggested an allopolyploid origin for the hexaploid species *J. foetidissima*, involving *J. thurifera* and *J. sabina* lineages. The tetraploid cytotypes of *J. seravschanica* were shown to originate from an allopolyploidy event, while no clear evidence of hybridization in the origin of the tetraploid *J. thurifera* and *J. chinensis* was detected. Furthermore, flow cytometry measurements on samples from the three studied populations in France and Spain revealed the presence of three ploidy levels: diploid for *J. sabina* samples, tetraploid for *J. thurifera*, and a rare triploid level found in few individuals. Based on chloroplast and nuclear markers, the triploid individuals were identified as hybrids resulting from a cross between the diploid *J. sabina* and the tetraploid *J. thurifera*. These findings contribute to our understanding of the polyploidy origin of *Juniperus* taxa and highlight the potential role of allopolyploidy in the evolution of this coniferous genus.

P.1224 Unravelling the reticulate evolutionary history of the Iberian endemic genus Phalacrocarpum (Anthemideae, Asteraceae)

David Criado-Ruiz[1,2], Irene Villa-Machío[1], Jaume Pellicer Moscardó[3], Oriane Hidalgo[3], Rosalía Piñeiro Portela[4], Gonzalo Nieto Feliner[1]

1 Real Jardín Botánico, CSIC, Madrid, Spain. 2 Facultad de Biología, Universidad Autónoma de Madrid, Madrid, Spain. 3 Institut Botànic de Barcelona, Barcelona, Spain. 4 Facultad de Ciencias, Universidad de A Coruña, A Coruña, Spain.

Phalacrocarpum (Anthemideae, Asteraceae) illustrates the difficulties of achieving a fine reconstruction of the evolutionary history of plant groups that contain reticulations. However, because it is restricted to mountains in the northwestern quadrant of the Iberian Peninsula, it provides a suitable spatial framework for inferring past range shifts and forced secondary contacts between populations along these chains. Current recognition of one species (*P. oppositifolium*) with three subspecies (*oppositifolium*, *anomalum*, *hoffmannseggii*) results from early reports of hybridization in contact areas. A recent study revealed unexpected results. The easternmost subsp. *anomalum* populations are so genetically distinct that they can be considered a cryptic subspecies; morphological and Sanger sequencing data suggested a contact zone between two subspecies in the Sanabria Valley and showed that populations from a large area in southern Galicia and northern Portugal do not match any of the three subspecies. We performed an integrative study based on 37 populations (263 samples) to investigate these findings. This includes phylogenomics —based on SNPs from genotyping-by-sequencing and full plastome sequences—, Bayesian genetic clustering, introgression tests, genome size estimation, environmental niche modeling, and geometric morphometrics. The phylogenetic frame obtained shows two monophyletic groups —the early diverging eastern cryptic subspecies and the *oppositifolium* populations of central Portugal— connected by a large grade that runs from NW to SE, roughly in line with an increase in genome size. Populations along this grade tend to constitute recognizable genetic groups, but not to group into monophyletic assemblages. This picture is consistent with a dynamic history of partial isolation and hybridization. Such a dynamism has also affected (1) the contact zone in the Sanabria Valley, which is better interpreted as a vestigial hybrid zone, and (2) the Galician and northern Portuguese populations, which resulted from ancient hybridization between subsp. *hoffmannseggii* and a sub-atlantic geneticgroup.

P.1225 When, where and how an allopolyploid species was born: the case of Gypsophila bermejoi G. López

Miguel de Luis[1], Carmen Bartolomé[1], Julio Álvarez-Jiménez[1]

1 Departamento de Ciencias de la Vida, Facultad de Ciencias, Universidad de Alcalá, Alcalá de Henares, Spain.

Gypsophila bermejoi G. López is an allopolyploid (2n = 68) species derived from the parental *G. struthium* L. subsp. *struthium* (2n =34) and *G. tomentosa* L. (2n =34). All these plants are gypsophytes endemic to the Iberian Peninsula. We have used ordination techniques to model their niches and potential distributions in the current climate, the Last Glacial Maximum (LGM) and the Middle Holocene. The niche of *G. bermejoi* is markedly smaller than that of its parental species. Models indicate that environmental conditions during the LGM did not allow the presence of this plant in the Iberian Peninsula. In that period the distribution areas of its parental species overlapped and could theoretically produce individuals of the hybrid species, but climatic conditions prevent the hybrid species from thriving. Therefore, we consider that the populations of *G. beremejoi* have a recent origin, after the end of the LGM. There is data pointing to an increase in the rate of unreduced gamete formation by plants under conditions of stress. Accordingly, a higher frequency of polyploid individuals would be expected in populations living under extreme environments. We have used Species Distribution Models and GIS to locate areas with low bioclimatic suitability for both parental taxa during the LGM, hypothesizing that the rate of tetraploid hybrid formation would be higher than expected where low suitability areas of both parental species overlap. That locations could be centers for hybrid tetraploid formation or potential cradles of this species. Indeed, potential Mid-Holocene cradles were also identified in this manner. The evolution of bioclimatic suitability in both LGM and Mid-Holocene cradles was studied to assess the possible survival of the hybrids, and the current distribution of *G. bermejoi* proved to be consistent with our hypothesis.

P.1226 Exploring the chromosomal diversity of Crocus chrysanthus Herb. in Turkey

Bilge S. Kaleli[1], Almıla Çiftçi[1], Rachel Mollman[1], Levent Şık[2], Osman Erol[1]

1 Istanbul University, Department of Biology, Botany Division, Vezneciler, Istanbul, Turkey. 2 Manisa Celal Bayar University, Biology Department, Botany Division, Manisa, Turkey.

Crocus L. (Iridaceae) is a geophyte genus with a wide distribution across Europe, Asia and North Africa; however, the greatest diversity and number of taxa are found in Turkey and Balkans. The *Crocus chrysanthus* Herb. complex grows primarily across southwest Anatolia and Turkey-in-Europe, and its cultivars and hybrids are also prized as ornamental plants. Although several *C. chrysanthus* populations distributed in Turkey have been published as distinct species, they are usually considered doubtful at best due to insufficient specimens or gaps in comparative analyses, and most have been synonymized or transferred to subspecific status. Considering the wide distribution and fluctuating reports on its chromosome number (2n=8–22), further exploration is necessary to find the natural boundaries of the taxa nestled within, and to determine ploidy levels across this complex. Chromosome number and morphology are considered reliable characters for distinguishing closely related taxa and have been especially useful for the genus *Crocus*. This complex has long been in need of detailed and geographically widespread cytogenetic studies, which will aid in the delimitation of what is most probably several closely related species. The current work, which aims to fill this gap through comprehensive cytogenetic studies across the known distribution of the complex in Turkey, is one part of an ongoing multidisciplinary scientific project (TÜBITAK 222Z016) which plans to resolve the relationships within the *C. chrysanthus* complex in Turkey. This study uses fluorescence in situ hybridization (FISH) and flow cytometry in order to reliably determine and compare chromosomal morphology and genome size. Results indicate significant differences between karyotypes and genome sizes among the observed *C. chrysanthus* populations.

P.1227 Role of the reproductive strategies and gene flow in the evolution of endemics in the oro-Mediterranean region

Adam Kantor[1], Jaromír Kučera[1], Zuzana Gajdošová[1], Roswitha Schmickl[2,3], Andrea Melichárková[1], Ali A. Dönmez[4], Sırrı Yüzbaşıoğlu[5], Zübeyde U. Aydın[4], Marek Slovák[1,2]

1 Institute of Botany, Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovakia. 2 Department of Botany, Faculty of Science, Charles University, Prague, Czechia. 3 Institute of Botany, The Czech Academy of Sciences, Průhonice, Czechia. 4 Department of Biology, Faculty of Science, Hacettepe University, Ankara, Tur-

key. 5 Department of Biology, Faculty of Science, Istanbul University, Istanbul, Turkey.

The evolution of mountain endemics has been the subject gaining considerable attention within a broader context. This project aims to bring novel insights into the mechanisms behind diversification and adaptation of these key components of biodiversity in the oro-Mediterranean belts, which are renowned for being part of the global biodiversity hotspots and hosting centers of endemism. Our studies focus on the endemic representatives of this region from the genera Daphne (Thymelaeaceae) confined to rocky slopes, and Picris (Asteraceae) inhabiting craggy grasslands. We use phylogenomic-based methods (Hyb-Seq, RADseq) combined with other cytogenetic, karyological and morphological analyses to investigate the significance of selected intrinsic and extrinsic traits in evolutionary history of the target groups. We are interested about the role of peculiar environmental conditions that they live in, as well as specific reproductive strategies of the individual genera or particular lineages within them (chasmogamy / cleistogamy; seed dispersal mediated by zoochory/anemochory; sexual / asexual reproduction). We want to elucidate how have these factors shaped the extant genetic diversity of the focused groups, and if and how they might facilitate or hamper gene flow among the closely related species or lineages. Answering the stated questions will result in better general understanding of the evolution of endemics inhabiting challenging habitats in mountains of the temperate zone, which will be beneficial also for the management of conservational efforts.

P.1228 Enhanced clonality explains the spatial genetic structure of polyploids in the largest diploid-autopolyploid primary contact zone

Barbora Šingliarová[1,2], Judita Zozomová-Lihová[1], Marek Šlenker[1], Patrik Mráz[2]

1 Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovakia. 2 Department of Botany, Charles University, Prague, Czechia.

Given the ubiquity of polyploidy in plants, it is paradoxical that we do not know which evolutionary mechanisms allow newly formed autopolyploids to establish successfully in nature. As a consequence of whole-genome multiplication (WGM), neoautopolyploids suffer from reduced fitness due to disrupted meiosis and the negative effect of majority-minority cytotype interaction. However, this negative effect of WGM can potentially be counterbalanced by the emergence of a new trait that enhances the reproduction of neo-autopolyploid and/or reduces the negative effects of interploidy crosses, thereby increasing its successful establishment. Our previous studies showed that *Pilosella rhodopea* (Asteraceae), an *oro-Mediterran*ean species, forms the largest diploid-autopolyploid primary contact zone ever recorded in angiosperms. Furthermore, our experiments revealed a strong trade-off between generative and vegetative reproduction in autopolyploids expressing a novel clonal trait – root sprouts. Increased vegetative clonal growth in autopolyploids appears to be a key mechanism for their successful establishment over large spatial scales. We hypothesize that the shift towards more intense clonality in autopolyploids should also be reflected in their clonal structure over small spatial scale. Here, we investigate the effect of contrasting vegetative growth between diploids and autopolyploids on their spatial structure using acombination of microsatellite genotyping in natural populations and acommon garden experiment. Our results confirmed our hypothesis: (i) diploid plants in natural populations are represented by unique multilocus genotypes and propagate via axillary rosettes at short distances in cultivation (up to several centimetres over season); (ii) in contrast, autopolyploids show a clonal pattern of genetic diversity, with some large clones (up to several metres) in the field and very rapid propagation via root sprouts observed in experimental cultivation (several tens of centimetres). Enhanced clonality of autopolyploids thus influences cytotype and genetic patterns at both global and local spatial scale.

P.1229 Deciphering the allopolyploid origin of Dactylorhiza cantabrica: a Hyb-Seq approach

Eva Pardo Otero[1], Manuel Pimentel Pereira[2], Elvira Sahuquillo Balbuena[2], Rosalía Piñeiro Portela[3]

1 Evolutionary Biology Research Group, Center of Information and Communication Technologies, University of A Coruña, A Coruña, Spain. 2 Evolutionary Biology Research Group, University of A Coruña, *A Coruña, Spain. 3 Evolutionary Biology Research Group, Interdisciplinary Centre of Chemistry and Biology, University of A Coruña, A Coruña, Spain.*

The orchid *Dactylorhiza cantabrica* H.A. Pedersen is a narrow endemic occurring at western Cantabrian Mountains in NW Spain. Previous allozyme and morphological studies suggest that it results from the hybridization of two widespread congeners: the triploid *D. insularis* and the diploid *D. sambucina*. However, this hypothesis has not been tested using multiple genetic markers, necessary to analyse phylogenies in complex genera such as *Dactylorhiza*. In this study, the Hyb-Seq technique is applied together with the universal Angiosperms353 probe kit to sequence multiple plastid and low-copy nuclear genes. The phylogenetic relationships between the three species, estimated based on 269 and 266 nuclear genes under concatenation and coalescent-based approaches, respectively, revealed highly-supported clades containing each putative parent, *D. insularis* and *D. sambucina*. The position of *D. cantabrica* was not well resolved, suggesting the existence of mixed inheritance, where different genes come from each parent. Phylogenetic networks, used for visualizing the conflict between nuclear gene trees, placed *D. cantabrica* between the two parents and revealed high levels of reticulation. In addition, nuclear genetic variation within and among species was explored with allele frequencies-based tools further supporting the intermediate position of *D. cantabrica* and the hypothesis of a recent hybrid origin. Finally, 75 plastid genes revealed that either *D. insularis* was the maternal donor or the existence of ancient introgression. Altogether, our results point to the allopolyploid origin of *D. cantabrica* from *D. insularis* and *D. sambucina*, as well as to the clear genetic differentiation of the two parental species.

P.1230 Unveiling molecular and cytogenetic aspects of Carpobrotus invasiveness in the Mediterranian Basin

Laura Valenzuela[1], Joan Pere Pascual-Díaz[1 2], Ana Novoa[3], Nokwanda P. Makunga[4], Jordi López-Pujol[1], Neus Nualart[1], Daniel Vitales[1], Sònia Garcia[1]

1 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 2 Facultat de Biociències, Universitat Autònoma de Barcelona, Bellaterra, Spain. 3 Department of Invasion Ecology, Institute of Botany, Academy of Sciences of the Czech Republic, Průhonice, Czech Republic. 4 Department of Botany and Zoology, Stellenbosch University, Stellenbosch, Private Bag X1, Matieland, South Africa.

Carpobrotus (family Aizoaceae), also known as ice plants, is a genus of succulents comprising from 12 to 25 species mainly native to South Africa, although a few are autochthonous to America and Oceania. Several species have become naturalized outside their native area, forming hybrid complexes in these regions and constituting one of the most concerning cases of plant invasions worldwide. Among these hybrids, the *Carpobrotus* aff. *acinaciformis* complex stands out, with a widespread presence in the Atlantic coasts of the Iberian Peninsula as well as in the Mediterranean region, a current hotspot of invasive alien plant species. The ecological aspects of the genus have been extensively studied, but there is a lack of genomic and cytogenetic knowledge. Interestingly, all *Carpobrotus* species and hybrids share the same chromosome number ($2n = 2x = 18$), making up an example of homoploid hybridization. Here we aim to understand the evolutionary history of native and hybrid (invasive and non-invasive) *Carpobrotus* populations. To achieve this goal, we used genomic and cytogenetic tools, including genome size assessments by flow cytometry, whole genome sequencing and karyotype/chromosome analyses by fluorescent *in situ* hybridization. We reconstructed the whole plastome and the repeatome, provided a preliminary phylogenetic framework, analysed the repeat composition, and in particular, leveraged the information of 5S ribosomal RNA genes diversity to understand the genomic composition of the studied populations. Additionally, this work contributes the first pictures of *Carpobrotus* chromosomes, including the labelling with 5S and 35S rDNA probes.

P.1231 Hybrid seed failure in Arabidopsis arenosa: molecular mechanisms of leaky triploid block

Susnata Salony[1], Filip Kolář[1, 2], Clément Lafon Placette[1]

1 Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic. 2 Czech Academy of Sciences, Institute of Botany, Průhonice, Czech Republic.

Hybrid seed failure due to polyploidization, such as whole genome duplication, is a significant post-zygotic reproductive barrier in plants. The imbalance between maternal and paternal contributions in the endosperm (nourishing tissue in the seeds) often leads to triploid inviability, known as the triploid block, especially in inter-ploidy crosses between diploids and their tetraploid descendants. This phenomenon is frequently observed in mixed-ploidy plants. While the mechanistic basis of the triploid block has been documented in model species, it remains unexplored whether natural ploidy-variable species share a similar mechanism. To investigate this, reciprocal crosses were conducted between diploid and auto-tetraploid *Arabidopsis arenosa*, followed by whole genome transcriptome profiling of young hybrid seeds (collected at 14 days after pollination). Gene ontology analyses revealed distinct pathways associated with reciprocal hybrids. Specifically, photosynthetic machinery-related processes were downregulated in transgressive paternal-excess hybrids, while defense-like responses were upregulated in transgressive maternal-excess hybrids. Notably, the lack of mitochondrial function associated with photosynthetic machinery could be linked to embryo arrest in paternal-excess hybrids as opposed to viable maternal-excess hybrids. These findings provide a foundation for further exploring whether different species share a common molecular mechanism behind the triploid block.

P.1232 New insights into the evolution and hybridization of daffodils using phylogenomic approaches

Ana Valdés-Florido[1], Letícia R. Novaes[1], Lisa Pokorny[2], Violeta Simón-Porcar[1], Enrique Maguilla[3], Gonzalo Nieto-Feliner[2], Isabel Larridon[4], Isabel Marques[5], Cristina Andrés Camacho[1], Zoila Díaz-Lifante[1], Juan Arroyo[1], Marcial Escudero[1]

1 University of Seville, Seville, Spain. 2 Real Jardín Botánico (CSIC), Madrid, Spain. 3 Pablo de Olavide University, Seville, Spain. 4 Royal Botanic Gardens, Kew, Richmond, UK. 5 University of Lisbon, Lisbon, Portugal.

Narcissus L. (Amaryllidaceae), a bulbous Mediterranean genus with ~80 species, has its centre of diversity in the Iberian Peninsula and NW Africa. In spite of abundant studies relying on morphology, karyology and Sanger sequencing approaches, the taxonomy of this morphologically variable genus remains unsettled. This is likely due to the high levels of natural hybridization *Narcissus* presents, as well as the extensive artificial selection it has been subject to, given its ornamental use, and further scape into the wild. The advent of high-throughput sequencing (HTS) technologies, coupled with the development of high-performance computing (HPC) approaches (to process the resulting wealth of data), have made it possible to address the evolution of complex groups, such as *Narcissus*. In here, we (i) implement both RADseq (with the *SbfI* restriction enzyme) and Hyb-Seq (with the universal Angiosperms353 probe set) approaches, (ii) reconstruct the phylogeny of this genus and address sources of phylogenomic conflict, relying on maximum likelihood based on concatenated gene sequences and multispecies coalescent (MSC) methods, as well as phylogenetic networks; and (iii) analyse diversification drivers in this emblematic Mediterranean genus, focusing on hybridization. Hyb-Seq was used to process 192 accessions, while 176 accessions were analyzed using RADseq, representing 58 and 56 taxa, respectively. Our bioinformatic workflow reconstructs the phylogenetic history of the genus with much higher resolution than previous attempts. Additionally, we compared the topologies obtained under either approach (Hyb-Seq vs. RADseq) and were able to confirm hybridization events within *Narcissus*. Our results shed light on the taxonomy, systematics, and evolution of *Narcissus*, and will inform further studies on critical aspects of its reproductive ecology, for which this genus is of paramount importance.

S.134. PRESERVATION AND PROMOTION OF TRADITIONAL ECOLOGICAL KNOWLEDGE IN THE ERA OF OPEN SCIENCE: BENEFITS AND CHALLENGES

P.1233 Communitarian experiences of biodiversity conservation in the Lacandon and Guatemalan Jungles. Diverse History of Salicaceae Sex Chromosomes

Deyan Wang[1], Yiling Li[1], Jiale Zhao[1],Wenlu Yang[1],Mengmeng Li[1],Lei Zhang[1],Ran Zhou[2], Brian J Sanderson[3], Ken Keefover-Ring[4], Tongming Yin[5], Lawrence B Smart[6], Stephen P DiFazio[2], Jianquan Liu[1], Matthew Olson[3], Tao Ma[1]

1 Key Laboratory for Bio-Resource and Eco-Environment of Ministry of Education & Sichuan Zoige Alpine Wetland Ecosystem National Observation and Research Station, College of Life Science, Sichuan University, Chengdu, China. 2 Department of Biology, West Virginia University, Morgantown, USA. 3 Department of Biological Sciences, Texas Tech University, Lubbock, USA. 4 Departments of Botany and Geography, University of Wisconsin-Madison, Madison, USA. 5 The Key Laboratory of Tree Genetics and Biotechnology of Jiangsu Province and Education Department of China, Nanjing Forestry University, Nanjing, China. 6 Horticulture Section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva, USA.

Salicaceae species have extremely diverse sex determination systems and frequent sex chromosome turnovers, providing an ideal model for studying the origin and evolution of plant sex chromosomes. Over the past few years, we have studied the sex determining systems and sex determining regions of multiple species using the phylogenetic relationships of Salicaceae as a framework. By accurately assembling the sex determining regions of these species, we conducted a comparative analysis of their sequence composition, gene content, and expression differences between males and females. The results showed that most of the sex chromosomes of these species originated recently, and there were significant differences in the sequence composition and gene content of their sex determining regions. The diversification history and possible driving forces of sex chromosome turnovers in Salicaceae were further analyzed through comparisons between species. Our studies improved the evolutionary trajectory of sex chromosomes in Salicaceae species, explore the evolutionary forces driving the repeated turnovers of their sex chromosomes, and provide a valuable reference for the study of sex chromosomes in other species.

P.1234 Taxonomic analysis of the useful native flora of Mexico through the BADEPLAM ethnobotanical database

Luis A. Bernal-Ramírez[1], Diana G. Flores-Camargo[2], Andrea Martínez-Ballesté[2]

1 CONAHCyT - Jardín Etnobotánico y Museo de Medicina Tradicional Centro INAH Morelos, Mexico. 2 Jardín Botánico, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, Mexico.

There is a close relationship between biological and cultural diversity in Mexico, which allows an ideal setting for the study of biocultural processes. The ethnobotanical database Base de Datos Etnobotánicos de Plantas Mexicanas (BADEPLAM) of the Botanical Garden at the Institute of Biology, UNAM, systematizes biocultural information in this country for more than 40 years. The analysis of their data allows us to understand the taxonomic trends in the use of biodiversity with original distribution. We validate the quality of the information by verifying the accepted taxonomic names. Synonyms and misspelled names were corrected. The distribution attributes of the species and the IUCN risk categories were assigned

through specialized information. BADEPLAM has 6950 species distributed in 1929 genera and 248 families, where 85% are native and only 15% exotic. The useful native flora in Mexico amounts to 5936 species, of which 1841 are endemic and 2137 are in some IUCN risk category. The best represented families are Fabaceae, Asteraceae and Poaceae, a pattern that persists in a large part of the ethnofloristic lists of the country and throughout America. The native floristic richness used is equivalent to 25% of all Mexican flora, which can be compared with that of other regions such as China, where 28% of its flora is used, a fact worth highlighting if we consider that the Chinese territory is four times larger than the Mexican. We infer that there are cultural coincidences in both nations, such as the relevance of traditional medicine and the consumption of foods with significant cultural value.

S.135. PRIORITISE, PLAN, ACT AND MONITOR PROMOTING AN INTEGRATED APPROACH TO THREATENED TREE CONSERVATION

P.1235 Population census of oak Quercus humboldtii Bonpl. (Fagaceae) in the Botanical Garden of Popayán-Colombia

Luis Gerardo Chilito López[1,2,*] Julieth Alexandra Chacón Paja[2]

*1 Botanical Garden of Popayán, Popayan, Colombia. 2 Popayán University Foundation, Popayan, Colombia. *luis.chilito@docente.fup.edu.co – jardinbotanico@fup.edu.co.*

The oak forests in Colombia are of great importance due to the ecological dynamics that they contain, and they also have a series of threats that have led them to be endangered. In the department of Cauca there are some oak relics and one of them is located in the Botanical Garden. The objective was to determine the population census of Quercus humboldtii Bonpl., in the Botanical Garden of Popayán. During the months of April to July 2022, the total count of individuals was carried out in different ex situ collections, in situ of the botanical garden and areas surrounding crop covers, taking as data: circumference at chest height, total height, cover of canopies and analysis of population structure, vertical stratification, and diameter distribution, dispersion pattern, phytosanitary status, abundance and density using the Acocks scale. The data were stored in an Excel spreadsheet. A total of 128 individuals registered. The ex situ Arboretum collection recorded 22 individuals (17%), the in situ Renacer microbasin 75 (58.5%), Corazones microbasin 2 (1.5%), Wettú 16 (12.5%) and areas surrounding crops 13 (10%). The vertical stratification 60% are found in the tree canopy stratum (18-25 m), the diameter distribution was recorded with 58% in class 2 (56 -110 cm), four stages were structured (seedlings, juveniles, adults 1 and adults 2), the dispersion pattern was grouped and 95% are in good phytosanitary condition. In terms of density and abundance, the Acocks scale presents occasional significance with 11 individuals/hectare. The distribution shows that the species' habitat has suffered alterations due to fragmentation of forest covers, due to the influence of anthropic factors, generating low abundance and regenerants, little connectivity between them and changes in the population structure.

P.1236 The timbre, Acaciella angustissima (Mill.) Britton & Rose (Fabaceae), is a potential flagship species for conserving and restoring

Rafael F. del Castillo1, Sonia Trujillo-Argueta[1]

1 CIIDIR Oaxaca, Instituto Politécnico Nacional, México.

Conserving and restoring semi-desertic shrublands are urgent due to the increasing land use pressure. These ecosystems are biodiversity rich, offer important ecosystem services, and are sources of useful species the local people. Promoting flagship species, i.e., "taxonomically distinctive, threatened, and charismatic species that can serve as icons for conservation efforts" is a promising strategy. Usually, flagship species are animals. Yet, some plant species fulfil the above characteristics. We explore this possibility in the timbre, *Acaciella angustissima*. This species is dominant in Mesoamerican scrublands, such as those of Central Valleys of Oaxaca, Mexico, which have been severely deforested by land use change and urbanism. Thus, conservation and restoration actions are urgently needed. We obtained the DNA barcode using *rbcla* and *MATK* of this species. Through photographic records and interviews with local people, we collected the uses of this species and gathered information about the plants, fungi, and animals directly associated with this species in Monte Albán, Oaxaca. The DNA sequences and their metadata were deposited in GenBank and BOLD. BLAST analyses gave 100 % similarity to sequence registers for *A. angustissima*. At least two vines and two bromeliads use this species for support. The timbre is associated with at least 35 insect species belonging to Hemiptera (6), Coleoptera (4), Lepidoptera (10), Diptera (4), Hymenoptera (2), and Orthoptera (4), through phytophagy (plant sap, leaves, or nectar), predation, pollination, cleptoparasitism, or support. At least four lichen morphospecies grow on the timbre cortex. *Zopherus nodulosus* (coleoptera) camouflages with the lichen *Heterodermia diademata,* which lives on the timbre cortex. Timbre is a main source of firewood, and exclusively hosts the tigrillo *Umbonia reclinata* a rare edible hemiptera. *Acaciella angustissima* is a valuable flagship species that provides shelter, food, or other resources to >40 species, including humans.

P.1237 Climate modelling as a tool for conservation in highly threatened regions: a case study for the Euro-Mediterranean

Giovanni B. Ferreiro-Lera[1], Aitor Álvarez-Santacoloma[1], Ángel Penas[1], Sara del Río González[1,2]

1 Department of Biodiversity and Environmental Management (Botany), Faculty of Biological and Environmental Sciences, University of León, León, Spain. 2 Mountain Livestock Institute (CSIC-ULE), León, Spain.

CMIP6 General Circulation Models (GCMs), the most recent cutting-edge climate open-access models from the World Climate Research Program (WCRP; https://esgf-node.llnl.gov/search/cmip6), outperforms its predecessors with improved simulated atmospheric circulation. However, species distribution studies are hardly in line with these developments. In fact, it is uncommon to assess the performance of the climatic models prior to their incorporation into Species Distribution Models (SDMs). Nevertheless, to avoid the "*garbage in-garbage out*" effect of SDMs, present and projected climatic data must be reliable. In this context, finding which GCMs are optimal for a specific study area at an appropriate resolution is essential. Furthermore, in regions highly threatened from both climatic and ecological perspectives, such as the European Mediterranean, risk assessments for species and habitats need to be as close to reality as possible to adopt early and effective protection and land management measures. In this study, 25 CMIP6 GCMs have been assessed regarding their ability to simulate Euro-Mediterranean bioclimate. Using a bioclimatic approach instead of raw climatic parameters will allow correlating changes in bioclimatic units with potential changes in Mediterranean vegetation. Köppen-Geiger and Rivas-Martínez bioclimatic classifications, as well as the ERA5-Land reference database, were applied. Skill-Scores (SS) used included chi-square value, Heidke SS, Peirce SS and Gerrity SS. ACCESS-EMS1-5, BCC-CSM2-MR and IPSL-CM6A-LR proved to be the most suitable globally. Subsequently, a consensus Random Forest model was obtained. This model was projected for three scenarios (SSP1-RCP2.6, SSP2-RCP4.5, and SSP5-RCP8.5) and three future timeframes (short, medium, and long term). Key findings in this regard include: i) loss of Temperate climates in favor of Arid/Mediterranean; ii) an increase in arid-thermal climates on the south; and iii) an increase in continental climates. With this synthesis we want to highlight the potential of modern climate simulations as part of an integrated approach to plant conservation.

P.1238 An integrated protocol for the non-invasive comprehensive characterization of the root system together with its interactors

Gabriella Sferra[1], Daniele Fantozzi[1], Dalila Trupiano[1], Gabriella S. Scippa[1]

1 University of Molise, Pesche, Italy.

Plant growth and development rely on the plastic response to abiotic and biotic interactors. In this perspective, the plants are considered as a part of an ecological unit which resilience is based on the mutual interaction among the unit components. A comprehensive analysis of the different units together with relationships among them would be beneficial to link the different unit functionalities with the overall performance of the plant, especially in the case of trees. Nowadays, specific demands about ecosystem services drive afforestation and reforestation projects in the direction of effective operational strategy (where and how use specific tree species) combined with careful tree management/monitoring and this is taking particular relevance due to the increasing urbanization process and due to the climate change scenario characterized by exacerbate impacting events. In this perspective, the root system is pivotal in the forest ecosystem functioning and the possibility to evaluate root health is crucial not only to tree stability and management but also to the safety of forests and environments in both urban and non-urban contexts. Thus, as part of the recovery and resilience plan (PNRR) driven by National Biodiversity Future Center (NBFC) of which the University of Molise (UNIMOL) is partner, we developed and tested an innovative non-invasive tool to identify and map the root system and to analyze its interactions with the biotic and abiotic components. We combined traditional methods based on the inspection of root morphology and physiology descriptors with bioinformatics-assisted methods which rely on omics data analysis and integration with imaging-based data and modelling. Collected data implement a database of root functional traits that will be exploited by machine learning approaches to model or to infer growth and developmental trends.

P.1239 Nutritional status of Pinus sylvestris and Quercus pyrenaica is improved in heterospecific neighbourhoods

Marina Tallón[1], Carmen Ureña[1], M. Esther Pérez-Corona[1], Enrique Andivia[1]

1 Departamento de Biodiversidad, Ecología y Evolución, Facultad de Ciencias Biológicas, Universidad Complutense de Madrid, Madrid, Spain.

Tree species admixture is considered as a key management strategy for improving forest ecosystem functioning under climate change due to niche complementarity between species. Mixing species with different leaf habit can increase carbon and nutrient stocks in forest soils. However, the effect of admixture on tree nutritional status has been less explored. In this study, we compared the foliar nutrient status of Pinus sylvestris and Quercus pyrenaica in mixed and monospecific stands in Mediterranean mountains. Our results showed interspecific differences in foliar nutrient concentration. Pines showed higher C concentrations while oaks had higher P concentrations in leaves, which resulted in higher C:N and N:P in pines. Despite no significant differences were found in the nutritional status of study species between mixed and monospecific stands, we found an improvement in the nutritional status of the trees of both species in mixed stands as the proportion of basal area of the other species increased in the vicinity. These results show that complementarity between these two species occurs at the local scale, which has practical implications for the design of forest management actions aimed at diversifying monospecific stands.

S.136. RANUNCULALES: FROM MORPHOLOGY TO PHYLOGENOMICS AND EVODEVO

P.1240 Alkaloid evolution in Ranunculales: a literature mining approach

Laetitia Carrive*[1], Karina Gonçalves-Gaspar[2], Pierre Champy[2], Sophie Nadot[2]

1 Université de Rennes, Rennes, France. 2 Université Paris-Saclay, Orsay, France.

Ranunculales are an order of angiosperms comprising ca. 4,500 species including common plants like buttercups and poppies. This order displays a vast diversity of specialized natural products, mainly alkaloids. For example, species containing isoquinolines such as opioids and curares, or diterpenoid alkaloids such as aconitins, have been used respectively as painkillers and narcotics, arrow hunting poisons, and animal managing poisons. These molecules may have played an important role in plant evolution, as they provide defense against herbivores. Although there is a rich phytochemical and ethnobotanical literature on specialized natural products, surprisingly little is known about their evolution. Here we explore this literature using a "literature mining" approach. We compare this strategy of dataset building to using a well referenced database (Dictionary of Natural Products). Substances found in Ranunculales are treated as phenotypical characters. Ancestral states are reconstructed on a phylogeny, and the presence of phylogenetic signal is tested. Results strongly vary among classes of molecules, from random evolution to well-supported synapomorphies for some clades. We state that adaptive hypotheses should be discussed in the light of the phylogenetic pattern of the characters they involve. This study also raises questions about the coding of chemical characters: how categories should be defined and how absence should be dealt with. The evolution of phytochemical characters opens new prospects for the understanding of plant natural history.

P.1241 How cell division orientations achieve branching chirality in leafy liverwort: 3D tissue analysis and mathematical modeling

Naoya Kamamoto[1], Koichi Fujimoto[1], Masaki Shimamura[1]

1 Hiroshima University, Higashi-Hiroshima, Japan.

The bryophyte apical stem cell (AC) rotates the division plane and arranges its differentiated daughters (merophytes) on the growing axis. When a merophyte divides to initiate a branch apical cell (bAC) in leafy liverworts, bAC also divides rotationally in a specific direction to develop shoot branching, depending on the initiation position. A bAC is initiated from the divided half at the forward side of the main axis rotation (anodic) produces the identical rotational orientation (homodromy), whereas that at the backward side (kathodic) produces the opposite rotational orientation (antidromy), indicating two types of branching chirality. Although branching chirality is a hallmark of the genera, how to achieve the chirality from bAC initiation position through bAC division rotation remains to be elucidated. Here we generated a 3D map of cell geometry, topology, and cell lineage of *Kurzia makinoana* to assess their roles in the division orientation and chirality. We found that AC rotational divisions are stably oriented in both the main axis and branches, even if the cell shapes are irregular. In contrast, the merophyte division orientation follows the own shape asymmetry or sometimes disrupted at branching, probably related to the irregular shape. These observations suggest that the division orientation in merophytes varies depending on the own geometry, while that in AC is regulated independently of its geometry. To infer how the AC rotational divisions achieve the branching chirality, we developed a mathematical model assuming that the age of surrounding cell walls biases the bAC division orientation. These model simulations reproduced that the bAC derived at the anodic and kathodic side inevitably resulted in homodromy and antidromy, respectively. These results suggest that geometry-dependent merophyte division initiates the age-dependent AC division rotation to achieve branching chirality thereby controlling the species diversity.

P.1242 Evolution of pollen in the Adesmia clade (Leguminosae, Dalbergieae)

Higor Antonio-Domingues[1,2], Ana Paula Fortuna Perez[3], Monica L Rossi[4], Rafael Felipe de Almeida[1], Adriana P Martinelli[4], Gwilym P. Lewis[1], Cynthia F.P. Luz[2]

1 Royal Botanic Gardens, Kew, United Kingdom. 2 Instituto de Pesquisas Ambientais, São Paulo, Brazil. 3 Universidade Estadual Paulista, Botucatu, Brazil. 4 Universidade de São Paulo, Piracicaba, Brazil.

Legumes comprise different pollen morphological types due to Leguminosae being one of the most diverse families of flowering plants. Taxa of the Adesmia clade (Papilionoideae, Dalbergieae) have been extensively palynologically studied in the last few years, evidencing pollen morphology's taxonomic relevance in this group. Building on these studies, we scored, coded, and mapped 16 pollen characters related to general morphology, ultrasculpture and ultrastructure into the most recent molecular phylogeny of the Adesmia clade. Quantitative and qualitative palynological data were also scored from our results for the ingroup (*Adesmia*, *Amicia*, *Poiretia*, *Nissolia* and *Zornia*) and outgroup (*Tipuana* and *Pterocarpus*) genera. All lineages of the Adesmia clade were recovered with at least one or more pollen homoplasies/apomorphies, except for *Adesmia*. The Adesmia clade was morphologically supported by colporus length, operculum ultrasculpture and nexine thickness. The Adesmia + ZAP clade (*Zornia* + *Amicia* + *Poiretia*) was supported by endoaperture length and the latter by features of the polar and equatorial axes. The remaining genera are characterised by nexine thickness (*Poiretia*), endoaperture type (*Amicia*), P/E, endoaperture type, and operculum ultrasculpture (*Zornia*). Morphological synapomorphies for *Adesmia* were unclear due to the reduced sampling in a genus with 206 accepted species. Even though most characters were found to be homoplastic across the Adesmia clade, they helped characterise all clades and most genera of this informal group. Future pollen studies on the Adesmia clade will enable the scoring and coding of additional characters and the proposition of a new classification system (subtribal) for this group.

P.1242 Testing different strategies to efficiently assemble high-quality plant genomes

Karbstein, Kevin[1,2,4*], Tomasello, Salvatore[1], Wagner, Natascha D.[1], Barke, Birthe H.[1], Paetzold, Claudia[3], Bradican, John P.[1,2], Preick, Michaela[5], Himmelbach, Axel[6], Stein, Nils[6,7], Irisarri, Iker[8,9,10], Pucker, Boras[11], Jan de Vries[8,9,12], Hörandl, Elvira[1]

*1 University of Göttingen, Albrecht-von-Haller Institute for Plant Sciences, Göttingen, Germany. 2 University of Göttingen, Georg-August University School of Science (GAUSS), Göttingen, Germany. 3 Senckenberg Naturhistorische Sammlungen, Dresden, Germany. 4 Max Planck Institute for Biogeochemistry, Jena, Germany. 5 Institute for Biochemistry and Biology, University of Potsdam, Potsdam, Germany. 6 Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben/Seeland, Germany. 7 Center of integrated Breeding Research, Germany. 8 University of Göttingen, Institute for Microbiology and Genetics, Göttingen, Germany. 9 University of Göttingen, Campus Institute Data Science, Göttingen, Germany. 10 Leibniz Institute for the Analysis of Biodiversity Change, Hamburg, Germany. 11 TU Braunschweig, Institute of Plant Biology, Braunschweig, Germany. 12 University of Göttingen, Göttingen Center for Molecular Biosciences, Göttingen, Germany. *kkarb@bgc-jena.mpg.de.*

Currently, it is still a challenge - in terms of laboratory effort and cost, as well as assembly quality - to reliably reconstruct large and complex genomes from non-model plants. This often hampers the study of evolutionarily complex groups characterized by hybridization, polyploidy, and/or apomixis. The large polyploid *Ranunculus auricomus* complex (Ranunculaceae) is an angiosperm model system for the study of apomixis, evolution, and biogeography. However, neither plastid, mitochondrial nor high-quality nuclear genomes are available, limiting phylogenomic, ecological, and taxonomic analyses. We tested different Illumina short-read, Oxford Nanopore Technology (ONT) or PacBio (HiFi) long-read, and Illumina-ONT/PacBio hybrid assembly approaches on the diploid species *R. cassubicifolius*, a sexual progenitor of the *R. auricomus* complex. Here, we will predominantly show results of different genome assembly strategies in terms of completeness, contiguity, and BUSCO quality scores. The best of 14 strategies will be presented in detail, which is characterized by >99% completeness with a haploid genome size of 3.2 Gbp, 99% single-copy and duplicated complete BUSCO genes found, a median contig length (N50) of 20 Mbp, and 40k predicted genes. The genomic information presented here helps to improve phylogenomic analyses in this species complex, and will enable advanced functional, evolutionary, biogeographic, and population genomic analyses for the *R. auricomus* complex, the genus, and beyond in Ranunculaceae in the future.

S.137. RECENT ADVANCES IN THE MEGADIVERSE LEGUME SUBFAMILY PAPILIONOIDEAE

P.1243 Evolution of pollen in the Adesmia clade (Leguminosae, Dalbergieae)

Higor Antonio-Domingues[1,2], Ana Paula Fortuna Perez[3], Monica L Rossi[4], Rafael Felipe de Almeida[1], Adriana P Martinelli[4], Gwilym P. Lewis[1], Cynthia F.P. Luz[2]

1 Royal Botanic Gardens, Kew, United Kingdom. 2 Instituto de Pesquisas Ambientais, São Paulo, Brazil. 3 Universidade Estadual Paulista, Botucatu, Brazil. 4 Universidade de São Paulo, Piracicaba, Brazil.

Legumes comprise different pollen morphological types due to Leguminosae being one of the most diverse families of flowering plants. Taxa of the Adesmia clade (Papilionoideae, Dalbergieae) have been extensively palynologically studied in the last few years, evidencing pollen morphology's taxonomic relevance in this group. Building on these studies, we scored, coded, and mapped 16 pollen characters related to general morphology, ultrasculpture and ultrastructure into the most recent molecular phylogeny of the Adesmia clade. Quantitative and qualitative palynological data were also scored from our results for the ingroup (*Adesmia*, *Amicia*, *Poiretia*, *Nissolia* and *Zornia*) and outgroup (*Tipuana* and *Pterocarpus*) genera. All lineages of the Adesmia clade were recovered with at least one or more pollen homoplasies/apomorphies, except for *Adesmia*. The Adesmia clade was morphologically supported by colporus length, operculum ultrasculpture and nexine thickness. The Adesmia + ZAP clade (*Zornia* + *Amicia* + *Poiretia*) was supported by endoaperture length and the latter by features of the polar and equatorial axes. The remaining genera are characterised by nexine thickness (*Poiretia*), endoaperture type (*Amicia*), P/E, endoaperture type, and operculum ultrasculpture (*Zornia*). Morphological synapomorphies for *Adesmia* were unclear due to the reduced sampling in a genus with 206 accepted species. Even though most characters were found to be homoplastic across the Adesmia clade, they helped characterise all clades and most genera of this informal group. Future pollen studies on the Adesmia clade will enable the scoring and coding of additional characters and the proposition of a new classification system (subtribal) for this group.

P.1244 A PhyloCode-based system for infrageneric classification of Astragalus (Fabaceae)

Nasim Azani[1], Daniele Buono[2], Diego F. Morales-Briones[2], Gudrun Kadereit[2], Anne Bruneau[3], Martin F. Wojciechowski[4], Shahin Zarre[1]

1 Department of Plant Science, University of Tehran, Tehran, Iran. 2 Fakultät für Biologie, Ludwig-Maximilians-Universität München, Munich, Germany. 3 Institut de Recherche en Biologie Végétale, Université de Montréal, Montreal, Canada. 4 School of Life Sciences, Arizona State University, Tempe, USA.

With about 3,000 species worldwide, *Astragalus* (Fabaceae) stands out as a highly diverse genus of flowering plants distributed throughout Eurasia and the Americas, representing a remarkable example of rapid species-level continental radiations. The genus is well-known for its complicated taxonomic history associated with outstanding ecological and morphological variation. In such big genera, recognizing infrageneric taxa is essential to achieve identification and an effective classification of species. Phylogenetic studies utilizing different nuclear and plastid markers have demonstrated that neither the traditional subgenera nor most of the previously recognized sections are supported as monophyletic. Here, we reconstruct the phylogenetic relationships of major clades within *Astragalus* based on analyses of a dataset of 400 taxa using both nuclear rDNA region (ITS) and plastid *trnK*/*matK* gene sequences to produce a new clade-based classification that reflects the current knowledge of relationships in the genus. Although the relationships among the clades, especially among nested lineages, are still not well resolved, the composition of the main clades remains consistent across all studies. In this updated classification system, the clade names chosen are primarily based on the former subgeneric groups

represented by the current constituent taxa. However, selecting other names from classical literature was necessary for some clades. Thus, within the currently defined monophyletic *Astragalus*, we recognize 12 well-supported subclades: *Glottis*, *Pseudosesbanella*, *Phaca*, *Trimeniaeus*, *Hamosa*, *Contortuplicata*, *Hemiphragmium*, *Cercidothrix*, *Brachylobium*, *Astracantha*, *Diholcos* and *Hypoglottis*. It is worth mentioning that 11 of these subclades are Eurasian in origin and distribution while about 450 species found in the Americas (the so-called Neo-Astragalus) are nested within the *Diholcos* clade, which also comprises a subclade of predominantly annual or short-living perennials showing a Mediterranean-North African distribution.

P.1245 Strategies for rediscovering missing species in the Brazilian Cerrado: a case study with Lupinus

Tânia M. Moura[1], Daniel P. Silva[1], Anderson R. Silva[1], Marcelo F. Simon[2]

1 Instituto Federal Goiano, Urutaí, Brazil. 2 Embrapa Recursos Genéticos e Biotecnologia, Brasília, Brazil.

Five of the thirteen *Lupinus* species occurring in the Brazilian Cerrado are endemic to this biome. Three species are known from some occurrences: *L. elaphoglossum* (1), *L. ovalifolius* (2), and *L. insignis* (3). We questioned whether the climatic conditions of Cerrado are still suitable for the occurrence of these endemic species or not. *Lupinus elaphoglossum* and *L. insignis* were last collected 50 years ago, while *L. ovalifolius*, known from only its type collection, was finally re-collected after 207 years (the last collection known in 2020). We used statistical models and methods based on time series and principal component analysis to determine areas suitable for the occurrence of *L. elaphoglossum* and *L. insignis*. Forty-nine environmental variables were gathered to predict the distribution of these two species. We analyzed climatic variation using data from several weather stations. We detected suitable areas where these two species may occur. We have detected that the maximum and the mean wind speeds were the only significant environmental variables, allowing us to infer the areas with the weather conditions most similar to those where the species were registered. Cerrado is still climatically suitable for these endemic species of *Lupinus*. Still, other physical or biological factors not considered here might influence the peculiar pattern of occurrence of these species in Cerrado. The five species of *Lupinus* endemic to the Cerrado were assessed as endangered or critically endangered according to the IUCN criteria. Our study suggests that additional rare taxa might be missing from the red list, requiring more conservation attention.

P.1246 Taxonomic and spatiotemporal evolutionary studies on liquorice (Papilionoideae, Glycyrrhizeae) based on genomic data

Lei Duan[1], Hong-Feng Chen[1], AJ Harris[1], Jun Wen[2]

1 South China Botanical Garden, Chinese Academy of Sciences, Guangdong, Guangzhou, China. 2 Department of Botany, Smithsonian Institution, Washington, USA.

Liquorice was represented by the tribe Glycyrrhizeae. Its long, strong root has been widely has broad economic importance for its utility in traditional medicine, as well as modern pharmaceutical products, cosmetics, food additives, and popular confectioneries. This tribe widely distributes in every continent except for Antarctica, but its spatiotemporal evolutionary history was unclear, also, its inter-tribal, inter-generic and inter-specific taxonomy are controversial. First, based on NGS data, we reinstated the long-forgotten tribe Glycyrrhizeae, including two genera: *Glycyrrhiza* and *Glycyrrhizopsis*. Then, by integrating machine-learning-based image recognition with phylogenetic analyses of chloroplast genomes and low-copy nuclear genes, which is the first application of the approach in plant systematic study, we merged the Central Asian endemic *Meristotropis* into *Glycyrrhiza* (13 species), and recognized two species within the Anatolian endemic *Glycyrrhizopsis*. Third, our historical biogeographic study indicated that the liquorice tribe was originated in Tethys region during the late Eocene. A vicariance event, possibly a response to the uplifting of the Turkish-Iranian Plateau, may have driven the divergence between *Glycyrrhiza* and *Glycyrrhizopsis* in the Middle Miocene. The third and fourth main elevations of the Qinghai-Tibetan Plateau may have led to the rapid radiation within *Glycyrrhiza*, the genus dispersed to eastern Asia, North America (through Bering Land Bridge), South America and Australia via long-distance dispersal during the Pliocene. The ancestor of *Glycyrrhiza* lacked glycyrrhizin, a key secondary metabolite that marks the medicinal efficacy of liquorice, and revealed that presence of glycyrrhizin evolved twice within *Glycyrrhiza*. Only the Old World medicinal clade is qualified for the medicinal liquorice, and according to solid molecular phylogenetic results, we treated the whole clade as the same species, *G. glabra*. The morphologically diverse species experienced rapid radiation and massive hybridization within the last million years, providing a good model for study on reticulate evolution.

P.1247 Erythrina L. (Phaseoleae, Papilionoideae, Leguminosae) of the world: a synoptic nomenclatural revision

Ramon Guedes-Oliveira[1], Ana Paula Fortuna Perez[2], Leandro C. Pederneiras[3], Vidal F. Mansano[3]

1 Escola Nacional de Botânica Tropical, Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 2 Departamento de Biodiversidade e Bioestatística, Universidade Estadual de São Paulo, Botucatu, Brazil. 3 Diretoria de Pesquisas, Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil.

Erythrina L. consists of a papilionoid legume genus whose species are spread across the tropical and subtropical regions of the world in a wide variety of habitats, from savannah lowland vegetations to dense moist montane forests. Before the establishment of the genus by Linnaeus in “Genera Plantarum”, the species were generally known as “coral trees” or “Corallodendron” in America, and “Mouricou” or “Gelala” in Asia. Since the first binomial names published for the genus in Linnaeus’ “Species Plantarum”, many authors around the world have made several works regarding *Erythrina* species across the centuries, from regional floras to taxonomic treatments, describing dozens of new species, besides the publication of new genera which were based on species of the genus. However, we acknowledged that many issues still remained concerning the nomenclatural status of many published names in *Erythrina*. Hence, we carried out a comprehensive search for all the scientific names, protologues, and type specimens related to the species of the genus, resulting in 412 names. After the revision, we recognize 119 species and four subspecies for the world, proposing 83 new lectotypes (74 first-step, nine second-step), two epitypes, and 21 new synonyms. Of the 412 names analyzed, we maintained 258 as synonyms, nine as unplaced, and excluded 26 of them for several reasons. For the Neotropical region, we recognize 72 species and two subspecies, proposing 34 new lectotypes and six new synonyms. For the African region, we recognize 35 species and one subspecies, proposing 39 new lectotypes, two epitypes, and three new synonyms. For the Asian-Pacific region, we recognize 15 species and one subspecies, proposing 10 new lectotypes, and 12 new synonyms. This work highlights the importance of digital databases, herbaria, and libraries, which made it possible for us to easily analyze protologues and preserved specimens from all over the world.

P.1248 Late Quaternary climate-change velocity in the areas of endemism of the orchids of Megamexico

Brandon E. Gutiérrez-Rodríguez[1], Marilyn Vásquez-Cruz[2], Victoria Sosa[1]

1 Red de Biología Evolutiva, Instituto de Ecología, Xalapa, Mexico. 2 Tecnológico Nacional de México ITS de Irapuato, Irapuato, Mexico.

Megamexico is a biogeographic region characterized by an elevated biodiversity, complex geological history, rugged topography, and climatic heterogeneity that have favored the presence of 1,732 species of orchids; more than half are endemic. The objective of this study is to determine whether climatic stability differed in areas of endemism from surrounding areas, to understand the role of climate in the maintenance of these areas of endemism for the orchids distributed in this biogeographic region. Areas of endemism and phylogenetic endemism were determined, and climate change velocity was estimated. A database was compiled to identify current climate preferences and multivariate analyses were carried out to identify the most significant variables. Climate change velocity was calculated in R using Climetric. The relationship between climate change velocity and areas of endemism was determined by regression analysis. Results showed that climate change velocity was low in the most important areas of endemism and phylogenetic endemism located in the southeast of Mexico in Chiapas, along with an area in of Guatemala and another in Nicaragua. These areas have probably acted as refuges over evolutionary time for the Orchidaceae of Megamexico, so they should be considered important in conservation planning.

P.1249 Understanding drivers of diversification in Astragalus (Fabaceae) on the Colorado Plateau of Western North America

Ross A. McCauley[1]

1 Department of Biology, Fort Lewis College, Durango, USA.

With over 120 species and 60 endemic taxa, the Colorado Plateau is a center for species diversification of *Astragalus* in North America. To help understand the patterns and drivers of speciation in this region, I focused on a set of 60 species occurring within a radius of ca. 150 km from the Four Corners, where the US states of Arizona, Utah, Colorado, and New Mexico meet near the center of the Colorado Plateau. Geographical distribution, species morphological characteristics, and substrate preferences were analyzed for each taxon. This data was combined with separate molecular phylogenies based on nuclear (ITS and ETS) and chloroplast (*ycf1*) regions. Analysis shows that diversification is driven my multiple factors including edaphic specialization, pollinator shifts driven by change in floral color, geographic isolation, and interspecific hybridization. These analyses help to provide insight into the patterns of species diversification and the environmental and organismal interactions giving rise to evolutionary novelty in this speciose group.

P.1250 Similar but not the same: Floral and inflorescence ontogeny in the Adesmia clade (Dalbergieae, Leguminosae)

Thiago Cobra e Monteiro[1], Marcus J.A. Falcão[2], Vidal F. Mansano[2], Ana Paula Fortuna Perez[1]

1 Departamento de Biodiversidade e Bioestatística, Universidade Estadual Paulista, Botucatu, São Paulo, Brazil. 2 Instituto de Pesquisas do Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil.

Papilionaceous flowers with a banner, two wing petals, and two fused keel petals, which involve the gynoecium and the androecium, characterize the subfamily Papilionoideae. However, changes in size and color and structural variations such as developmental suppressions, abortions, reductions, torsions, or acquisition of floral parts occur in Papilionoideae. Those changes are driven by pollinator preferences and protection against herbivory (e.g., pollen and nectar pillars and seed predators). In the Adesmia clade of tribe Dalbergieae, the flowers are yellow and papilionaceous and do not change much between genera except for some androecium variations (free stamen in *Adesmia* and heteroanthery in *Zornia* and *Poiretia*). However, after conducting floral and inflorescence ontogeny of one representative of four of the five genera within the clade, we found several unique features. All species investigated have short plastocrony between the development of sepals and other floral organs, which is highly abnormal in Papilionoideae. *Nissolia longiflora* presented a unique inflorescence type, never described accurately before. *Adesmia psoraleoides* did not present bracteoles development, and the calyx has a lateral initiation. These two rare features suggest a morphogenetic role of the bracteoles shaping the unidirectional sepal development in other Papilionoideae. We also found disk-shaped nectaries in *N. longiflora* and *A. psoraleoides*, a novel feature for the Adesmia clade that may be a useful morphological character to taxonomy. *Poiretia coriifolia* and *Zornia reticulata* present distichous inflorescences, with two well-developed bracteoles and abortion of the bract early in development. Both genera do not present disk-shaped nectaries, but *Zornia* has osmophores in the standard petal. Secondary pollen presentation occurs in *Poiretia* and *Zornia* but is more pronounced in *Zornia,* where it appears to have the same phases of development reported to *Crotalaria juncea*.

P.1251 Bioprospecting in both domestic and wild species of the genus Vigna Savi: the Bowman-Birk inhibitors

Elisa Toini[1,2], Davide Panzeri[1,2], Giovanni Zecca[1,2], Massimo Labra[1,2], Fabrizio Grassi[1,2]

1 Università degli studi Milano Bicocca, Milano, Italy.
2 National Biodiversity Future Center, Palermo, Italy.

The *Vigna* Savi genus, of the Fabaceae family, includes different important crops, such as *Vigna unguiculata* (cowpea), *Vigna angularis* (adzuki bean), and others. They can grow in dry climates and poor soils, and their seeds are abundant both in nutrients and nutraceutical compounds. Variants of these plants are also present in the wild while the majority of the *Vigna* species were never domesticated. Among the useful compounds of these plants are the Bowman-Birk protease inhibitors (BBI), molecules produced as defensive mechanism against insect attacks. Various nutraceutical effects of these proteins on humans have been demonstrated, including chemopreventive and anticarcinogenic ones. This study analysed the natural genetic variability of two BBI isoforms in different species of the genus *Vigna*. In particular, the two isoforms encode for a trypsin-trypsin BBI, characterized by two trypsin-specific domains (BBI-TT) and the second one, a trypsin-chymotrypsin BBI, characterized by one trypsin and one chymotrypsin-specific domain (BBI-TC). For this purpose, the sequences of both genes were first obtained from 12 published genomes. Then DNA was extracted from 44 *Vigna* species and different primers were used to amplify and then sequence both genes. Ultimately, the BBI-TT were obtained from 34 species, revealing 55 haplotypes corresponding to 40 isoforms and 32 mature proteins. Meanwhile the BBI-TC were obtained from 40 species, revealing 70 haplotypes corresponding to 56 isoforms and 39 mature proteins. A phylogenetic tree of both genes was constructed to study their evolution and to apply an ancestral sequence reconstruction analysis. Furthermore, sites under selective pressure were identified with different algorithm approaches. In conclusion, this work provided insights about the evolution of these genes in *Vigna* and allowed the detection of several natural forms of BBI. These natural proteins could potentially be used to improve the defences of cultivated plants or for pharmaceutical and nutritional purposes.

S.139. RELICT PLANT VULNERABILITY TO CLIMATE CHANGE

P.1253 Vulnerability and mesomorphy of selected tropical plants: A guide to choice of plant for desert encroachment control and revegetation

Jonathan O. Adinde[1], Osita J. Uche[1], Uche J. Anieke[1]

1 Enugu State Polytechnic, Iwollo, Enugu State, Nigeria.

Desert encroachment is a major challenging environmental problem facing sub-sahara Africa resulting in climate change and conflicts between farmers and herders. Attempts to control it through tree planting often fail due to wrong choice of plants among other factors hence, the need for the application of Wood anatomy indices in the choice of plants. In the study, Vulnerability and Mesomorphy of selected tropical plants namely: *Ixora coccinea*, *Gmelina arborea*, *Pentaclethra macrophylla* and *Ceiba pentandra* were studied to determine their adaptability to desert encroached areas. Slides of transverse sectioned samples and macerated samples from the plants were prepared and viewed under light microscope with 20 replications. Vessel diameter, vessel length and vessel density per square millimeter of the plants were observed for each of the samples and used to calculate Vulnerability and Mesomorphy values. The results showed that *Gmelina arborea* has vessel diameter of 203.4μm, vessel length of 378.2μm, vessel density of 7.85, high Vulnerability value of 25.91 and high Mesomorphy of 9,799.162. *Pentaclethra macrophylla* has vessel diameter of 379.8μm, vessel length of 304.6μm, vessel density of 16, high Vulnerability values of 23.74 and high Mesomorphy value of 7,230.44. *Ceiba pentandra* has vessel diameter of 229.2μm, vessel length of 697.8μm, vessel density of 6.8, high Vulnerability value 33.71, high Mesomorphy values 23,522.84, while *Ixora coccinea* has vessel diameter of 113.4μm, vessel length of 216.8μm, vessel density of 161.9, low Vulnerability value of 0.6877 and low Mesomorphy value of 149.09. The relationship between Vulnerability and Mesomorphy values and plants adaptability in conditions of water stress was discussed. Gmelina arborea, *Pentaclethra macrophylla* and *Ceiba pentandra* with high mesomorphy and vulnerability values are vulnerable to water stress condition characteristic of desertified areas while *Ixora coccinea* with low mesomorphy and vulnerability values is not vulnerable to water stress condition.

P.1254 Life cycle and phenological growth stages in Arum rupicola in its natural habitat based on BBCH scale in three consecutive years

Sajad Alipour[1], Nasim Safari[1]

1 Department of Horticultural Science, Faculty of Agriculture, Ferdowsi University of Mashhad, Mashhad, Iran.

Studying the phenology of valuable native plants is very important and effective for better introduction and protection of theirs. *Arum rupicola* Boiss. is one of the native bulbous plants with ornamental and medicinal value. According to BBCH (Biologische Bundesanstalt, Bundessortenamt und CHemische Industrie) scale, from sprouting to winter rest, six main principal stages are described for sprouting, leaf development, inflorescence emergence, flowering, fruit development, fruit maturity, senescence and beginning of dormancy. This research was done from January 2020 to December 2023. Data on this study were collected once a week in the course of the vegetative season and with a 30-day interval during the dormant season. The results showed, sprouting was approximately the same in three consecutive years (late February). In comparison to the second and third years, the leaves' development and inflorescence appearance occurred ten days earlier in the first year. In the first year, blooming occurred in the first decade of May but in the second and third year it occurred after 15 May. Also, seed capsule formation was recorded ten days earlier in the first year (late of May). The summer dormancy approximately occurred in late spring in three consecutive years. And, the results of t-test showed that there were significant differences in leaf number, plant height, flower stem length, and flower diameter in the first years in comparison with the second and third year (P ≤ P.5). Therefore, the aim of this study is to investigate the phenological stages of the Arum rupicola in order to deeper understanding of the climate change effect on the growth cycle of this vulnerable species.

P.1255 Seed biology of relict Juniperus drupacea in the westernmost area of its global distribution (Mt. Parnon, Greece)

Evangelia N. Daskalakou[1], Spyridon Oikonomidis[2], Costas A. Thanos[2]

1 Institute of Mediterranean Forest Ecosystems, Hellenic Agricultural Organization - DIMITRA, Athens, Greece. 2 Department of Biology, National and Kapodistrian University of Athens, Athens, Greece.

Juniperus drupacea Labill. is a dioecious tree (or shrub) predominantly found in Turkey, Syria, Lebanon, and Israel, with its European native range limited to Greece, specifically in Mt. Parnon and a small section of Mt. Taygetos (SE Peloponnese). In Europe, *J. drupacea* is classified as endangered (EN) by the IUCN Red List, facing primary threats such as sapling grazing, timber overexploitation, and climate change. Cone collections of *J. drupacea* were carried out during the fall (Oct-Nov) over a 4-year period (2020-2023). For the examination of cone and seed morphology, 20 mature cones were randomly gathered from 10 sites across the entire massif of Mt. Parnon. An additional batch of 829 cones was analysed for the seed count per cone. The average cone mass was determined to be 3539 mg, each cone containing 1-5 sound seeds (average of 2.3 seeds per cone), with an average seed mass of 33.9 mg. Furthermore, seeds underwent varying periods of pre-chilling (up to 32 weeks) and were subsequently germinated at 15 °C in darkness. In addition, germination was tested without pre-chilling at two alternating temperatures (25/15 and 20/10 °C, 12/12 h) and the effect of GA_3 (1000 ppm) on germination, with or without prior chilling, was investigated as well. *J. drupacea* seed germination is indifferent to light conditions and although chilling for up to 16 weeks leads to a faster germination rate, final germination percentage is not increased compared to non-chilled seeds. Based on viability tests (TTZ), seeds stored within the woody cones (with their external leathery layer either intact or removed) demonstrated high viability for a long period (>15 yrs). Finally, experimental data are analysed through the lenses of both climate change and conservation purposes.

P.1256 Will warming affect the reproduction of plants at high elevations in the Andes?

Karol D. Dueñas-F[1], Eloisa Lasso[1]

1 Laboratorio de Ecología y Fisiología Vegetal, Departamento de Ciencias Biológicas, Universidad de Los Andes, Bogota, Colombia.

Páramos are tropical high-mountain ecosystems particularly vulnerable to global warming. Páramo plants sustain a diverse array of animals, regulate the local climate, and trap and retain water, ensuring that the páramo acts as a key water reservoir for the region. Successful reproduction is essential to ensure the continued existence of these plants and the services they provide. Hence, it is pivotal to understand how warming will impact their reproductive biology to understand the potential effects of climate change on biodiversity and ecological stability in the Tropical Andes. To this end, we studied the reproduction of plants that have been growing for seven years inside open-top chambers (OTCs) and in control plots beside them. These OTCs act as greenhouses, warming the air temperature by approx. 2°C, simulating the temperatures expected at the end of this century. We followed the phenology of *Arcytophyllum nitidum, Castilleja integrifolia, Diplostephium phylicoides, Geranium multiceps, Pernettya prostrata, Vaccinium floribundum* and *Valeriana pilosa* to understand if flowering time is changing in response to warming. Additionally, we recorded flower, fruit, and seed production for *P. prostrata, V. floribundum* and *C. integrifolia* in warmed and control plots. We assessed female fertility by analyzing ovule production and male fertility by evaluating the amount of viable pollen. Two species, *V. pilosa, and D. phyllodes,* flowered earlier in warmer conditions. Most species reduced flower and fruit production in warmer conditions. Ovule production was not affected by the warming, but some species show a lower percentage of pollen grain germination. Seed quality seems to decrease in the OTCs. Preliminary data indicates that the reproduction of some Páramo species will be negatively affected by warming. The findings from this research are crucial to assess if páramo plants can maintain theirpopulations over time in a warmer world and provide valuable insights for conservation.

P.1257 A new infrageneric classification of Paullinia (Paullinieae, Sapindaceae)

Pedro Acevedo-Rodríguez[1], Genise Somner[2], Joyce G. Onyenedum[3], Chun Su[3]

1 Department of Botany, Smithsonian National Museum of Natural History, Washington, USA. 2 Universidade Federal Rural do Rio de Janeiro, Departamento de Botânica, Rio de Janeiro, Brazil. 3 Department of Environmental Studies, New York University, New York, USA.

Paullinia (Sapindaceae) is a monophyletic genus of tendrilled climbing plants that currently include about 220 species native to the Neotropics from Mexico south to northern Argentina and the Antilles. The infrageneric classification of *Paullinia* dates back to the work of Radlkofer (1895, 1931) who proposed 13 sections, primarily based on fruit morphology. Recent analyses based on two molecular markers and the sampling of few species (5-22%) suggest that most of Radlkofer's sections are polyphyletic, as the resulting clades cluster together species that may have either similar or different fruit morphologies. In this study, we generated new nuclear DNA sequence data, covering ~56% of species, using target sequence capture method with the Angiosperms353 universal probe set. Through the analyses of coalescence-based and concatenated phylogenetic trees, constructed from the 353 recovered genes across 271 samples (126 species), we expect to resolve the intrageneric relationships within *Paullinia.* The resulting topologies will be evaluated on the light of all possible morphological characters in order to propose an infrageneric classification for the genus.

P.1258 Floral glands anatomy, fragrance, and pollinators in two sympatric species of Pilocarpus (Rutaceae)

Éllen S. Garcia[1,*], Anelize Barboza[1], Mariana T. Araújo[1], Maria JF Caliman[1], Milton Groppo[1].

1 Department of Biology, Faculty of Philosophy, Sciences and Letters at Ribeirão Preto, Universidade de São Paulo, Brazil.[*]ellengarcia@usp.br.

Angiosperms use many floral signals that can attract both floral visitors and effective pollinators, such as floral odor, which allows insects to identify flowers as a source of resources. With this in mind, the aim of this work was to study the floral biology of *Pilocarpus pennatifolius* and Pilocarpus spicatus, species from the Rutaceae family, identifying the characteristics used by these species to attract pollinators. To this end, an anatomical study was carried out using cross-sectional histological sections of the flowers, made using a rotary microtome, analysis of floral fragrance compounds using the Solid Phase Microextraction (SPME) technique and a study of floral visitors using the "Fixed Sample" observation method. As a result, both species had the nectary fused to the ovary, but only visually distinguishable in *Pilocarpus pennatifolius*, which also had a greater number of stomata and secretory cavities, as well as the presence of druses and papillose epidermis, not, observed in *Pilocarpus spicatus*. Both species presented compounds belonging mainly to the terpene group in their fragrances. *Pilocarpus pennatifolius* had ten more compounds (37), with trans-caryophyllene having the highest concentration (24.89%). In *Pilocarpus spicatus*, the compound with the highest relative percentage was alpha pinene (42.18%) and, in both species, the compound alpha cubebene had the lowest concentration, P.2% and 0.16%, respectively. In *Pilocarpus pennatifolius*, 13 more families of flower visitors were observed, the most representative being the order Diptera. These data suggest that, in the species studied, the quantity of compounds in the fragrances and their unique combinations may interfere with the diversity and quantity of floral visitors and, consequently, with effective pollinators. Finally, this study reaffirmed the information obtained about the species, as well as defining the compounds that make up the fragrance of *Pilocarpus spicatus*.

P.1259 Laticifers in vascular plants

Erika Prado[1], Diego Demarco[1]

1 Department of Botany, Institute of Biosciences, University of Sao Paulo, Sao Paulo, Brazil.

Laticifers are specialized latex-secreting structures whose primary function is defense against herbivory and microorganisms. Laticifers are found in several families of vascular plants and have taxonomic and phylogenetic importance. However, several misinterpretations are found in the literature, in which laticifers had been reported for families that do not have them. Thus, a review of this secretory structure is needed to access its real distribution and evolution. The aim of this study was to characterize and distinguish laticifers from other secretory structures, identifying their typology, ontogeny and distribution. We analyzed 63 families described as having at least one latescent species but confirmed the occurrence of latex in only 34 families, many times without phylogenetic relationship. This finding showed that laticifers appeared multiple times in the evolution of vascular plants. We demonstrated that 18 so-called latescent families actually have resin ducts or secretory idioblasts. All laticifers investigated are articulated and can be classified as anastomosing or non-anastomosing, branched or unbranched. No evidence of non-articulated laticifers and intrusive autonomous growth was observed. Our results contributed significantly to the knowledge on laticifers and promotes a better understanding of their distribution, mode of growth, and evolution in vascular plants.

P.1261 Occurrence of bundle sheath extensions in leaves of Anacardiaceae

Rosa Mateos Escobar[1], Teresa Terrazas[1]

1 Universidad Nacional Autónoma de México. Mexico City, Mexico.

Bundle sheath extensions are vertical prolongations of the bundle sheath that contact one or both epidermises. In the presence of extensions, the leaf is termed heterobaric; in their absence, it is termed homobaric. The presence of bundle sheath extensions has an impact on the mechanical and physiological properties of the leaf (when the extensions contact both epidermises the gas exchange in the mesophyll is diminished). The tissue that constitutes extensions can be parenchyma, sclerenchyma, or collenchyma. It has been reported that heterobaric leaves are most likely found in shrubs and trees at the top of the canopy and in canopy gaps, whereas homobaric leaves have been associated with species growing in sub-canopies and understories. Since most of the species in Anacardiaceae are shrubs or trees we hypothesize that the leaves of the family are heterobaric. Our purpose was to determine if the presence of bundle sheath extensions is a common feature of the Anacardiaceae. Fifty-eight of the 79 genera recognized in the family were studied. The leaves were removed from herbaria. Cross sections of the medium third part of the leaf blade were made and stained with safranin-fast green. Leaf sections were analyzed under bright field and polarized light microscopy. Bundle sheath extensions were identified in 93% of the studied species. Only 10 species in 8 different genera, as *Drymicarpus*, *Operculicarya*, and *Solenocarpus*, lack extensions. The type of cells in the extensions varies, being more than 80% of sclerenchyma. Most of the species possessing extensions are shrubs and trees of the canopy. Homobaric leaves occur in monotypic genera, such as *Haplorhus* and *Malosma*, and polytypic genera, as in the case of *Buchanania* and *Mangifera*. It is concluded that bundle sheath extensions are a conserved trait in the Anacardiaceae.

S.141. SEEDS, SALINITY AND SURVIVAL: A FUNCTIONAL PERSPECTIVE

P.1262 Understanding the increase of plant density of Hoffmannseggia aphylla (Fabaceae): Evidence of "el niño Southern oscillation" years

Felipe S. Carevic[1,2], Roberto Contreras[2,3]

1 Laboratorio de Ecología Vegetal, Facultad de Recursos Naturales Renovables, Universidad Arturo Prat, Iquique, Chile. 2 Millennium Nucleus on Applied Historical Ecology for Arid Forests, Santiago de Chile, Chile. 3 Centro Regional de Investigación y Desarrollo Sustentable de Atacama, Universidad de Atacama, Copiapó, Chile.

Studies on the natural regeneration of plant species under hyperaridity conditions have been scarce, mainly because of the low germination percentage of the species under these conditions. Presumably, sporadic phenomena such as the El Niño Southern Oscillation (ENSO) could have a positive effect on the natural germination of these species, although this effect has not yet been satisfactorily explored. To test the crucial assumption of our statement, a hyperarid region (average rainfall below 5 mm/year) was used as a model to determine the effect of ENSO years on the natural regeneration rate of adult individuals of the endemic legume Hoffmannseggia aphylla (retama) in the Atacama Desert, northern Chile. Thus, the vegetation density of an endemic leguminous species in a sector of the Pampa del Tamarugal, Tarapacá Region, northern Chile, was analyzed for six years. The density of this species increased during ENSO years, mainly dueto water flows from the highest sectors of the Tamarugal pampas, such as the town of Pica, in addition to the increase in humidity and summer rainfall. Our results highlight the transcendence of the ENSO in the regeneration of leguminous plants.

P.1263 Salinity tolerance of seeds and seedlings and their integration in a biosaline production system aimed at dry forest restoration

Bárbara F. Dantas[1]

1 Embrapa Semiárido, Petrolina, Brazil.

Dry forests are highly threatened by climate change and agricultural pressures. The Brazilian Caatinga is a largely threatened, highly complex, diverse and endemic dry forest ecosystem, which is vulnerable to desertification and has surpassed the longest drought (2011-2022) in the past 100 years. Drought and deforestation have decreased c. 40% the amount of original surface potable water over the last 35 years and groundwater is usually brackish. In the desalination process, besides the potable water, a highly saline and pollutant water (brine) is generated, which can be used in biosaline agriculture with careful monitoring of crops and soil. We propose a '*biosaline restoration*' by an alternative use of non-potable brackish water to produce native tree seedlings for Caatinga revegetation. In this study we selected species and tested several alternative sources to potable water to irrigate forest seedlings in nurseries, which have high water expenditure. The trail was performed in a completely randomized design with three irrigation water sources (biosaline fish cropping water; brackish groundwater and tap water) and four replications with five seedlings. We found Fabaceae species which have fast germinating salt tolerant seeds had similar seedling growth in tap or brackish water. Also, an irrigation water source with conductivity levels of up to 7 dS.m^{-1} did not compromise the seed germination and seedlings growth of the Caatinga native Fabaceae *Anadenanthera colubrina* (Vell.) Brenan; *Cenostigma pyramidale* (Tul.) Gagnon & G.P.Lewis; *Cenostigma microphyllum* (Mart. ex G.Don) Gagnon & G.P.Lewis and *Erythrina velutina* Willd. Furthermore, biochar, produced from agro-industrial waste, can be added to the substrate to enhance seedlings tolerance; minimize the effect of brackish water on development; promote the sequestration of C in the soil and increase water and nutrient retention. This therefore is an alternative and low input technique for restoration aiming native tree seedling production.

P.1264 Mechanisms of tolerance to increasing levels of salinity in Spartina patens (Aiton) Muhl. seedlings

Adrián Sapiña-Solano[1], Oscar Vicente[1], Monica Boscaiu[2], Mario X. Ruiz-González[1], Sara González Orenga[1,3,4]

1 Universitat Politècnica de València, Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Valencia, Spain. 2 Universitat Politècnica de València, Instituto Agroforestal del Mediterráneo, Valencia, Spain. 3 Universidade de Vigo, Departamento de Bioloxía Vexetal e Ciencias do Solo, Facultade de Bioloxía, Vigo, Spain. 4 Universidade de Vigo, Instituto de Agroecoloxía e Alimentación, Ourense, Spain.

Invasive species are promoters of biodiversity loss and ecosystem degradation worldwide. Coastal habitats such as dunes, saltmarshes and wetlands, have become highly threatened environments. The Mediterranean basin is very vulnerable to biological invasions, due to altered conditions as consequence of climate change effects. In addition to their ability to outcompete native vegetation and efficient dissemination strategies, invasive species typically exhibit high levels of stress tolerance. On the coast of the Valencian Community can be found an invasive species native to the Atlantic coast of North America that has spread worldwide, due to its rapid propagation in the last few decades, *Spartina patens* (Ait.) Muhl. Thus, it deserves special attention, particularly in protected areas like the Albufera Natural Park included in Natura 2000. Its colonisation reduces ecosystem's biodiversity and has an impact on vulnerable or protected species, e.g., the reduction of *Limonium albuferae* populations, a critically endangered species, was detected during the last years. Both native and invasive species are exposed to climate change effects such as salination and drought. Plants face abiotic stresses by displaying different mechanisms: 1) the regulation of the cellular osmotic pressure through ion transport, regulation of photosynthetic pigments concentration and the change in osmolytes concentration; 2) the inactivation of reactive oxygen species (ROS) to face oxidative stress by the activation of enzymatic and non-enzymatic antioxidant machinery. Understanding the tolerance of invasive plants to abiotic stress might contribute to ecosystem management and conservation policies. *S. patens* was sampled from Albufera Natural Park (València, Spain) and exposed to 0, 200, 400, 600 and 800 mM of NaCl for 18 days. When plants began to show signs of withering, we recorded biomass parameters and analysed their mechanisms of tolerance. The blockage of sodium, chloride and calcium at the root level was the main defence against salt of *S. patens*

P.1265 Tolerance and recovery capacity to water and salt stress of Juncus balticus, a dominant Salar de Atacama salt flat plant

Adrian Sanhueza[1,2], Francisco A. Squeo[1,2]

*1 Biology Department, University of La Serena, Chile.
2 Institute of Ecology and Biodiversity, Chile.*

In Andean salt flats (Salar), water deficit conditions and high salinity can negatively affect plants' fitness, inhibiting them. These conditions could be likely aggravated by industrial activity and climate change. To understand the vegetation Salar plant's cope mechanisms to this type of stress, we made an experiment of hydroponic growing of Juncus balticus, adding different concentrations of polyethylene glycol and NaCl that reach waters potentials of 0, -1, -1.5, -2 and -2.5 MPa, simulating rising intensities of water deficit and high salinity conditions. After two months under these conditions, half of the plants were subjected to a recovery stage, in which we maintained them in a nutrient solution at a water potential of 0 MPa. Our results show that below a water potential of -1.5 MPa, plant growth stops and below -2 MPa, plant survival drops below 50%. Aswell thus, the results were confirmed by another functional traits measurement performed. On the other hand, the recovery study found that plants can restart growth through aerial biomass turnover, however, this growth is less vigorous in plants subjected to lower water potentials and in those subjected to salt stress.

P.1266 Salinity tolerance strategies of the halophyte Suaeda maritima during seed germination

Charlotte Seal[1], Camille-Madeleine Szymansky[1,2], Adele Muscolo[3], Margaret Yeo[1], Louise Colville[1], Innes Clatworthy[4], Tobias Salge[4]

1 Royal Botanic Gardens, Kew, UK. 2 University of Toulouse III Paul Sabatier, France. 3 Mediterranean University of Reggio Calabria, Italy. 4 Natural History Museum, London, UK.

Coastal ecosystems, such as saltmarshes, provide a number of ecosystem services including a critical role in 'blue' carbon storage, but are under threat from global sea level rise. Their vegetation is comprised of halophytes, salt-tolerant plants, that are exposed to high concentrations of salt and frequent flooding. Many halophytes naturally regenerate from seed, yet the combination of traits associated with salinity tolerance in seeds is still poorly characterised. Here, we focus on elucidating two mechanisms that are commonly utilised by adult halophyte plants: (1) ion accumulation and elemental localisation, and (2) enhanced antioxidant capacity to protect against oxidative stress, in seeds of the saltmarsh halophyte *Suaeda maritima* during over-wintering and germination. Our approach uses a halotime model to characterise the saline germination niche, along with techniques in microscopy, spectrometry and biochemistry to provide a mechanistic understanding. We show that seeds of *S. maritima* utilise seawater to their benefit during germination, thriving in highly saline environments.

S.142. SOLANACEAE: BIOLOGY, SYSTEMATICS AND EVOLUTION

P.1267 Preliminary cytological studies in the tribe Browallieae (Solanaceae)

David Hoyos[1], Rocío Deanna[1,2], Franco Chiarini[1]

1 Instituto Multidisciplinario de Biología Vegetal, Córdoba, Argentina. 2 Departamento de Ciencias Farmacéuticas, Facultad de Ciencias Químicas, UNC, Córdoba, Argentina.

Browallieae belongs to the subfamily Cestroideae and comprises *Browallia* L., with 23 accepted species, and the monotypic *Streptosolen* Miers. Although the tribe is monophyletic, its genera do not form separate clades. The cytological knowledge for this group is limited to chromosome counts for three species, two diploids (2n = 22) and one tetraploid (2n = 44) whereas chromosome measurements are known for only one species. Karyotype analyses can elucidate synapomorphies among the tribes of Cestroideae and provide evidence to clarify the boundaries between species of Browallieae. We aim to infer ploidy level and chromosome morphology for the three most conflictive species of Browallieae: *B. americana* L., *B. speciosa* Hook. and *S. jamesonii* (Benth.) Miers. Chromosome preparations were made from root meristems and pretreated in 8-hydroxyquinoline. The basic chromosome number of the three species was x = 11; *B. americana* and *S. jamesonii* are diploids and *B. speciosa* is a tetraploid; this latter presented the highest chromosomal asymmetry indexes. Concerning size, we recorded chromosomes between 0.9–6.4 µm, where diploids had the longest and the tetraploid species the smallest chromosomes. Assuming x=12 as the basic number of the family Solanaceae, our results suggest at least two events of chromosome rearrangements:

one number reduction in the divergence of Browallieae and its sister clade Cestreae, and another one in the divergence of Cestreae, whose basic number is x=12. The differentiation between *Browallia* and *Streptosolen* may be limited to small cumulative cryptic rearrangements, which are not evident with classical techniques. In addition, ploidy level played an important role in the differentiation of species within Browallieae. Our chromosome data supports the similarity between *Browallia* and *Streptosolen*, already noticed in molecular phylogenies, and outstands the importance of integration of cytological analyses with molecular and morphological evidence to resolve circumscription problems in Browallieae.

P.1268 Preliminary phylogenetic hypothesis of the genus Chamaesaracha (Solanaceae)

Camila Ogas[1], Carolina Callegari[1], Rocío Deanna[1]

1 Instituto Multidisciplinario de Biología Vegetal (UNC-CONICET), Córdoba, Argentina.

Chamaesaracha (A.Gray) Benth. is a genus that belongs to the tribe Physalideae and is native to the United States, Mexico, and Central America. It contains 12 species with conflictive taxonomic circumscription. These species are herbs with flowers with yellowish-white rotate corollas, and fruiting calyx appressed around a greenish berry. *Chamaesaracha* is not monophyletic; most of the taxa form a clade of 'arid' species, sister to the genus *Quincula* Raf., but a single species escapes this main clade and is closely related to other genera in *Physalideae* (*C. rzedowskiana* Hunz. with *Leucophysalis* Rydb., *Capsicophysalis* (Bitter) Averett & M.Martínez, and *Cataracta* Zamora-Tav., O.Vargas & M.Martínez). However, the major taxonomic challenges lie at the species level due to morphological similarities that make the specific limits diffuse. Therefore, our objective was to resolve the circumscription of the species by incorporating more collections and molecular data. DNA was extracted from at least three populations of 10 species, and four molecular markers (*Leafy*, *waxy*, *trnLF*, ITS) were amplified. Alignments and phylogenetic analyses were conducted using Maximum Likelihood. Sequences available in Genbank were added, including one species of each genus of the subtribe Physalidinae. *Lycianthes* (Dunal) Hassl. was used as the outgroup. The subtribe resolves as in previous phylogenetic studies, obtaining a non-monophyletic *Chamaesaracha.* Within the genus, the clades resolved were poorly resolved, highlighting the need for more molecular data to resolve this complex group. Most of the species resulted in non-monophyletic taxa, although we found two clades clearly distinguished by their indumentum. Although we did not resolve the species' circumscriptions, this is the basis for further studies integrating genomics with morphological information to resolve the relationships and propose taxonomic changes.

P.1269 Building a global online multi-access identification key to the mega-diverse and economically important genus Solanum

Rebecca Hilgenhof[1], Sandra Knapp[2], Leandro Giacomin[3], Xavier Aubriot[4], Eric J. Tepe[5], Lynn Bohs[6], Iris E. Peralta[7], Christopher T. Martine[8], Rocío Deanna[9], Franco Chiarini[9], Gloria Barboza[9], Yuri Gouvêa[10], João R. Stehmann[10], Andrés Orejuela[11], Clara I. Orozco[11], Tiina Särkinen[1]

1 Royal Botanic Garden Edinburgh, 20a Inverleith Row, Edinburgh, United Kingdom. 2 Natural History Museum, London, United Kingdom. 3 Departamento de Sistemática & Ecologia, Universidade Federal da Paraíba, Cidade Universitária, Paraíba, Brazil. 4 Université Paris-Saclay, CNRS, AgroParisTech, Écologie, Systématique et Évolution, Orsay, France. 5 University of Cincinnati, Department of Biological Sciences, Cincinnati, U.S.A. 6 University of Utah, Department of Biology, Salt Lake City, U.S.A. 7 Faculty of Agricultural Sciences, National University of Cuyo, Luján, Mendoza, Argentina; and IADIZA CCT CONICET Mendoza, Argentina. 8 Department of Biology, Bucknell University, Lewisburg, U.S.A. 9 Instituto Multidisciplinario de Biología Vegetal (CONICET-UNC), Córdoba, Argentina. 10 Departamento de Botânica, ICB, Universidade Federal de Minas Gerais, Minas Gerais, Brazil. 11 Instituto de Ciencias Naturales, Universidad Nacional de Colombia, Bogotá, Colombia.

Identification keys are important taxonomic tools that aid in the identification of unknown biological entities to varying ranks. Traditional dichotomous keys are limited by their single point of access, where the sequence and structure of identification steps and characters used are fixed by the author. Those that address large numbers of taxa become lengthy and complex to follow, making their application challenging, especially when dealing with species-rich groups that display high intraspecific plasticity. *Solanum* is a genus of such magnitude. With 1,245 currently accepted species displaying high morphological diversity, it is considered a mega-diverse genus. Accurate identification is crucial within this economically important group, which includes the cultivated tomato and potato as well as many other crops and crop wild relatives. To aid with the identification of *Solanum* species, we have built two freely available global online multi-access identification keys constructed using the taxonomic management software Xper^3. The first key allows the identification of all 68 clades currently recognized within *Solanum*. The second serves to identify 752 individual species, including all non-spiny species worldwide, as well as African and Asian spiny species. To enable effective identification, we recorded geography for each taxon, in addition to 52 characters covering 21 vegetative and 27 reproductive structures. Terminology used within the keys is explained using both text and photographic plates, rendering the keys user-friendly for both experts and non-experts alike. The *Solanum* keys are hosted at the Solanaceae Source website, where users can access detailed information such as individual species descriptions and photographs. The species-level key presented here is a first identification key framework for *Solanum* and will be followed by “add-ons” for the groups that are still lacking up-to-date taxonomic treatments such as, for example, the Geminata, New World spiny, and Australian spiny clades.

P.1270 The value of morphological traits to separate species in Cestrum (Solanaceae)

Hector J. Lazarte[1], Carla Maldonado[1], Rocío Deanna[2]

1 Herbario Nacional de Bolivia, Instittuo de Ecología, Carrera de Biología, Universidad Mayor de San Andrés, La Paz, Bolivia. 2 Instituto Multidisciplinario de Biología Vegetal, Córdoba, Argentina.

Cestrum L. is a genus of Solanaceae widely distributed throughout the Americas. Extending from southern Florida to Chile, *Cestrum* is the second largest genus of Solanaceae, reaching almost 220 species. Less than 40 species (ca. 15%) of *Cestrum* have been included in the phylogeny of the family and a small section was further studied. Previous results have shown unresolved topologies or with very low support, even including multiple molecular markers. Our objective was to test if species phylogenetically unresolved with only molecular markers, can be separated using morphological characters. To pursue this, we morphologically analyzed and compared five closely related species found in Bolivia resolved as a polytomy in the last phylogenetic studies. We recovered 17 continuous and three discrete characters for 10 specimens of these five species: *C. strigulatum, C. concglomeratum, C. reflexum, C. rigidum and C. megalophylum.* The data were obtained through measurements in Image J and analyzed using a Non-metric Multidimensional Scalling (NMDS) in R. *Cestrum reflexum and C. rigidum* exhibited strong morphological similarities, particularly emphasizing the size of the corolla in both species. Notably, *C. rigidum* was the only species consistently found with stipules among the five studied. Additionally, *C. conglomeratum* and *C. megalophyllum* displayed remarkable similarity, mainly due to their larger leaves compared to other species. *Cestrum megalophyllum* stood out prominently in this category. Conversely, *C. strigulatum* was the only species that did not show clear morphological similarities with the other analyzed species. The NMDS analysis revealed distinctive morphological similarities of these species, allowing us to identify clusters that correspond to each species and providing a deeper insight into their Similitudes.

P.1271 Unraveling the molecular basis of andromonoecy induction under heat stress conditions in Solanum melongena

Silvia Manrique[1], Gloria Villanueva[1], Marina Martínez-López[1], Mariola Plazas[1], Pietro Gramazio[1], Miguel Chapa[1,2], Aureliano Bombarely[2], Santiago Vilanova[1], Jaime Prohens[1]

1 Instituto Universitario de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Valencia, Spain. 2 Instituto de Biología Molecular y Celular de Plantas (CSIC-UPV), Valencia, Spain.

Climate change poses a significant challenge to global agriculture, and the Mediterranean region is particularly susceptible to its adverse effects. In this context, understanding plant responses to stress becomes imperative for mitigating yield losses. Several species of the genus *Solanum*, exhibit andromonoecy, a sexual system characterized by the coexistence of hermaphrodite and male flowers. Specifically, *Solanum melongena* displays functional andromonoecy, where "male" flowers possess a non-functional gynoecium because the reduced development of the stigma and the style avoids the fertilization of the ovules. Under heat stress conditions, there is an observed increase in functionally-male flowers, suggesting that this increase is a mechanism to optimize resource allocation in response to environmental challenges. Our lab developed an early-flowering, dwarf eggplant variety, ("Micromel,") more amenable for molecular studies. Utilizing Micromel plants, we performed transcriptomic and metabolomic analyses on pistils of flowers grown under control or heat stress conditions. Our findings reveal that heat stress induces autophagy, contributing to the increase of functionally-male flowers. Understanding the molecular mechanisms underlying the induction of functional andromonoecy in response to heat stress not only provides insights into plant reproductive strategies but also offers avenues for enhancing stress tolerance in agricultural systems. By deciphering how plants allocate resources under stress, we can develop strategies to mitigate the impacts of climate change on plants both for agricultural and conservation purposes.

P.1272 Exploring morphological variation in three related species of Solanum sect. Petota ser. Commersoniana and ser. Tuberosa (Solanaceae)

Rodrigo Nicolao[1], Morgan R. Gostel[2], Caroline M. Castro[3], Gustavo Heiden[3]

1 Universidade Federal de Pelotas, Pelotas, Brazil. 2 Botanical Research Institute of Texas, Fort Worth, USA. 3 Embrapa Clima Temperado, Pelotas, Brazil.

Solanum sect. *Petota* (Solanaceae) comprises potatoes *(S. tuberosum),* the third most important food crop on Earth, five domesticated potato species, and 107 wild relatives. Potatoes are widely distributed in the Americas. *Solanum* sect. *Petota* ser. Commersoniana is unique as one of the few South American groups that occur outside of the Andes, extending into Argentina, Paraguay, Uruguay and Southern Brazil. This group has a complex taxonomic history and the number and rank of taxa belonging to series Commersoniana (currently two spp., *S. commersonii* and *S. malmeanum)* remains unclear. *Solanum chacoense* is sympatric with both species in series Commersoniana, but morphologically distinct and recognized in a distinct taxonomic series Tuberosa. Interestingly, a hybridization event between *S. commersonii* and *S. chacoensehas* been proposed to explain the origin of *S. malmeanum. Solanum commersonii* and *S. malmeanum* (1EBN) are compatible to each other and partially compatible with *S. chacoense* (2EBN) under artificial crosses, but the mechanisms involved and barriers to hybridization are poorly understood. A morphological study was conducted to clarify the taxonomy of *S.* ser. Commersoniana. 254 individuals from *S. chacoense, S. commersonii,* and *S. malmeanum* were studied from herbarium vouchers for comparative morphometric analysis. A multivariate morphometric approach was used to reveal species-specific patterns among 53 morphological traits. Principal coordinates analysis (PCoA) revealed no separation of two morphological groups overall, with *S. chacoense* represented in the first and *S. commersonii* in the second. *Solanum malmeanum* was observed across both coordinates. Canonical discriminant analysis (CDA) identified the most distinct groups, with *S. chacoense* in one group and *S. commersonii* and *S. malmeanum* in another group, but with lower support. Overall classification success rate exceeded 84%. *S. chacoense* is morphologically distinct from *S. commersonii* and *S. malmeanum.* Further molecular and geographic analyses are needed to explore distinction among these wild species of potato.

P.1273 Advancing eggplant genetics, domestication and breeding research through the development of a first MAGIC population

José Luna[1], Andrea Arrones[1], Giulio Mangino[1], Virginia Baraja[1], Mariola Plazas[1], Jaime Prohens[1], Pietro Gramazio[1], Santiago Vilanova[1]

1 Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Valencia, Spain.

Eggplant (*Solanum melongena*) is a globally important crop that, despite its significance, lags behind other important crops in the development of experimental populations for genetics, domestication and breeding research. Addressing this gap, our research team has developed an eight-parent Multiparent Advanced Generation Inter-Cross (MAGIC) population to investigate the genetic architecture of complex traits in eggplant, as well as to provide insights into the domestication process. The parents of this first eggplant MAGIC population are seven genetically diverse accessions of eggplant and one close wild relative (*S. incanum*). The eight parents were intercrossed using a funnel scheme to obtain a segregating eight-way hybrid generation, which was subsequently selfed for five generations using a single seed descent (SSD) approach to maximize variation in the MAGIC population. As a result, 325 S5 recombinant MAGIC lines were obtained, each of which is a genetic mosaic of the eight founder genomes. This S5 generation of the MAGIC has been genotyped using skim whole-genome resequencing at 3X coverage. Furthermore, parental genomes were resequenced at high coverage (20X). Therefore, 433,335 high-quality markers were found to be polymorphic. In addition, the MAGIC population was phenotyped in two environments for 56 traits, which span a wide range of characteristics, from morphological features to fruit composition traits. First results reveal a large variation in the MAGIC population, with new phenotypes and transgressive individuals for many of the traits evaluated. Genome-Wide Association Studies (GWAS) were performed to identify quantitative key genomic regions for the traits evaluated and for identifying novel candidate genes. Apart from the significance of this first eggplant MAGIC population for eggplant research in genetics, domestication and breeding, some of the recombinant MAGIC lines may be of interest for being incorporated into breeding pipelines.

P.1274 Development of an inter-specific MAGIC population combining Solanum lycopersicum var. cerasiforme and S. pimpinellifolium genomes

Andrea Arrones[1], Oussama Antar[1], Leandro Pereira-Dias[1], Andrea Solana[1], Paola Ferrante[2], Giuseppe Aprea[2], Mariola Plazas[1], Jaime Prohens[1], María José Díez[1], Giovanni Giuliano[2], Pietro Gramazio[1], Santiago Vilanova[1]

1 Instituto de Conservación y Mejora de la Agrodiversidad Valenciana, Universitat Politècnica de València, Valencia, Spain. 2 Agenzia Nazionale Per Le Nuove Tecnologie, L'energia e Lo Sviluppo Economico Sostenibile, Casaccia Research Centre, Rome, Italy.

We developed an interspecific Multi-parent Advanced Generation Inter-Cross (MAGIC) population by inter-crossing four accessions each of *Solanum lycopersicum* var. *cerasiforme* (SLC) and *S. pimpinellifolium* (SP) spanning the range of geographical diversity and phenotypic and genetic variation of both taxa. These two taxa are the closest relatives to cultivated tomato *S. lycopersicum* var. *lycopersicum* (SLL), offering a unique opportunity to provide insights into the genetics of traits involved in the early domestication process. Our selection of the eight MAGIC founders was strategically based on representing the genetic diversity and geographical distribution of SLC and SP, maximizing variation in origin, morphology, and genetic diversity. This selection strategy was instrumental in capturing a broad spectrum of diversity, with the founders demonstrating a wide morphological diversity. Whole-genome resequencing of the eight accessions unveiled over 12 million variants, with a significant proportion (46.3%) being private. The MAGIC population, comprising 354 lines developed through successive generations of inter-crossing and selfing, was genotyped using Single Primer Enrichment Technology (SPET) and a new tomato panel developed by ENEA composed by 12k SNPs and resulted in 6,488 polymorphic SNPs. The genotyping data revealed high homozygosity (average 93.69%) and a balanced representation (11.62% to 14.16%) of the founder genomes. GWAS analysis identified strong associations for key domestication traits like fruit weight, plant anthocyanin, and flowering time, pinpointing both previously known and novel QTLs and candidate genes. The new intraspecific tomato MAGIC population has a high potential for tomato researchers and breeders, aiding in the understanding of tomato domestication and allowing the detection of new genes and alleles of potential interest in breeding.

P.1275 Genome and chromosome size evolution on the Cyphomandra clade (Solanaceae): architecture of the genome

Mariela Sader[1], Amalia Ibiapino[1], Mariana Baez[2], Amanda Camara[3]

1 Instituto Multidisciplinario de Biología Vegetal, Universidad de Córdoba-CONICET, Córdoba, Argentina, msader@imbiv.unc.edu.ar. 2 Plant Breeding Department, Bonn University, Bonn, Germany. 3 Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany, camara@ipk-gatersleben.de

Some genomes can accumulate a high number of repetitive sequences. These gather at heterochromatic, inactive regions serving organizational roles beyond forming centromeres and telomeres. But their tendency to aggregate suggests that there must be a limit to their abundance. Over recent years, polymer simulation of chromatin has become a powerful tool to understand chromatin dynamics. Previous models, reproducing the higher compaction of heterochromatic regions compared to euchromatic regions in interphase nuclei, indicate that the differences in compaction drive phase separation. With polymer simulations, we analyzed varied distributions of heterochromatic regions over the genome, regarding nuclear position, compaction, and diffusion to understand their effects on the dynamics of the nucleus and in the evolution of repetitive fractions within a clade. We compare the organization of euchromatin and heterochromatin in the nucleus with a genomic composition analysis, focusing on the repetitive fraction of the genome, in different species of the clade Cyphomandra. This clade is composed of a group of plants within the Solanum L. genus (Solanaceae family), commonly known as the nightshade family. The Cyphomandra clade includes several species of shrubs and small trees native to Central and South America and bears a broad variation in the repetitive fraction of its genomes, Cyphomandra genome sizes mean=10.71 pg, range 6.80-24.80 pg (Solanum genome sizes mean = 1.40 pg, range 0.60-24.8 pg). So, considering this variation in genomic sizes, in this project, we are searching for correlations between the physical nuclear organization of their chromatin and influences on the evolution of the species in this clade.

P.1276 Repetitive DNA in the Cyphomandra clade (Solanum, Solanaceae)

M.A. Sader[1,*], M. Vaio[2], J.D. Urdampilleta[1,**]

*1Instituto Multidisciplinario de Biología Vegetal, Universidad de Córdoba-CONICET, Córdoba, Argentina, 2 Laboratorio de Evolución y Domesticación de las Plantas, Departamento de Biología Vegetal, Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay. * msader@imbiv.unc.edu.ar, **jurdampilleta@imbiv.unc.edu.ar*

The genus *Solanum* is quite diverse, containing a wide range of species including important crops like tomatoes, potatoes, and eggplants, as well as many wild species. The Cyphomandra clade is a group within the *Solanum* (Solanaceae), commonly known as the nightshade family. One of the most well-known members of this clade is *S. betaceum* (tree tomato or tamarillo). Members of the Cyphomandra are typically found in tropical and subtropical regions and their fruits are generally edible and used in culinary applications. Genome sizes (GS) within *Solanum* can vary significantly and Cyphomandra has giant genomes (*Solanum* GS mean=1.40pg, range 0.60-24.8pg, and Cyphomandra GS mean=10.71pg, range 6.80-24.80pg) compared to its cultivated relatives: tomato (*S. lycopersicum,* 950Mb), potato (*S. tuberosum*, 844 Mb) and eggplant (*S. melongena*, 1,120 Mb). Giant genomes are characterized by often containing a high number of repetitive sequences and non-coding DNA. To understand and characterize the repetitive fraction, we sequenced DNA from four species (*S. betaceum, S. glaucophyllum, S. confusum, S. stuckertii)* using low coverage (0.1×). We also estimated the genome size, performed a clustering analysis, and mapped the most abundant repeats using FISH. The estimated GS were 12.5pg, 17.3pg, 21.7pg and 23pg for *S. glaucophyllum, S. stuckertii, S.confusum,* and *S. betaceum* respectively. The repetitive fraction constitutes 54%, 53%, 63%, and 76% of the genome respectively, with the Ty3/gypsy-Tekay retrotransposon being the most abundant except in *S. glaucophyllum* (Ty3/gypsy-Ogre). Furthermore, we identified four distinct satellite DNA families in *S. confusum*, *S. stuckertii* and *S. betaceum*, with 0.45%, 1.93%, and 0.85% of repetitive fraction respectively, and 9 families in *S. glaucophyllum* (1.52%). We observed that in the species exists an accumulation of repetitive DNA sequences, especially retrotransposons, and different satellite families, confirming that these genomes are highly dynamic in their repetitive fraction.

P.1277 Solanaceae: trichome morphology and the acyl-sugar pathway, associations between gene expression and form

Gina P. Sierra-Reyes[1], Federico Roda-Fornaguera[1]

1 Max Planck Tandem Groups. Universidad Nacional de Colombia. Bogotá, Colombia.

Acyl sugars (ASs) are defense metabolites typically found in species with glandular trichomes. They hold great potential as natural pesticides that can enhance adaptability and crop productivity. ASs have a relatively short pathway and few constituents: sugar cores and acyl chains. However, they exhibit a vast diversity and variability within and across species. ASATs are the most crucial enzymes in creating diversity in the ASs pathway. These metabolites have been primarily studied in the Solanaceae family. Specifically, type I/IV trichomes in tomato (*Solanum lycopersicum*) produce ASs. Nevertheless, ASs have been detected in other species with different trichome types. Despite the implicit associations between the morphology of trichomes and the acyl-sugar pathway, the relationship between them has not been tested across species. We have analyzed the transcriptomes of leaf and trichome fraction from 10 species from *Solanum*, and of leaves from 34 species of Solanaceae, which vary between simple, simple glandular, stellate, and stellate glandular trichomes. Through differential gene expression analysis, we found that there is not a perfect match between glandular trichomes and ASATs. This is the case in some *Capsicum, Jaltomata, Lycianthes* and *Solanum* species which did not present glandular trichomes but expressed ASATs. However, there is a tendency to find ASATs in glandular trichomes, for both simple and stellate trichomes. ASATs and trichome types do not seem to be correlated, but some ASATs were more associated with certain genera (*Solanum*, *Brugmansia* and the tribe Physalideae). ASAT4 appears to be present in both glandular and non-glandular trichomes. Using enrichment analysis, we found some possible new enzymes that modified the sugar core of acyl-sugars, belonging to the transferase and glycosyltransferase terms. In the future, we aim to link genes from the acyl-sugar pathway with morphogenic genes of trichomes to better understand their relationship.

P.1278 Evolutionary conservation and functional significance of NLRs in Solanum: insights into plant immune responses

Giuseppe Trotta[1,2], Laura A. Randarevitch[1,3], Laura E. Rose[1,2, 3]

1 Institute for Population Genetics, Heinrich Heine University, Düsseldorf, Germany. 2 iGRAD-Plant. 3 Cluster of Excellence on Plant Sciences (CEPLAS), Germany.

Plants lack a mobile immune system, therefore they must recognize pathogens and deploy defence responses at a cell-autonomous level. This strategy engages resistance genes (R-genes). Some R-genes are dedicated to pathogen perception, while others are dedicated to executing the resistance response. In many cases, the resistance response results in a macroscopic region of cell death, called the hypersensitive response. We evaluated the expression levels of resistance genes within and between species of tomato. Within *Solanum lycopersicum,* a subset of resistance genes is constitutively expressed at low to moderate levels: these genes were defined as “core R-genes”. Two core R-gene groups were conserved across species, suggesting a crucial role in plant defence. Notably, one of these genes is homologous to the *ZAR1* gene in *Arabidopsis thaliana*. The ZAR1 protein forms a pentameric structure upon pathogen detection. This structure is known as the resistosome and functions as a calcium channel, promoting cell death. Another class of resistance genes, including 3 NRCs, appear to function like ZAR1, but emerged more recently, after the division between Rosids and Asterids. Our findings indicate that certain core R-genes are retained over evolutionarily long periods of time and may perform similar or related functions in plant defence. In our poster, we will present data detailing the rate of evolution and patterns of protein substitution observed in these core R-genes within and between groups of Solanum.

S.143. SPATIAL MODELLING OF PLANT NICHES AND DISTRIBUTIONS IN THE ANTHROPOCENE

P.1279 Patterns of floristic inventory and plant collections in Myanmar

Thant Sin Aung[1,2], Alice C. Hughes[3], Phyo Kay Khine[4], Bo Liu[5], Xiao-Li Shen[1], Ke-Ping Ma[1,2]

1 State Key Laboratory of Vegetation and Environmental Change, Institute of Botany, Chinese Academy of Sciences, Beijing, China. 2 University of Chinese Academy of Sciences, Beijing, China. 3 University of Hong Kong Department of Ecology and Biodiversity: The University of Hong Kong School of Biological Sciences, China. 4 Center for Integrative Conservation, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun, Yunnan, China. 5 Minzu University of China, Beijing, China.

Myanmar is one of the most biodiverse countries in the Asia-Pacific region, because of a wide range of climate and environmental heterogeneity. Floristic diversity in Myanmar is largely unknown resulting in a lack of comprehensive conservation plans. We developed a database of higher plants in Myanmar derived from herbarium specimens and literature sources, and analyzed patterns of diversity inventories and collection inconsistencies, aiming to provide a baseline floristic data of Myanmar and act as a guide for future research efforts. We collected 1,329,354 records of 16,218 taxa. Results show that the collection densities at the township level were variable and 5% of townships had no floristic collections. The collection density was lowest (1.3%) in the Kayah-Karen Montane Rain Forests, which covered 8 % of Myanmar's total area and no ecoregion averaged greater than one specimen/km². The highest sampling densities were found in the Mandalay Region, Chin State, and Yangon Region. Despite the past three centuries of floristic collections, knowledge of the distribution of the vast majority of plant taxa is still limited, particularly for gymnosperms, pteridophytes, and bryophytes. More botanical surveys and further analysis are needed to fill floristic-knowledge gaps to represent Myanmar's diversity. An important strategy to promote knowledge of the biodiversity patterns in Myanmar is to improve the collection and digitalization of specimens and to strengthen cooperation among countries.

P.1280 Assessing vulnerability to climate change of the Atractylis species in the Canary Islands

Víctor Bello-Rodríguez[1], Juan José García-Alvarado[1], Jonay Cubas[1], Jorge Rey Medina[1], Juana María González-Mancebo[1]

1 Departamento de Botánica, Ecología y Fisiología Vegetal, Universidad de La Laguna, La Laguna, España

Climate change is significantly altering species distribution and abundance, posing a particular threat to endangered species which are characterized by their scarcity. An example of this are *Atractylis preauxiana* and *Atractylis arbuscula*, two endangered endemics from the coastal scrublands of Tenerife and Gran Canaria, and Gran Canaria and Lanzarote respectively. In this study we assess their vulnerability to climate change following the methods proposed by (González Mancebo et al., (2023), which consider several factors such as seed production, invasive herbivore impact and species distribution models under current (1990-2019) and future (RCP 8.5 2041-2060 and 2061-2080) scenarios. Models predict potential area losses greater than 50% in all cases, with notable differences between islands for the same species. Their halophilic nature limits the possibilities of migration to higher altitudes, but models predict the persistence of some populations. Thus, among the main results is the recommendation of coastal areas to restore on each of the islands. However, both species have restrictions on their adaptive capacity. Both are very palatable to invasive herbivores such as the European rabbit, and although they can have moderate seed production, droughts significantly reduce productivity, even causing the mortality of juveniles and adults. The results also show the need for effective control of the European rabbit and the restoration of the biodiversity of accompanying species that could also persist in future scenarios.

P.1281 Updated global maps for the oak (Quercus spp.) sections

Kristel van Zuijlen[1], Jan Borgelt[2], Thomas Denk[1]

1 Swedish Museum of Natural History, Stockholm, Sweden. 2 Industrial Ecology Programme, Norwegian University of Science and Technology, Trondheim, Norway.

The more than 400 species of oaks (*Quercus* L., Fagaceae) are organized in two subgenera, *Cerris* and *Quercus*, which in turn are categorized in eight different sections: *Cyclobalanopsis*, *Cerris*, *Ilex*, Lobatae, *Protobalanus*, *Ponticae*, *Virentes* and *Quercus*. With the recently updated oak phylogeny, we are able to provide updated maps and climate envelopes for each of the sections. We utilized open-access data on species' native ranges in conjunction with geographic occurrence records to extract relevant bioclimatic variables and generated species distribution models (SDMs) for each species. Here, we present these distribution maps and explore their implications for forest management practices, focusing on risk assessment and the development of sustainable afforestation strategies amid global climate change.

P.1282 Spatial risk modelling of plant invasions: application in Mediterranean sea cliffs with endemic species

Bosch-Guiu, A.*[1], Rodríguez-González, R.[1], Nualart, N.[1], Gómez-Bellver, C.[1], Ibáñez, N.[1], García, S.[1], Melero, R.[1], Vitales, D.[1], López-Pujol, J.[1]

*1 Botanical Institute of Barcelona, CSIC-CMCNB, Barcelona, Spain. *arnau.bosch@csic.es.*

The use of spatial risk models is a valuable tool for predicting the likelihood of invasive plant species to spread, establish, and persist in the environment. This predictive approach identifies priority areas with a higher risk of invasion, aiding land managers to make better decisions on prevention, early eradication, or containment interventions. In line with this, one of the objectives of LIFE medCLIFFS (see below) involves the application of "Riskmapr", a tool originally developed and tested by Froese et al. (2019) that was designed to map the risk of invasion of an alien species, enabling a rapid response against plant invasions. The method considers that habitat suitability (i.e., invasion risk without considering propagule pressure) and habitat susceptibility (i.e., invasion risk considering propagule pressure) are influenced by risk factors that reflect the environmental and biological conditions needed for the invasive species to grow and spread. LIFE medCLIFFS is a five-year project (2021-2026) co-funded by the LIFE Programme of the European Union, with the aim of enhancing the management of invasive plant species in coastal areas while providing exportable models for similar projects seeking to manage plant invasions in Mediterranean regions. The project focuses on the habitat of community interest "Vegetated Mediterranean Sea cliffs with endemic *Limonium* spp." (HCI 1240), specifically targeting the Costa Brava (NE Spain). This region is one of the most heavily impacted by invasive plant species along the Spanish coastline. In the initial phase, the project focuses on invasive *Opuntia ficus-indica*, *Carpobrotus* spp., and *Gazania rigens* affecting the Cap de Creus Natural Park and its surrounding areas. The obtained risk maps—by means of the "Riskmapr" tool—will be overlaid with the distribution areas of endemic and threatened species (*Limonium geronense*, *L. tremolsii*, and *Seseli farrenyi*) to improve management practices in the natural park.

P.1283 Biogeographical and climatic change impact analysis on priority species in Sierra de las Nieves National Park (Málaga, Spain)

Camacho-Romero, Miguel[1], Casimiro-Soriguer Solanas, Federico[1], Hidalgo-Triana, Noelia[1]

1 University of Málaga, Málaga, Spain.

Sierra de las Nieves National Park (SNNP), located at the south-western border of the Baetic Range, represents one of Iberian´s region with the greatest number of ecosystems and species of interest. The factors that explain such biodiversity are: historical relevance as a glacial refuge area in a Mediterranean region; a high altitude with the representation of the thermo- to oro-Mediterranean thermotypes; and its unique high diversity of lithologies, especially, given the presence of serpentine rocks highlight. In our study, the Favourability Function was used to analyse possible factors such as climate, lithology and topography that may be explain which are the areas of establishment of several taxa of interest for conservation or priority species within the boundaries of the SNNP, as well as to predict the possible impact of climate change (CC) on the distribution patterns of those species within the SNNP. The results showed that, according to the factors considered, more than 75% of the studied taxa have their distribution patterns affected by the climatic variables present within the boundaries of the SNNP, being the aridity index the most frequent. This highlights the relevance and the necessity of predicting the effects of CC, in the coming years, inside this National Park in order to be able to establish management and conservation measures.

P.1284 Niche modeling of Helichrysum (Compositae) under future climate change scenarios in the African sky-islands

Elvira Castillo-Almansa[1], Rubén G. Mateo[1,2], Mercè Galbany-Casals[3], Carme Blanco-Gavaldà[3], Lucía D. Moreyra[4], Cristina Roquet[3], Christian Brochmann[5], Abel Gizaw[5], Desalegn Chala[5], Alfonso Susanna[4], Juan A. Calleja[1,2]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain 3. Systematics and Evolution of Vascular Plants—Associated Unit to CSIC, Autonomous University of Barcelona, Bellaterra, Spain. 4. Instituto Botánico de Barcelona, CSIC, Barcelona, Spain. 5. Natural History Museum, University of Oslo, Oslo, Norway.

The current biodiversity crisis is driven by multiple factors and one that is gaining relevance is climate change. Extensive research has been conducted on the impact of climate pattern alterations on species across diverse ecosystems. However, East African mountain systems, despite their unique characteristics, remain understudied. The plateaux and peaks of East Africa (2,000 – 5,895 m) form isolated high-altitude archipelagos (sky-islands) with distinct climatic features. The total area is very small if compared to other ecosystems, but they host an extraordinary biological uniqueness especially concentrated in the highest vegetation belts: the Afromontane Region (ca. 1,000 – 3,200 m) which encompasses high mountain forests up to the treeline, and the Afroalpine Region (ca. > 3,200 m) which comprises shrublands and grasslands with some taxa exhibiting gigantism. The genus *Helichrysum* (ca. 600 spp.) exhibits notable diversity in Africa (ca. 300 spp.). Different *Helichrysum* lineages have repeatedly colonized the East African sky-islands, leading to the diversification of Afromontane (ca. 60) and Afroalpine (ca. 12) species, many of which are endemic. Recent research has unravelled the evolutionary and biogeographic origins of these lineages, but the vulnerability of these species to ongoing climate change remains poorly understood. This study focuses on six Afromontane and nine Afroalpine *Helichrysum* species. Through the integration of three statistical algorithms (generalized linear models, boosted regression trees and random forest), we generate consensus models to depict their current climatic niche and project their spatial evolution under different future climate scenarios. This effort contributes to our understanding of their vulnerability to climate change. Additionally, it provides insights into the broader impact of climate change on the *Helichrysum* lineage pool and the vulnerability of the unique sky-island archipelagos of Africa.

P.1285 Species distribution modeling of Ligularia sibirica and L. glauca in changing climates

Alina G. Cîșlariu[1], Dragoș Ș. Măntoiu[2], Emanuel Ș. Baltag[3], Iulian Gherghel[4], Ciprian C. Mânzu[5]

1 Department of Botany and Microbiology, Faculty of Biology, University of Bucharest, Bucharest, Romania. 2 Wilderness Research and Consultancy, Bucharest, Romania. 3 Marine Biological Station Prof. Dr. Ioan Borcea, Agigea, "Alexandru Ioan Cuza" University of Iași, Iași, Romania. 4 Department of Exact Sciences and Natural Sciences, Institute of Interdisciplinary Research, "Alexandru Ioan Cuza" University of Iași, Iași, Romania. 5 Faculty of Biology, "Alexandru Ioan Cuza" University of Iași, Iași, Romania.

Ligularia genus has originated in the eastern Palearctic Region and currently has over 120 species. Only two of these species, *Ligularia sibirica* and *L. glauca* have managed to naturally colonise the Western Palearctic regions through a series of dispersion events. However, the potential routes and timing of these events remain unclear. This study aims to identify potential dispersal corridors from East to West Palearctic for *Ligularia sibirica* and *L. glauca*, along with determining the timing of these events, using the available historical bioclimatic datasets. Ensemble Species Distribution models were employed to project suitable areas under the current conditions, using bioclimatic variables. These models were then projected onto past climatic conditions (Late Holocene, Mid Holocene, Early Holocene, Last Glacial Maximum, and the last Interglacial period) to recreate potential suitable habitats, taking into account the current ecological niche. Potential dispersal corridors were identified by merging the least cost paths for all climatic periods. The analyses were performed using ArcGIS and R software. Our findings suggest both species may have colonised Europe prior to the Last Interglacial period. Notably, *Ligularia sibirica* appears to have thrived during colder and more humid climates, facilitating connectivity through the Ural Mountains. In the case of *L. glauca*, a potential corridor to Europe appears to have existed through a southern passage (south of the Caspian Sea) across the plains north of the Black Sea. The post-glacial trajectory of *L. sibirica* in Europe can be explained by re-establishing connections with Asian populations and through relict populations. Conversely, the post-glacial evolution of *L. glauca* appears to have led to a concentration in populations in the plains of western and central Asia, while European populations remained isolated. The study provides valuable information for establishing effective conservation and management strategies, particularly in the context of changing climatic conditions.

P.1286 From Sisyrinchium to grasslands: Urgency in protecting Brazil's forgotten grassland ecosystems

Dani J. G.[1], Esser L. F.[2], Souza-Chies, T. T.[1]

1 Programa de Pós-Graduação em Botânica da Universidade Federal do Rio Grande do Sul, Brazil. 2 Programa de Pós-Graduação em Ecologia de Ambientes Aquáticos Continentais da Universidade Estadual de Maringá, Brazil.

Neotropical grasslands are often overlooked in terms of conservation, particularly in Brazil, despite the presence of diverse grassland types representing biodiversity hotspots. Within these environments, especially in the *campos sulinos*, the genus *Sisyrinchium* (Iridaceae) is well-represented, hosting some endemic species. Nevertheless, the conservation of species within this genus remains underexplored. Our main objective is to evaluate the adequacy of Brazilian conservation areas for the current and future occurrence range of two *Sisyrinchium* species: *S. plicatulum* Ravenna and *S. weirii* Baker. The selection of these two species is based on their distinct morphological groups within the genus and their widespread distribution in Brazil, allowing for broader coverage. Ecological niche models (ENM) were developed using an ensemble approach for both species, with projections for 2050 and 2070 employing the widely adopted MIROC6circulation model. Two emissions scenarios (SSP126 - low emissions, SSP585 - high emissions) were considered, highlighting potential variations. Projections were overlaid onto maps containing all Brazilian conservation areas. The projections indicate a decline in suitable habitats for the two species, particularly under more pessimistic scenarios, especially *S. weirii*. Our findings underscore the inadequate coverage of protected areas for both *S. plicatulum* and *S. weirii* in all scenarios. The disparity between current and future projections emphasizes the urgent need to expand protected areas, encompassing a larger territory to ensure the preservation of *Sisyrinchium*. Critical investigations are required to propose new protected areas, especially in *campos sulinos*, to secure lineage preservation. Our study offers valuable insights into *Sisyrinchium* conservation in Brazil and the grasslands of the South and Southeast. We emphasize the importance of these environments, which is reinforced by studies emphasizing their urgent need for conservation. We emphasize the vital role of current Brazilian protected areas for *Sisyrinchium* conservation.

P.1287 Impacts of climate change on floristic regions

Samuel Minev-Benzecry[1], Barnabas H. Daru[1]

1 Department of Biology, Stanford University, Stanford, USA.

Biogeographic regions reflect the organization of biotas over long evolutionary timescales but face alterations from recent anthropogenic climate change. Here, we model species distributions for plant species under present and future climates and use this data to generate floristic regions based on phylogenetic dissimilarity. We found declines in phylogenetic beta diversity, leading to a future homogenization of floristic regions. While some biogeographic boundaries will persist, climate change will alter deeper boundaries. Such boundary alterations will track areas that experienced past climate velocities, and sharp transitions in precipitation seasonality and elevation. Our findings suggest that human activities may now surpass the geological forces that shaped floristic regions over millions of years, calling for the mitigation of climate impacts to meet international biodiversity targets.

P.1288 Spatial phylogenetic of the native flora in the Southern Cone of South America

Lone Aagesen[1], Diego Salariato[1], Amalia Scataglini[1], Juan Acosta[1], Renée H. Fortunato[1, 2]

1 Instituto de Botánica Darwinion (CONICET-ANCEFN), San Isidro, Buenos Aires, Argentina. 2 Escuela Superior de Ingeniería, Informática y Ciencias Agroalimentarias, Universidad de Morón, Morón, Buenos Aires, Argentina.

Inspired by large scale studies from all over the world, researches at the Darwinion Botanical Institute are currently assembling spatial and phylogenetic datasets, aiming to analyze the distribution of the native Southern Cone vascular flora in a phylogenetic context. Working at generic level, we will explore several diversity metrics and randomization tests within the framework of Phylogenetic Diversity. We aim to identify which areas contain the largest amount of vascular plant evolution, which areas contain the oldest lineages and where new ones are evolving. However, the history of individual plant families inevitably gets lost, when the big picture of spatial phylogenetic diversity patterns is assembled for all vascular plants. We therefor plan to analyze selected families such as Poaceae, Fabaceae, and Asteraceae on their own, because of their unique evolutions within different timeframes and/or in distinct ecoregions of the Southern Cone. We have recently concluded the analysis of the grass family. Grasses appear to have been present in South America since its early evolution as tropical understory species more than 60 My years ago. We found that tropical humid regions hold the highest phylogenetic diversity with no observed bias in branch lengths, indicating that niche conservatism dominates the diversity pattern of grasses in the Southern Cone. We found significantly low phylogenetic diversity in the Arid Chaco and in the Patagonian Steppe, which suggest ecological filtering in both warm and cold arid regions. The Patagonian Steppe also holds significantly longer branches than expected by chance, as the native grass flora is mainly composed of distantly related Pooideae genera with a northern hemisphere origin. Short branches are found in the Uruguayan Savanna suggesting that these grasslands could be a cradle for grass diversity within the Southern Cone. We are currently assembling the data for Legumes that appear to tell a different history.

P.1289 Landscape connectivity of Spain’s main vegetation formations: current and future perspectives

Sergio González[1], Teresa Goicolea[2], Juan Ignacio García-Viñas[1], Aitor Gastón[1], Rubén G. Mateo[2]

1 ETSI Montes, Forestal y del Medio Natural, Universidad Politécnica de Madrid, Madrid, Spain. 2 Departamento de Biología, Universidad Autónoma de Madrid, Madrid, Spain.

Landscape connectivity of ecosystems plays a critical role in maintaining biodiversity and facilitating species movement, especially in the face of environmental changes. This study focuses on assessing the current and future landscape connectivity of Spain’s 12 main vegetation formations, considering both their current distributions and potential future scenarios. We integrate hierarchical species distribution models to predict the distribution of key species and utilize dynamic least cost path connectivity models to analyze current and projected future connectivity. Our analysis accounts for the main dispersal vector for each species, the influence of the landscape matrix and the dispersal capacity of species on connectivity patterns to provide a comprehensive understanding of how landscape features and species traits interact to shape connectivity across different vegetation formations. We assess the current state of landscape connectivity and project potential changes under future climate scenarios. This approach enables us to identify critical corridors and barriers to species movement within and between vegetation formations, aiding in the development of effective conservation strategies and land management practices.

P.1290 Invasion history and invasive potential of Kalanchoe ×houghtonii and its parental species (K. daigremontiana, K. tubiflora)

Isaac Ojea-Jiménez[1], Estefany Goncalves[2], Laura Mena[1], Joan Pere Pascual-Díaz[1], Mònica Utjés[1], Neus Nualart[1], Jordi López-Pujol[1, 3]

1 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 2 Departamento de Botánica y Fisiología Vegetal, Universidad de Málaga, Málaga, Spain. 3 Escuela de Ciencias Ambientales, Universidad Espíritu Santo, Samborondón, Equador.

Invasive alien species are considered one of the main threats to global biodiversity, and ornamental horticulture has become one of the main introduction pathways of alien species. A paradigmatic example is that of the so-called "mother of thousands", *Kalanchoe ×houghtonii* D.B. Ward, a hybrid that until recently was thought to be exclusively the result of the artificial crossing between *K. daigremontiana* Raym.-Halmet & H. Perrier and *K. tubiflora* Eckl. & Zeyh. The two parental species are native to Madagascar but have become established, as the hybrid, in several regions worldwide. The three taxa have been reported as invasive in several parts of the world, particularly in dry or relatively dry subtropical regions (e.g., Mediterranean Basin, Australia, southern US and Mexico, southern China), given to their very extended use as ornamental (and medicinal) plants and also because of their vigorous asexual reproduction (by means of bulbils that are formed in the leaf margins). With the main objective of analyzing which of these taxa shows the highest invasive potential, we have proceeded for each of them to: (1) explore the geographic pattern of their worldwide distribution, (2) trace their spatial and temporal colonization history, (3) predict their potential distribution through Ecological Niche Modelling to different scenarios of climate change, (4) compare their ecological niches and (5) classify their invasive risk through the IUCN's Environmental Impact Classification for Alien Taxa (EICAT).

P.1291 Modelling the potential area of occupancy of habitat types at a biogeographical scale

Jorge González Le Barbier[1], José V. Roces-Díaz[1], Borja Jiménez-Alfaro[1]

1 Biodiversity Research Institute, University of Oviedo, Mieres, Spain.

Understanding the distribution of ecosystems in large geographic areas is essential for biodiversity conservation. In Europe, ecosystem assessments are based on the EUNIS habitat classification, a hierarchical system based on the relative dominance of plant species in functional or ecological habitat types. In this study, we use a vegetation database linked to the EUNIS classification to model the potential area of occupancy of habitat types in the Ibero-Atlantic biogeographic region of northern Spain. Our main aim was to evaluate the role of climatic and edaphic drivers in the distribution of habitat types related to forest, shrubland and grassland ecosystems. We also evaluated whether early- and late-successional habitats differed in their ecological drivers within the study area. We computed distribution models based on habitat occurrences using multiple edaphic and climatic predictors. The models were computed with Random Forest (RF) using geographically stratified cross-validation, after preliminary tests with Generalized Linear Models (GLM), Generalized Additive Models (GAM) and Gradient Boosting Models (GBM). Our results detected the minimum temperature of the coldest month as the most important driver in most habitat types, in agreement with the regional climatic gradient ranging from warm temperate coastal areas to high mountain ecosystems. The models computed for late-successional habitats outperformed the early-successional ones (ROC-based AUC = 0.86 and 0.75, respectively). We also found meaningful correlations between habitat types which are generally expected to be linked in successional stages. Our results suggest that correlative models based on the occurrence of ecosystem or habitat types are useful to understand spatial patterns of biodiversity and to test hypothesis about the climatic drivers of early- and late-successional habitats. Modelling the potential area of occupancy of habitat types is also a preliminary step for downscaling higher-resolution models based on remote sensing.

P.1292 From the present to the future: bioclimatic mapping and projections in the United States and Puerto Rico

Alejandro González-Pérez[1], Norma Y. Ochoa-Ramos[1], Ángel Penas[1] Sara del Río González[2]

1 Department of Biodiversity and Environmental Management (Botany Area). Faculty of Biological and Environmental Sciences. University of Leon, León, Spain. 2 Department of Biodiversity and Environmental Management (Botany Area). Faculty of Biological and Environmental Sciences, University of Leon, Mountain Livestock Institute CSIC-UNILEON, León, Spain.

The Intergovernmental Panel on Climate Change (IPCC) projections for the end of the century stated that global average temperatures over the period 2081-2100 are likely to be 1.5ºC higher than the pre-industrial values in pessimistic scenarios RCP4.5 and RCP8.5. Climate variables such as temperature and precipitation, alongside factors like sea level are disturbed by global warming in the United States. In some areas, droughts are more frequent and severe, whereas others experience more torrential rains and floods. Bioclimatology, the study of the relationship between climate and living organisms, plays a crucial role in understanding and mitigating the impact of climate change on ecosystems and human health. The objective of this research was to design the current bioclimatic map (1979-2018) for the United States and Puerto Rico, following the methodology of Rivas-Martínez. Moreover, we projected future changes with CMIP6 (GFDL-ESM4; IPSL-CM6A-LR; MPI-ESM1-2-HR; MRI-ESM2-0; UKESM1-0-LL) atmospheric circulation models for the temporary horizon 2041-2070 and 2071-2100, and for three Shared Socioeconomic Pathways (SSP 2.6; 7.0 and 8.5) data available in the CHELSA database. For this purpose, we applied Boolean logic and map algebra in ArcGISPro. The results were presented in maps and show a wide range of bioclimatic units, thermotypes, ambrotypes, continentality, and variants. Future projection outcomes revealed in general an increase in both lower levels of thermotypes and ombrotypes. The changes compared were detailed in this study.

P.1293 Future prospects of the conservation of endangered vascular plants amidst climate change in the Iberian Peninsula

Heiko Hentschel[1], Jennifer Morales-Barbero[1], Rubén G. Mateo[1,2]

1 Departamento de Biología, Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain. 2 Centro de investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain.

Climate change poses a significant challenge to plant biodiversity, affecting it from chorological, phenological, and physiological perspectives. However, the effects of this threat remains poorly understood for threatened Iberian flora. The potential impacts of climate change on the chorology of threatened Iberian plant species remain unknown, with earlier studies such as Felicísimo *et al.* (2011) being outdated. Additionally, the effects of climate change on conservation measures for these taxa, particularly concerning the conservation objectives of Natural Protected Areas (NPAs), are not well understood. This study aims to assess the vulnerability of threatened flora to climate change and evaluate the effectiveness of the current NPAs as conservation tools in future climate change scenarios. For this purpose, we developed species distribution models (SDMs) for 51 different taxa, considering climatic and edaphic variables, using an ensemble forecasting modelling technique. The SDMs for the future climate change scenarios were projected considering two different representative concentration pathway (4.5 and 8.5), two general circulation models (MIT and HadGEM2) and two-time horizons (2050 and 2070). The results of this work have the potential to identify priority taxa for conservation efforts and serve as a guide in planning conservation measures considering climate change factors. The SDMs could be used in the search for new populations of the studied taxa.

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P.1294 Crop wild relatives and the role of herbaria in future food crop security

Makenzie E. Mabry[1], Tori M. Ford[1], Jonathan Barz[1], Sebastian Fernandez[1], Tyler Radtke[1], Douglas E. Soltis[1,2], Pamela S. Soltis[1]

1 Florida Museum of Natural History, University of Florida, Gainesville, USA. 2 Department of Biology, University of Florida, Gainesville, USA.

Although Nicolai Vavilov recognized the potential of crop wild relatives (CWR) in the early 1900s, with the advent of genome editing techniques like CRISPR, scientists worldwide are now able to fully leverage the potential of CWRs as a source of diversity for cultivated populations. With global crop production facing increasing threats from climate change, plant biologists are tasked with finding ways to continue production of crops that can withstand changes to environmental conditions and to increase production to supply a growing population. CWRs provide a source of diversity that can be used to meet these demands. While there are concerted efforts to increase collections of CWRs in germplasms, herbaria have been an overlooked resource. Additionally, many herbarium records now have digital equivalents which can be used to address large research questions. Occurrence records from iDigBio and the Global Biodiversity Information Facility (GBIF) repositories were downloaded for CWRs of several important crop species. Following data cleaning, we performed ecological niche modeling to determine global niche suitability for both current and future climate scenarios. We hope this study highlights the important role of herbaria in future crop breeding efforts, especially in the face of climate change.

P.1295 Plant facilitation increases climatic disequilibrium across a broad geographic gradient

Jordi Margalef-Marrase[1], Jorge Prieto-Rubio[1], Miguel Verdú del Campo[1]

1 Centro de Investigaciones sobre Desertificación, CSIC, Montcada, Spain.

Climate change is increasing stress on many plant populations due to changes in abiotic conditions. Locally, these environmental changes can lead to the extinction of certain species within the community, especially those that are already at their environmental tolerance limits, either at their distribution edge or ecological niche limit. We might expect, therefore, that there is a relationship between climatic suitability or niche-derived indices and the survival and/or resilience of populations being affected by these environmental changes. However, this relationship is not entirely clear in some communities because other non-abiotic factors, such as plant-plant interactions or plant-soil community interactions, may modulate the response of these species to adverse conditions induced by climate change. Indeed, in semi-arid or dry temperate environments, plant-plant interactions can be beneficial for certain species within the community. Some species can generate changes in microclimate and the pedosphere, enabling other species to live in conditions they couldn't inhabit otherwise. This type of positive interactions is called facilitation. In this way, positive interaction -facilitation- can provoke a climatic disequilibrium in the community of recruits and saplings. We hypothesize that recruits that grow beneath adult canopies (nurse canopies) are more able to persist even if they are far from their climatic optima, while recruits and saplings in open areas - without facilitation - tend to be closer to their climatic optima. Here, we test whether facilitation can mitigate climatic stress induced by climate change. More specifically, we test if the species that benefit from facilitation exhibit more climatic disequilibrium compared to others that live outside the nurse canopy effect-gap. Our primary results shown that facilitation may mitigate climatic change induced extinctions. Facilitation generated below-canopy climatic disequilibrated community and further, they can maintain more diverse species community in comparison with the open community.

P.1296 Enhancing plant atlases completeness through graph analysis tool

Jennifer Morales-Barbero[1], Herlander Lima[2], Juan Carlos Moreno Saiz[1, 3], Ignacio Ramos[1], Rubén G. Mateo[1, 3], Miguel Á. Rodríguez[2]

1 Departamento de Biología, Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain. 2 GloCEE - Global Change Ecology and Evolution Group, Department of Life Sciences, University of Al-

cálá, Alcalá de Henares, Spain. 3 Centro de investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain.

Biodiversity atlases are crucial for both fundamental and applied research, including ecology, biogeography and biodiversity conservation. Despite their significance, most biodiversity datasets are incomplete, limiting what can be learned from them, hindering progress in ecology and evolutionary research, and compromising biodiversity conservation strategies and resources. Assessing and understanding the spatial distribution and extent of knowledge gaps in biodiversity datasets is pivotal for guiding effective future sampling efforts. To tackle this challenge, we present how novel graph analysis tools—a robust yet underexplored approach in ecology—can effectively predict and identify missing information within biodiversity inventories. When treating a multi-species distribution dataset as a bipartite graph of species by sites, graph reconstruction algorithms have the ability to estimate the probability of species and sites being linked based on their membership in specific “communities”, facilitating the identification of potential unrecorded species presences at specific sites. Amongst the myriad of algorithms devised for network reconstruction and link prediction, the Hierarchical Stochastic Block Models (HSBM) stands up for its statistical rigor and proven effectiveness. Applying HSBM (implemented in the recent R’s *hsbm* package) to the Atlas of the Vascular Flora of the Iberian Peninsula biodiversity hotspot (AFLIBER), our methodology reveals specific areas with under-sampled plant species (areas with a higher likelihood of harboring unrecorded species), particularly in mountainous regions and the eastern Iberian Peninsula. These findings can guide prioritization of future data collection efforts, improving AFLIBER’s completeness and enhancing our understanding of plant biodiversity in the Iberian Peninsula. Future perspectives involve expanding this methodology to other biodiversity datasets and atlases, integrating it into broader conservation and management frameworks.

P.1297 Impact of climate and land use change on the distribution of orchids in Estonia

Davide Nepote Valentin[1], Chiara Richiardi[1,2], Martino Adamo[1,3], Stefano Mammola[3,4], Tiiu Kull[5]

1 Department of Life Sciences and Systems Biology, University of Torino, Torino, Italy. 2 Technology Laboratory for the Dynamics of Structures and Prevention of Seismic and Hydrogeological Risk, Bologna, Italy. 3 National Biodiversity Future Center, Palermo, Italy. 4 Molecular Ecology Group, Water Research Institute, National Research Council of Italy, Verbania Pallanza, Italy. 5 Department of Biodiversity and Nature Tourism, Estonian University of Life Sciences, Tartu, Estonia.

Terrestrial orchids are undergoing marked population declines worldwide, due to habitat loss and climate change. In Europe, northward shifts in orchid distributions have been observed, suggesting northern countries as refugia in the next decades. Estonia is one of the orchid-richest countries in northern Europe and can be regarded as a well suited indicator of present and future impact of climate change on orchid distributions, despite its populations are already declining. In this context, predicting species distributions under climate and land use change exposure can help us implement effective conservation strategies. We used species distribution modeling (SDM) to predict the distribution of 34 orchid species in Estonia. We used bioclimatic and land use variables as environmental predictors, considering both climate predictions under fossil-fueled development pathways and land use urban and agricultural expansion scenarios from present to 2100. Our results indicate that the western Estonian islands and coasts are the most suitable areas for orchid distributions, yielding the highest predicted species diversity. However, western territories might also be the most impacted by range losses for several orchid species. Wide expansions eastwards for species growing preferentially on calcareous soils are predicted. However, these shifts are unlikely to occur due to a lack of calcareous soils connecting western and eastern Estonia and due to dispersal limitations, making it unrealistic for these orchids to disperse over such large distances in a few decades. As a result, western islands and coasts – currently the hotspot for calcicolous orchids in Estonia – might progressively become less suitable for several species. Additionally, wider range losses are predicted for non-calcicolous orchids, most of them with preference for woodlands or wetlands and three of them at risk of disappearing by 2060. Northern countries' role as orchid refuges might be not so straightforward, therefore further conservation strategies are recommended.

P.1298 Poor georeferencing overestimate species potential distribution: the effect of spatial uncertainty in species distribution modelling

Renato Otárola[1], Juan Reyes-Valentin[1], Sergio Estay[2,3], Paulette I. Naulin[1]

1 Laboratorio Biología de Plantas, Universidad de Chile, Santiago, Chile. 2 Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Valdivia, Chile. 3 Center of Applied Ecology and Sustainability), Pontificia Universidad Católica de Chile, Santiago, Chile.

Data digitization, integration and sharing have exponentially increased data volume and availability, particularly in biodiversity sciences. However, this growth has raised concerns regarding potential "big errors," such as data validity and accuracy. Ecological niche is a region inside a multidimensional space where various factors influence species development. Species distribution models (SDM) represent the geographic area where the environmental factors of the ecological niche of a species are met. SDM have become a widely used tool in various contexts, such as species conservation plans and guidelines, specimen sampling, and prioritization for restoration areas. Biodiversity data quality affects the usability of SDMs. Erroneous or incomplete georeferencing of data causes spatial uncertainty of occurrence records, leading to misrepresentation of the species distribution after modelling process. The study purpose was to evaluate the differences between SDM suitability for data with contrasting quality, using the Fabaceae tree Neltuma chilensis as a case study. Two databases were constructed. The first comprised all the natural distribution occurrences contained in GBIF of the species. The second was the same database, but with occurrences in Chile replaced by field data collected in the country following high data quality standards. For each database, the spatial uncertainty index was calculated, and an SDM was elaborated. Analysis focused on the relation between index value and SDMs suitability. Spatial uncertainty index and SDM suitability presented big differences between databases. Index value and suitability area were positively related. Data with more uncertainty models bigger distribution area. The results highlight the importance of georeferencing process for high quality spatial data in species occurrences. Usage of deficiently georeferenced data produces overestimation of species distribution. This could lead to misinformed decision-making outcomes.

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P.1299 Exploring the future of endangered epiphytic moss: a climate and biotic interaction perspective

Adrian Wysocki[1], Sylwia Wierzcholska[1], Kamil Konowalik[2], Jarosław Proćków[1]

1 Department of Plant Biology, Wrocław University of Environmental and Life Sciences, Wrocław, Poland. 2 Department of Botany and Plant Ecology, Wrocław University of Environmental and Life Sciences, Wrocław, Poland.

Our research focusses on endangered epiphytic moss *Dicranum viride*, a Natura 2000 species with a European conservation priority. We employed advanced Species Distribution Modelling (SDM) and niche dynamics techniques to investigate the intricate relationship between its potential distribution and the availability of specific phorophyte species (living trees that serve as hosts for an epiphyte) in the context of future climate change. We used the GFDL-ESM4 Earth system model in the projections, which encompasses atmospheric and ecosystem dynamics, as well as ocean and land physics. The time span for our analysis extended from 2071 to 2100, allowing us to examine long-term projections. Within this timeframe, we considered three different Shared Socioeconomic Pathways (SSP) scenarios. We implemented a novel SDM approach by incorporating biotic interactions (with preferred phorophyte species) into the projections. To determine the impact of our innovative approach, we also made projections of the species studied based solely on climate data for comparisons. The predicted decline in the vast majority of areas currently suitable for this endangered epiphyte is of great concern. Depending on the scale of climate change induced by anthropogenic radiative forcing, the range of *D. viride* may exhibit noticeable shifts toward the northern regions of the European continent. Furthermore, our analysis indicates that future refuges for this species in central Europe may be limited only to its mountainous regions. Our findings demonstrate that the inclusion of biotic interactions with phorophytes significantly enhances the performance of distribution models compared to those that rely solely on climatic data. This highlights the crucial role of the availability of phorophytes in shaping the potential distribution of epiphytic mosses, with *D. viride* serving as a prime example. Furthermore, we also emphasise the importance of incorporating biotic interactions into SDMs, rather than relying solely on climatic factors.

P.1300 Modelling the present potential habitat distribution of the near threatened endemic species Silene marizii: implications for conservation.

Rubén Ramírez-Rodríguez[1], João Rocha[2,3], Antonio L. Crespí[2,4], Francisco Amich[1]

1 Evolution, Taxonomy and Conservation Group (ECOMED), Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain. 2 Herbarium, Department of Biology and Environment, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal. 3 Chemistry Center-Vila Real, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal. 4 Centre for the Research and Technology of Agro-Environmental and Biological Sciences, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal. rubenrr2608@gmail.com

Species distribution models (SDMs) have been successfully used in spatial ecology, biodiversity conservation and environmental management. SDMs are correlative models using species ocurrences and environmental variables to understand how the environment influences in the native distribution range of a target species. There are different SDM algorithm methods, but Maxent is a machine learning SDM algorithm that performs well in species with small sample size as rare and narrow endemic species, in which often presence-only data are available (without absences). We selected as model species *Silene marizii*, a near threatened endemic species distributed in the central-western Spain and north-western Portugal. The aims were to: (i) model the current potential habitat distribution; (ii) identify the main environmental variables that determine its range of distribution; and (iii) suggest suitable areas for searching new populations, prioritizing conservation areas and performing reintroduction and translocation sites, if necessary. A total of 90 occurrences were used together with 34 predictors (23 bioclimatic, 7 edaphic and 4 topographic). The Maxent model performed well with a high predictive accuracy. The predictors that most contributed to the model were related to some aspects of the biology and ecology of the species. Our results were robust and the model had the sufficient predictive power to be applied in conservation and management proposes, such as searching for new populations or identifying suitable areas for reintroductions and translocations.

P.1301 Distribution changes of Pinus koraiensis in the Quaternary: a case study using a Species Distribution Model

Takuto Shitara[1]

1 Tama Forest Science Garden, Forestry and Forest Products Research Institute, Japan.

Pinus koraiensis Siebold et Zucc. (Korean pine) is one of the dominant canopy tree species in the cool and cold temperate conifer and mixed conifer–broad-leaved forests in Northeast Asia (the Amur and Maritime provinces of the Russian Far East, northeast China, the Korean Peninsula, and the Japanese Archipelago). This species occurred in only a few montane areas of Japan, showing present-day disjunct geographical distribution patterns. In Japan, this species widely occurred during the Last Glacial Maximum (LGM; approximately 22,000 years ago) and rapidly reduced from most areas in response to global warming. However, how and why post-LGM climate changes have influenced this distribution shift remains controversial. I identified the climatic factors that have influenced the distribution of *P. koraiensis* and determined how paleoclimate change has affected the distribution and development of present-day species using a species distribution model (SDM). Projected suitable habitats of this species under the LGM showed broad distributions in Japan expected Hokkaido. Furthermore, I identified that an increase in the minimum temperature in winter and precipitation in summer affected the retreat of their suitable habitats in Japan post-LGM. On the other hand, the suitable habitats expanded northward from the Korean peninsula post-LGM. Differences in these distribution processes between Japan and mainland Northeast Asia would have led to the formation of disjunct distribution in the present.

P.1302 Can species distribution modelling recreate the greening of the Sahara?

Irene Solano Regadera[1], Ignacio A. Lazagabaster[1,3], Chris D. Thomas[2], Jakob Bro-Jørgensen[1]

1 Department of Ecology and Behaviour, University of Liverpool, UK. 2 Leverhulme Centre for Anthropocene Biodiversity, Department of Biology, University of York, UK. 3 Centro Nacional de Investigación sobre Evolución Humana CENIEH, Spain.

During the Holocene, a pronounced humid phase occurred in North Africa (12,000-5,000 BP), known as the African Humid Period (AHP), which transformed the Sahara into a vegetated region with diverse plant communities. The scarcity of fossil records and the challenges in reproducing the AHP in paleoclimatic simulations hinder the reconstruction of this Holocene Saharan environment. Some studies propose that, aside from the African southern monsoon, additional moisture sources like Mediterranean winter rains contributed to increased precipitation during the AHP. This study aims to reconstruct the Sahara's Holocene paleobotanical environment to establish whether it was vegetated with both Mediterranean and sub-Saharan communities, and thereby assess the significance of southern monsoon versus Mediterranean winter rains in creating the AHP. In contrast to previous research on the AHP, this study employs Species Distribution Modelling, applying multiple algorithms and improved paleoclimatic simulation, to hindcast the Holocene ranges of plant species in Northern Africa using available evidence.

P.1303 Ecological niche modeling of 20 species of medicinal plants from the state of Hidalgo, Mexico

Valdés-Vásquez I. F.[1], Cuervo-Robayo A.P.[2], Monroy-Ata A.[1], Defossez E.[3], Villaseñor J.L.[4], Morrone J.J.[5], Bye-Boettler R.A.[6], Calmé S.[7], Osorio-Olvera L.O.[8], Reyes-Chilpa R.[9], De-Nova J.A.[10], Couturier-Stéphane R.A.[11], Ramírez-Barahona S.A.[4], Beltrán-Rodríguez L.A.[12], Mas J.F.[13], Yáñez Arenas C.A.[14], Aguilar-Contreras A.[15], Cristians-Niizawa S.[6], Morales-Manilla L.M.[16], Bollo-Manent M.[16] Heike-Vibrans L.[17], Torrescano-Valle N.[18], Ortiz-Bermúdez E.[4], Estrada-Márquez A.S.[4], Espinosa-Organista D.N.[19], Santiago-Alvarado M.[19], Guevara-Fefer P.[20]

1 Unidad de Investigación en Ecología Vegetal, FES Zaragoza Universidad Nacional Autónoma de México, México. 2 Laboratorio Nacional CONAHCYT de Biología del Cambio Climático, Instituto de Biología UNAM, México. 3 Laboratory of Functional Ecology, Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland. 4 Departamento de Botánica, Instituto de Biología UNAM, México. 5 Departamento de Biología Evolutiva, Facultad de Ciencias UNAM, México. 6 Laboratorio de Etnobotánica, Jardín Botánico IB UNAM, México. 7 Department of Biology, Université de Sherbrooke, Québec, Canada. 8 Departamento de Ecología de la Biodiversidad, Instituto de Ecología UNAM, México. 9 Departamento de Productos Naturales, Instituto de Química UNAM, México. 10 Instituto de Investigación de Zonas Desérticas, Universidad Autónoma de San Luis Potosí, México. 11 Laboratorio de Análisis Geoespacial, Instituto de Geografía UNAM, CDMX, México. 12 Laboratorio de Etnobotánica Ecológica, IB UNAM, México. 13 Laboratorio de Análisis Espacial, ENES Morelia UNAM, Michoacán, México. 14 Laboratorio de Ecología Geográfica, Unidad Académica Sisal, ENES Mérida UNAM, Yucatán, México. 15 Unidad de Investigación de Plantas Medicinales, Herbario Medicinal IMSS, México. 16 Laboratorio Universitario de Drones, ENES Morelia UNAM, Michoacán, México. 17 Departamento de Botánica, Colegio de Postgraduados, Universidad Chapingo, Estado de México, México. 18 Departamento de Conservación de la Biodiversidad, El Colegio de la Frontera Sur Unidad Chetumal, Quintana Roo, México. 19 Unidad de Investigación en Biogeografía y Conservación, FES

Zaragoza UNAM, México. 20 Laboratorio de Fitoquímica, Facultad de Ciencias UNAM, México.

Mexico is the second country with the greatest diversity of medicinal plant species in the world after China. We know remarkably little about how phytochemical diversity is distributed across the plant kingdom and environment. The objective of this work was to analyze the ecological relationship between phytochemical components of medicinal plants and climatic variables through ecological niche modeling of species present on a fine scale, in the state of Hidalgo, Mexico, is an area with high floristic diversity. This was done based on records of each species in international databases, to subsequently filter, purify, and clean with spatial data mining, to create thematic maps of the species at the state level, which belong to six types of vegetation, from 400 registered species, 20 representative species were selected from that area in different ecoregions. In temperate and cool climate ecosystems, such as cloud forests, native species of pteridoflora such as *Pleopeltis polylepis* (Polypodiaceae), *Dryopteris filix-mas* (Dryopteridaceae), an epiphyte *Stanhopea tigrina* (Orchidaceae); in the pine-oak forest are *Montanoa tomentosa* (Asteraceae) and *Liquidambar styraciflua* (Altingiaceae) were selected; in the tropical forest are *Passiflora exsudans* (Passifloraceae), *Tigridia azufrensis* (Iridaceae), *Tabernaemontana alba* (Apocynaceae) and *Agastache mexicana* (Lamiaceae); in arid and semiarid areas of xeric scrub, the endemic species native to Mexico such as *Agave salmiana* (Agavaceae), *Ceratozamia latifolia* (Zamiaceae), *Echinocactus platyacanthus* and *Myrtillocactus geometrizans* (Cactaceae), *Jatropha dioica* (Euphorbiaceae), *Prosopis laevigata* (Fabaceae), *Fouquieria splendens* (Fouquieriaceae) and the state-endemic epiphyte *Tillandsia mauryana* (Bromeliaceae); finally, in induced grassland was analyzed to *Dysphania ambrosioides* (Amaranthaceae), *Yucca filifera* (Asparagaceae) and *Castilleja tenuiflora* (Orobanchaceae). The results were classified according to the function of species, with spatial analysis by botanical family and secondary phytochemicals. It's concluded that species with an affinity for a temperate and semi-arid climate have a greater diversity of medicinal plants than those with a warm and humid climate.

P.1304 Tree species abundance shifts are influenced by functional differences within communities

Albert Vilà-Cabrera[1], Miriam Bravo-Hernández[1], Julen Astigarraga[1], Cristina Grajera-Antolín[1], Susanne Suvanto[2], Thomas A.M. Pugh[3,4], Miguel A. Zavala[1], Adriane Esquivel-Muelbert[3], André Thibaut[5], Andrzej Talarczyk[6], Leen Govaere[7], Emil Cienciala[8], Georges Kunstler[9], Jonas Fridman[10], Julien Barrere[9], Marta Rodríguez-Rey[1], Mart-Jan Schelhaas[11], Sara Villén-Pérez[1], Paloma Ruiz-Benito[1]

1 Universidad de Alcalá, Madrid, Spain. 2 Natural Resources Institute Finland (Luke), Helsinki, Finland. 3 University of Birminghan, Birmingham, UK. 4 Lund University, Lund, Sweden. 5 Service Public de Wallonie, Jambes, Belgium. 6 Forest and Natural Resources Research Centre Foundation, Warsaw, Poland. 7 Nature and Forest Agency, Brussels, Belgium. 8 Institute of Forest Ecosystem Research, Jilove, Czech Republic. 9 Université Grenoble Alpes, INRAE, Grenoble, France. 10 Swedish University of Agricultural Sciences, Umeå, Sweden. 11 Wageningen Environmental Research, Wageningen, Netherlands.

Forest ecosystems are major C sinks of the terrestrial biosphere, but climate- and land-use change strongly impact their structure and distribution. Therefore, understanding the factors that regulate changes in tree species abundances is essential to define mitigation and adaptation priorities. While the spatial variation in climate and forest stand development is well known to explain species abundance shifts over large geographical areas, the contributing role of interspecific interactions remains unclear. Given that different species tend to co-occur across their distributions, it can be expected that species responses also depend on the identity and function of other species in the community. Here we used National Forest Inventories across Europe to study how changes in tree species abundances over large gradients of climate and forest stand development depend on interspecific differences in key functional traits related to drought tolerance and resource use. We found that functional differences within communities were consistently associated with species abundance shifts across for-

est types, climatic contexts, and stand development stages. Our trait-based approach can improve our predictive understanding of species distribution shifts and support conservation and management strategies targeting positive biodiversity effects on the C storage capacity of forest ecosystems.

P.1305 Differential impacts of climate change on specialist butterflies and their host plants

Linde N. Wieringa[1], Harith Farooq [2,3], André Freitas[4], Alexandre Antonelli[5,6,7,8]

1 Ludwig-Maximilians-Universität München, München, Germany. 2 University of Copenhagen, Copenhagen, Denmark. 3 Lúrio University, Pemba, Mozambique. 4 Universidade Estadual de Campinas, Campinas, Brazil. 5 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 6 University of Gothenburg, Göteborg, Sweden. 7 Wuhan Botanical Garden, Wuhan, China. 8 University of Oxford, Oxford, United Kingdom.

Climate plays a crucial role in shaping the distribution of species around the world. Biotic interactions further impose constraints on the extent of a species' range, limiting its establishment. Even though the impacts of climate change on species range shifts and potential mismatches of interacting species are increasingly acknowledged, the influence of biotic interactions on the distribution of insect species in tropical biomes remains largely unexplored. We investigated the impacts of climate change on the distribution of six monophagous (feeding on a single or small group of related larval host plants) butterfly species endemic to Brazil's Atlantic Forest. We generated validated data sets of species occurrences from museum specimens and other sources and then incorporated the co-occurrence of the studied butterflies and their respective larval host plants, following an ensemble modeling technique for both present-day and future climatic scenarios. We predict that five out of the six butterfly species and all six host plant species will experience range contractions under the pessimistic climate scenario, with range losses of up to -89% (A. chalciope). In the optimistic climate scenario, considerably fewer –7 out of 12 – species are predicted to contract their range. Our results show that both biotic interactions and climate play a limiting role in determining species distributions: butterflies make incomplete use of their host plant range, being simultaneously constrained by host availability. These findings suggest that specialist species may be at greater risk from climate change than currently assumed, and that insect partners may be at greater risk than their hosts. This study showcases the importance of incorporating biotic interactions in biogeographical, ecological and conservation research.

S.144. SPEEDING UP CONSERVATION IN POORLY KNOWN ORGANISM GROUPS – NEW APPROACHES TO BRYOPHYTE CONSERVATION

P.1306 Functional traits predicting mosses extinction risk.

Sinan Gürlek[1,*], Ana Claudia Araújo[2,**], Neil A. Brummitt[2]

*1 Imperial College London, Silwood Park, Ascot, UK, *sg522@ic.ac.uk. 2 Natural History Museum, Cromwell Road, South Kensington, London, UK, **a.araujo@nhm.ac.uk*

Mosses are an early lineage of plants, very diverse, comprising around 13,000 species, and providing crucial ecosystem services. Yet, less than 3% of known species had their extinction risk globally evaluated. From circa 300 mosses species, presenting fully conservation assessments, over 30% are threatened (classified as Vulnerable (VU), Endangered (EN) or Critically Endangered (CR)) while another 10% was classified as Data Deficient (DD). Bryological functional traits have been investigated to overcome the lengthy process of species risk assessment and improve outcomes speedily and efficiently. Functional traits are known to predict the extinction risk of species, thus a matrix was produced comprising of 15 functional traits acquired from circa 739 moss species from around the world. Traits were extracted from morphological description found in taxonomic references applying automated machine learning techniques. Binary generalised-linear models show as preliminary results that species sex (monoicous/dioicous); sexual reproduction, capsule and seta length, as well as substrate breadth, are strong traits to apply as indicative of species at risk of extinction. The application of the models developed, as preliminary investigation, is valuable to speedily identify which mosses species are more likely to become threatened, particularly when faced with habitat loss. Thus, human time and effort, scientific investigation and financial investment could be directed effectively towards those species more susceptible to extinction.

P.1307 In vitro investigation of the copper requirements of the Endangered liverworts Cephaloziella nicholsonii and C. massalongoi

Christina Campbell[1], Daniel L. Kelly[2], Noeleen Smyth[3], Neil Lockhart[4], David T. Holyoak[5], David Long[6]

1 National Botanic Gardens of Ireland, Dublin, Ireland. 2 Trinity College, University of Dublin, Ireland. 3 University College Dublin, Ireland. 4 National Parks and Wildlife Service, Dublin, Ireland. 5 Independent Researcher. 6 Royal Botanic Garden Edinburgh, Scotland, UK.

In addition to acting as a repository for rare and threatened species and their genetic diversity, *ex situ* conservation collections and techniques, such as *in vitro* cultivation (tissue culture), can be used to investigate life history traits and nutrient requirements. Many rare specialised bryophyte species have adapted to metal-rich soil habitats, such as found at former mine sites, which are toxic to most other plant species. Some of the bryophyte species found in these habitats are facultative metallophytes, and others are regarded as strict metallophytes, the so-called 'copper mosses'. It is a general assumption in the literature that the liverworts *Cephaloziella nicholsonii* Douin and *C. massalongoi* (Spruce) Müll.Frib, both categorised as Endangered in the IUCN Red List for Europe, are also strict metallophytes and obligate copper bryophytes. This *in vitro* experiment investigated the growth and gemma production of these two species from different sites in Ireland and Britain on treatment plates of 0 ppm, 3 ppm, 6 ppm, 12 ppm, 24 ppm, 48 ppm and 96 ppm copper. Results show that elevated copper is not an obligate requirement for optimum growth. Differences in response to the copper treatment levels among populations evident within both species could possibly be due to ecotypic variation. The results have implications for the species' conservation and also highlight the need for a taxonomic revision of the *Cephaloziella* genus.

P.1308 Besides Brazilian Pampa richness bryophyte: a functional structure approach

Elisa T. Aires[1], Talita S. Dewes[2], Wanessa V. S. M. Batista[3], Jéssica S. Lima[4], Denilson F. Peralta[4], Juçara Bordin[1]

1 State University of Rio Grande do Sul, São Francisco de Paula, Brazil. 2 Federal University of Rio Grande do Sul, Porto Alegre, Brazil. 3 University of Pernambuco, Petrolina, Brazil. 4 Environmental Research Institute, São Paulo, Brazil.

Studies and knowledge regarding the floristic diversity of the Brazilian Pampa Biome have increased in recent years, revealing greater richness compared to other grassland ecosystems. However, studies on bryophytes are limited and focused on small areas. The aim of this study is to present an ecological analysis of the bryophyte functional composition and site types where species were recorded. Based on literature data, 318 bryophyte species native to the Pampa (216 Bryophyta, 99 Marchantiophyta, and 3 Anthocerotophyta) were classified according to seven morphofunctional traits related to humidity and sunlight conditions. The relationships were then analyzed using Principal Component Analyses (PCA) considering the community-weighted mean (CWM) per trait. Nonlinear and linear data were used at the biome and site type scales, respectively. The PCA revealed that mat and thalloid life forms, as well as costa, exhibited the highest correlation with the first axis (20.4% variance), while turf life form, pH and light tolerance guilds were more relevant in the second axis (16.52%). Regarding the functional composition per site type, considering hornworts and liverworts, and mosses separately, the cumulative variance in the first two PCA axes was quite explanatory (89.9 and 84.5%, respectively). Differences in bryophyte functional composition were observed between sites affected by human impact (trails, forest edge), and aquatic and inland forest sites. Our results are consistent with literature: species with life forms tolerant to desiccation (turf and cushion) predominated in sites affected by human impact (stressed/unstable areas), while forest interiors (preserved/stable places) were characterized by species with life forms vulnerable to desiccation (fan, dendroid, pendant). This approach provides unexplored new data to understand bryophyte functional structure in the Brazilian Pampa, which is essential to elucidating the future effects of environmental change on this important group of plants and their implications for ecosystem processes.

P.1309 Working towards a Red List for Antarctic Bryophyta using IUCN criteria

Maria Clara Gil Laydner[1], Brenda Lopes Emerick Neves[1], Clara Katharina Vaz[1], Eduardo Toledo de Amorim[2], Paulo Eduardo Aguiar Saraiva Câmara[1]

1 Universidade de Brasília, Brasília, Brazil. 2 Centro Nacional de Conservação da Flora/Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil.

The knowledge on Antarctic plants is limited due to the extreme conditions of the continent, but recent research has revealed important discoveries about its biodiversity. Antarctic bryoflora has generally been considered low threatened. However, this may not be true for rare species. Considering this, our study sought to understand the current conservation status of the five endemic species of Antarctic mosses: *Coscinodon lawianus, Schistidium lewis-smithii, S. steerei, S. leptoneurum,* and *S. deceptionense*. King George Island is one of the areas most affected by anthropogenic activities on the continent, thus a regional assessment was made for two common bryophyte species: *Roaldia revoluta* and *Bryum pseudotriquetrum*. By assessing their extinction risk following IUCN criteria, the endemic species *C. lawianus, S. lewis-smithii* and *S. leptoneurum* met the Critically Endangered category (CR), while *S. steerei* and *S. deceptionense* were listed in the Data Deficient (DD) category. For the regional assessment, both species met the Vulnerable (VU) category. This diagnosis highlights the need for conservation measures for these species. Regardless of two endemic species being listed in the Data Deficient (DD) category, this does not imply that they are free from threats. These results reflect the exceedingly small botanical collections in the region, and difficulties in the identification and taxonomic classification of these species create uncertainties. Nevertheless, threats such as climate change and increased human activity on the continent are already affecting floristic diversity. Therefore, it is essential to better understand the current distribution and abundance of these species to provide proper legislative protection and guide the implementation of conservation programs and protected areas. This study stands for the first investigation into the threat status of Antarctic plant species.

P.1310 Revisiting the flora of two exceptional Antarctic sites: Deception Island and Elephant Island

Maria Clara Gil Laydner[1], Alan Camelo e Silva[1], Paulo E.A.S. Câmara[1]

1 Department of Botany, University of Brasília, Brasília, Brazil.

Deception Island and Elephant Island are situated on the South Shetland Archipelago, in the Antarctic Peninsula. Deception Island is one of few active volcanoes in Antarctica, most recently erupting in 1967, 1969 and 1970, with further eruptions expected. A unique feature is the presence of localized terrestrial sites that are geothermally active, including several fumaroles. Their associated warmth and moisture provide ideal conditions for mosses to grow. With the combination of its unique botanical diversity, aesthetic and scientific values, historical importance, the presence of active research stations, and being one of the most popular visitor sites in Antarctica, Deception Island has been designated as Antarctica Specially Managed Area (ASMA 4). Within the ASMA, Antarctica Specially Protected Area (ASPA 140) has been designated, which includes 11 distinct subsites, each with distinct vegetation features. Elephant Island hosts a remarkable diversity of moss species and is one of the northernmost areas in Antarctica, making it an important site to investigate climate change effects. The island also has an important historical value, as it was where the crew of Shackleton's Endurance expedition sheltered. However, the island has no protected areas. The island's challenging terrain and its extensive glaciers have made botanical collections difficult to obtain so prior knowledge was limited, with sparse collections. At present, 57 moss species are considered to occur on Deception Island. Of these, 13 are not recorded elsewhere in Antarctica and two are apparently endemic to the island. However, in recent collections from the past 10 years only 29 species from 10 families were identified. For Elephant Island, 50 moss species across 14 families were recorded, revealing it harbours nearly half of Antarctica's moss diversity, missing a legislated protection. Here, we map these collections and update the islands' known diversity to better inform future conservation decisions and their management plans.

P.1311 Bryophyte account for the Flora of Singapore

Boon-Chuan Ho[1]

1 Singapore Botanic Gardens, National Parks Board, Singapore, Republic of Singapore.

Singapore is a small low-lying tropical island-state sitting at the heart of Southeast Asia. The Singapore Botanic Gardens has embarked on the Flora of Singapore project, which will treat all groups of embryophytes. It is generally uncommon to include bryophytes in a flora project. In Southeast Asia, only a handful of regional moss floras are available but a complete regional bryophyte flora, i.e. including liverworts, mosses and hornworts, has not been available so far. With an area about 734.3 km^2 including some 22 % of reclaimed land, Singapore has recorded about 280 species of bryophytes, including 19 species and 7 genera that have been published as new records for the country land since the commencement of the Flora project in 2017. In the Flora account, all accepted species, genera and families will be accompanied by descriptions and other general information. Identification keys to genera and lower ranks, as well as selected illustrations will also be provided. When completed, the bryophyte account for the Flora of Singapore will be a useful guide and reference for the identification of lowland bryophytes of tropical southeast Asia.

P.1312 A systematic review of the success of translocation experiments for bryophyte species.

Izadora Kervin[1,*], Jennifer Rowntree[1,**]
Scott Davidson[1,***], Neil Bell[2,****]

*1 Faculty of Science and Engineering, University of Plymouth, Plymouth, UK. 2. Royal Botanical Gardens, Edinburgh, Edinburgh, UK. *izadora.kervin@plymouth.ac.uk; **jennifer.rowntree@plymouth.ac.uk; ***scott.davidson@plymouth.ac.uk; ****Edinburgh. nbell@rbge.org.uk*

An estimated one-fifth of all botanical species are at risk of extinction with the most vulnerable of these species being bryophytes. This is due to them being poikilohydric, causing bryophytes to be sensitive to changes in the environment. Translocation and reintroduction practices can be used to help reintroduce species into their native ranges, and ultimately help reduce the risk of extinction. However, currently there are no available guidelines specifically tailored towards the translocation and reintroduction of bryophyte species. We undertook a systematic review to advance our understanding of successful translocation and reintroduction projects. Using a standardised methodology, we systematically searched literature databases for articles on bryophyte translocations. The initial search of literature was filtered to 138 relevant articles (WoS = 132, EthOs = 4, and Scorpus = 1), in which the subject and focus were assessed. The remaining papers, the estimates of location of the translocation, distance transferred, reason for translocation, bryophyte species, duration of experiments and transplant method were extracted. The results show that most transplant experiments are for biomonitoring projects, with very little literature dealing with bryophyte transplants for conservation efforts. Most of these studies are short-term experiments with very limited long-term translocation projects. There were also disparities between bryophyte species utilised, for example, out of the 138 journal articles there was a total of 30 bryophyte species, of which 84.06% were moss species and only 15.93% were liverworts. This suggests that liverwort species are underrepresented within translocation and reintroduction experiments. This systematic review has highlighted a research gap in the frequency of academic papers focusing on conservation-based translocation experiments. To speed up bryophyte conservation we need to focus on increasing research efforts for translocations and reintroduction projects. Furthermore, we need to develop standardized guidelines for bryophyte reintroduction and translocations.

P.1313 Sphagnum magellanicum complex at the edge: species identification and genetic diversity in the Pyrenees

Aaron Pérez-Haase[1], Joan Cuscó-Borràs[1,2,3], Magni Olsen Kyrkjeeide[4], Eulàlia Pladevall-Izard[1], Jordi López-Pujol[2], Nil Escolà-Lamora[1], Kristian Hassel[5], Víctor Lecegui-Carnero[1], Núria Garcia-Jacas[2]

1 University of Barcelona and IRBio, Barcelona, Spain. 2 Institut Botànic de Barcelona (CSIC-CMCNB), Barcelona, Spain. 3 Universidad de Sevilla, Sevilla, *Spain. 4 Norwegian Institute for Nature Research, Trondheim, Norway. 5 Norwegian University of Science and Technology, Trondheim, Norway.*

The taxonomic complex of *Sphagnum magellanicum* Brid. is widespread across cold regions worldwide. Recent molecular and morphological studies have identified two species within this complex in Europe: *Sphagnum medium* Limpr. and *S. divinum* Flatberg & Hassel. Both species have a distribution spanning the Northern Hemisphere. In the southern European mountains, notably the Pyrenees and the ranges of the Iberian Peninsula, they reach their southern limit. Here, the species are less abundant, and their distribution remains poorly understood. Moreover, because of its scarcity, *S. magellanicum* is listed as a threatened species in this region. Recent morphological studies have identified the presence of both European species within the region but have also highlighted numerous ambiguous specimens. To elucidate the taxonomic identity of the *S. magellanicum* complex in the French and Spanish Pyrenees and assess its genetic diversity, we genotyped a total of 252 ramets from 12 populations using nine microsatellites. The selected populations covered the primary ecological gradients and the whole Pyrenean distribution of the species. Microsatellite analysis revealed the presence of *S. divinum* and *S. medium* in the Pyrenees, but often in clear disagreement with previous identifications based on their morphology. Thus, most populations previously identified as *S. medium* are genetically identified as *S. divinum*. Regarding genetic conservation status, Pyrenean populations exhibited reduced genetic diversity, consisting of one or a few clones per locality. As for the ten populations of *S. divinum*, structure analysis identified five distinct groups demonstrating some geographical coherence but also spatial gaps. We argue that Pyrenean populations deserve increased attention in the reassessment and delineation of morphological boundaries between the two European species within this group. Moreover, new red list assessments are needed for the two species separately.

P.1314 Investigating the role of epigenetic inheritance in Crassulacean Acid Metabolism (CAM) photosynthesis in Cistanthe longiscapa

Dauerman, Sophie[1], Chomentowska, Anri[1], Edwards, Erika[1]

1 Yale University, Department of Ecology and Evolutionary Biology, New Haven, USA.

Cistanthe longiscapa is a charismatic annual plant in the family Montiaceae. Native to the Atacama Desert in Chile, *C. longiscapa* experiences drought stress after mass-flowering following El Niño events. This plant performs CAM photosynthesis, which involves nighttime fixation of CO_2 into malic acid and its decarboxylation during the day. This is beneficial because CAM limits daytime water loss – *C. longiscapa* is a facultative CAM plant, upregulating CAM during drought. Gas exchange monitoring revealed that the CAM cycle remains activated after rewatering, even once daytime stomatal conductance has returned to pre-drought levels. This indicates changes in expression of CAM genes that persist after the cessation of the environmental signal. One plausible explanation for the phenomenon is epigenetic changes, such as DNA methylation. In this study, we investigate the role of epigenetic modification in the regulation of functional CAM photosynthesis. We grew parental *C. longiscapa* individuals in two treatments – under drought or fully watered – and monitored plant growth. We characterized the CAM phenotypes by measuring overnight accumulation of titratable acid and tracking gas exchange data. We collected seeds from both treatments, then grew the seeds in separate batches such that F1 progeny from each treatment were grown under full-water and drought, effectively setting up four treatments. We compared CAM phenotypes of these F1 progeny, testing whether the magnitude of CAM remains upregulated in the progeny of drought plants compared to the progeny of watered plants. We also compared the timing of onset of CAM following the start of drought. In all, our experiment contributes to the literature on the role of epigenetics in conferring drought tolerance between generations by conducting the first epigenetic inheritance experiment in a facultative CAM species.

P.1315 Hyophila loxorhyncha (Pottiaceae) reinstates among neglected bryophytes of South America

Omar Rodríguez[1], María T. Gallego[1], Juan A. Jiménez[1], Juan Guerra[1], María J. Cano[1].

1 Department of Plant Biology, Botany Department, Faculty of Biology, University of Murcia, Murcia, Spain.

Assessing diversity in Pottiaceae family is among the major tasks in our taxonomic study (https://pottiaceae.com/). The currently ongoing morphological and molecular analysis of the genus *Trichostomum* Bruch in South America has allowed us to study material of this genus deposited in the main European and American herbaria and our own collections kept at MUB. We have found some specimens from Brazil, Bolivia and Paraguay that do not match with any Pottiaceae species presently recognized in these countries (Costa 2016; Churchill et al. 2009). After carrying a study of the type material of Trichostomoideae reported in this area, we have identified them as *Hyophila loxorhyncha* Müll. Hal. ex Ångstr, a neglected taxon known only from the type locality in Minas Gerais (Ångström 1876), and others in Rio de Janeiro published by V. F. Brotherus at the end of the 19th century. We present a complete description of this species, and its main distinctive morphological characters are discussed. Based on our results, we can confirm that *H. loxorhyncha* has a wider distribution extending into central Brazil and is cited for the first time in Bolivia and Paraguay. A preliminary approach of the phylogenetic position of this species within the Pottiaceae based on molecular markers is also provided.

P.1316 Towards a new bryophyte Red Data Book of Slovakia

Pavel Širka[1,*], Patrícia Singh[2], Marta Múťňanová[3], Marko Sabovljević[4,5], Eliška Kolářová[6], Katarína Mišíková[7]

*1 Technical University in Zvolen, Slovakia. 2 Masaryk University in Brno, Czech Republic. 3 State Nature Conservancy of the Slovak Republic, Banská Bystrica, Slovakia. 4 Pavol Jozef Šafárik University in Košice, Slovakia. 5 University of Belgrade, Serbia. 6 U Jam 24, Plzeň, Czech Republic. 7 Department of Botany, Faculty of Natural Sciences, Comenius University in Bratislava, Slovakia. *pavel.sirka@tuzvo.sk.*

This study presents a comprehensive assessment of the bryophyte flora in Slovakia, focusing on selected species of hornworts, liverworts, and mosses. The investigation contributes to the compilation of an updated Red Data Book of bryophytes of the Slovak Republic, shedding light on the ecological significance of these taxa from a wide range of habitats within such bryologically under-explored country. Based on new data from extensive field surveys, literature excerption and herbarium studies, we documented the geographic distribution of 52 selected species and evaluated their conservation status applying IUCN criteria. Species selection was made upon the latest country red lists. Furthermore, our study shows the potential threats to these emblematic species, emphasizing the impact of habitat destruction and global climate change. These factors pose a significant risk to the survival of several species, particularly those with restricted habitats or specific or narrow ecological requirements. Recognizing the intricate relationship between bryophytes and their environment, we underscore the urgent need for conservation efforts to mitigate these threats. In addition to its significance for researchers and policymakers, the Red Data Book can serve as a valuable tool for public awareness and education. Non-vascular plants often belong to the less-explored realms of biodiversity, and their inclusion in such publications provides a platform to highlight their ecological importance. By bringing attention to these "unpopular" taxonomic groups, the Red Data Book not only enhances public understanding of biodiversity but also fosters a sense of responsibility towards the conservation of often-overlooked species. This educational aspect is crucial in engaging the public and non-experts, cultivating a broader understanding of the complex web of life and the need for collective efforts to preserve even the most inconspicuous components of our natural heritage. Here, we present what has been done up to date and further plans on bryophyte conservation in Slovakia.

S.145. SPEEDING UP OUR UNDERSTANDING OF ADAPTIVE EVOLUTION WITH GENOMICS

P.1317 The interplay between selection and the genomic landscape during the domestication of grain amaranth

Corbinian Graf[1], Markus Stetter[1]

1 University of Cologne, Cologne, Germany.

The process of adaptation is vital for populations facing changing environments. A number of potentially adaptive traits have been studied intensively, but intrinsic traits like the genomic landscape i.e., the composition and structure of the genome, have received less attention. Multiple features of the genomic landscape influence the molecular outcome of adaptation and recent evidence indicates that some features might be under selection themselves. However, the interplay between the genomic landscape and adaptation remains unclear. To address the effect of selection on the genomic landscape, we employ the domestication of crops as a model to study adaptation. Grain amaranth is a pseudocereal from the Americas that has been domesticated independently three times from the same wild species. Our goal is to understand how parallel selection during the three independent domestications of grain amaranth changed their genomic landscape. We combine quantitative and comparative genomics to estimate the recombination rates and chromatin structures along this adaptive gradient. We are constructing recombination maps for each of the three grain species and their wild relatives. Furthermore, we assess open chromatin of two tissues of 19 individuals from wild and domesticated amaranth. We identified common and species-specific chromatin features, showing that overall chromatin composition is conserved along this adaptation gradient. We find specific regions in the genome that are differentially open between wild and domesticated amaranth, suggesting their involvement in the domestication process. The combination of chromatin structure and recombination landscapes along the selection gradient from wild to domesticated amaranth can give insights into the interplay between the genomic landscape and plant adaptation. Hence, our model of repeated adaptation provides the opportunity to understand if and how genome space is shaped by selection.

P.1318 Comparative transcriptomics reveals conserved and dynamic parts of the angiosperm transcriptome

Alexandra M. Kasianova[1], Anna V. Klepikova[2], Alexey A. Penin[2], Maria D. Logacheva[1]

1 Center for Molecular and Cellular Biology, Skolkovo Institute of Science and Technology, Moscow, Russia. 2 Laboratory of Plant Genomics, Institute for Information, Transmission Problems of the RAS, Moscow, Russia.

Angiosperms are the dominant group among land plants, being the most numerous and occupying all major ecological niches. This success is in many aspects mediated by their unique genome structure shaped by multiple polyploidization events. Duplicated genes, resulting from polyploidization are a substrate for evolutionary processes leading to their structural and functional divergence. The understanding of similarities or differences in biological functions of orthologous genes between species gives cue to the understanding of the emergence of morphological or physiological novelties; it is however challenging based on gene sequence only. We used the genome-wide data on gene expression profiles as a complementary source of information on gene function. To do this we selected genomic and RNA-Seq data for 16 angiosperm species representing all major groups (basal angiosperms, rosids, asterids, monocots). At first step genes from different species were combined into orthogroups based on the sequence similarity. Within the resulting orthogroups, using the previously developed machine learning tool ISEEML, we identified the sets of genes with conservative expression profiles (expressogroups) that form an ancestral transcriptome and divergent genes with species- or lineage-specific expression profiles. We analyzed expressogroups and genes with non-conserved expression profiles and found that the expression pattern of divergent genes is predominantly narrow. Also, divergent genes are preferentially expressed in roots, stamens and seeds. These genes are actively involved in plant defense processes against biotic and abiotic stresses and take part in the production of secondary metabolites. Conservative part has broad expression patterns, mostly lacks organ-specific expression and is involved in the processes of organelle formation, the cell division and protein synthesis. The reconstructed ancestral angiosperm transcriptome makes it possible to study both the biological processes basic for all flowering plants and to identify dynamic parts of the genetic networks specific to certain taxonomic groups.

P.1319 Beyond sweet potato: origin, evolution and development of storage roots in wild Ipomoea species

Pablo Muñoz-Rodríguez[1], Javier Fuertes Aguilar[2], Cristina Marinho[2], Miguel Ángel García García[2], Aida Díaz Mansilla[2], Lluís García Mir[2], Isabel Sanmartín[2], Elisa Román Gómez[2], N. Ivalú Cacho González[3], Enoc Efer Jara Peña[4], John R.I. Wood[5], Jaume Pellicer Moscardó[6], Oriane Hidalgo[6], Pilar Cubas Domínguez[7], Robert W. Scotland[8]

1 Universidad Complutense de Madrid, Madrid, Spain. 2 Real Jardín Botánico de Madrid-CSIC, Spain. 3 Instituto de Biología, Universidad Nacional Autónoma de México, Mexico City, Mexico. 4 Universidad Nacional Mayor de San Marcos, Lima, Perú. 5 Royal Botanic Gardens, Kew, London, United Kingdom. 6 Institut Botànic de Barcelona (CSIC), Barcelona, Spain. 7 Centro Nacional de Biotecnología (CSIC), Madrid, Spain. 8 University of Oxford, Oxford, United Kingdom.

Sweet potato, *Ipomoea batatas* (L.) Lam., is one of the most consumed crops worldwide. Cultivated in all tropical and subtropical regions of the world for its edible storage roots, *I. batatas* is the best-known species of the genus *Ipomoea* (Convolvulaceae) but it is not the only species in the genus that develops storage roots nor the only one consumed by humans. At least 80 wild *Ipomoea* species have been reported to develop underground storage organs, some of them as big as those in *I. batatas* or even bigger, and also edible. The study of these wild undomesticated species can provide important information to understand the origin of the sweet potato roots and the role of storage roots in species diversification and adaptation, and to identify new sources of genetic diversity for crop improvement. Their conservation is paramount for food security and preservation of genetic resources. In this poster, we will present preliminary results of an ongoing project that integrates genomic and transcriptomic analyses with morphological and anatomical study of herbarium collections and plants in the field and in greenhouse environments. Specifically, the aim of this project is three-fold: 1) to generate a robust evolutionary framework to study the origin and evolution of storage roots in *Ipomoea*; 2) to investigate storage root development in wild non-domesticated *Ipomoea*; and 3) to investigate whether wild species of *Ipomoea* with edible roots present traits of interest for sweet potato breeding -such as resistance to pathogens or adaptability to changing environmental conditions.

P.1320 Recurrent adaptation to whole genome duplication in wild Arabidopsis

Alison D. Scott[1], Polina Y Novikova[1]

1 Max Planck Institute for Plant Breeding Research, Cologne, Germany.

Polyploidy is a critical and dynamic evolutionary mechanism present throughout the tree of life. While polyploids occur more frequently at higher latitudes, Siberia remains largely unexplored with regard to polyploid occurrence. With field collections and widely distributed herbarium specimens, we identified previously unknown tetraploid populations of Siberian *Arabidopsis lyrata* via genotyping and cytogenetic approaches. Selection scans between diploid and tetraploid populations of Siberian A. lyrata revealed that loci under selection in tetraploid populations include key players in meiosis. As polyploidy is also a recurrent state within the genus Arabidopsis, we assessed adaptations to whole genome duplication by comparing the newly identified tetraploid Siberian populations to the well described polyploids in *Arabidopsis arenosa* and European *A. lyrata*. Existing work showed *A.* arenosa tetraploids manage polyploid meiosis by limiting crossovers to one per chromosome, and European tetraploid *A. lyrata* have benefitted from introgression with *A. arenosa*, facilitating adaptation to whole genome duplication. Given the vast geographical distance between European and Siberian A. lyrata, and the fact that *A. arenosa* does not occur in Siberia, we test the hypothesis that Siberian A. lyrata tetraploids have independently adopted a similar strategy to mitigate the impacts of polyploidy on meiosis and endoreduplication. Preliminary data suggest repeated adaptation to polyploidy in Siberian *A. lyrata* and its European counterparts alike, simultaneously drawing from standing variation, de novo variants, and long-range haplotype sharing from Europe to Siberia.

S.146. STILL STANDING: RIBOSOMAL DNA SIGNIFICANCE IN CURRENT PLANT RESEARCH

P.1321 Two types of 5S rDNA repeats in ecotypes of greater duckweed, Spirodela polyrhiza (Lemnaceae), demonstrate contrasting evolutional dynamics

Anton Stepanenko[1,2,3], Guimin Chen[2], Nikolai Borisjuk[2]

1 Institute of Cell Biology and Genetic Engineering, National Academy of Sciences, Kyiv, Ukraine. 2 School of Life Sciences, Huaiyin Normal University, Huai'an, China. 3 Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany.

The greater duckweed, *Spirodela polyrhiza*, is a monocotyledonous aquatic plant in the family Lemnaceae, which contains five genera that include 36 species. Notwithstanding the reduced size and morphology, duckweeds represent a surprisingly diverse group of plants with huge potential to explore various genetic, physiological and biochemical pathways and practical opportunities. Because of the abundant representation in eukaryotic genomes and specific molecular organization of the highly conservative sequences encoding a ribosomal RNA (rRNA) and a variable intergenic spacer (IGS), the 5S rDNA has been broadly used as a molecular tool to study genome organization, molecular evolution and phylogenetics. Here, we characterized 5S rRNA genes in 25 *S. polyrhiza* ecotypes of worldwide origin by sequencing at least ten representative rDNA units for each ecotype. Sequence analysis revealed 5S rDNA repeats with two types of IGS in each ecotype. The shorter (type-S) repeats contain the IGS of 400bp with very low variability, whereas the longer (type-L) repeats of 1056-1084bp demonstrated significant intra- and inter-genomic differences. As revealed by quantitative PCR, the number of 5S rRNA genes in the investigated duckweed ecotypes ranged between 63±12 and 198±25, one of the lowest 5S rDNA copy numbers reported for the flowering plants. The separate measurement of type-L and type-S rDNA units showed that 5S rDNA repeats with type-L IGS are prevalent in the European ecotypes compared to the ecotypes originating from the tropics. However, this observation is rather a tendency than a direct correlation, suggesting a high level of the species geographic mobility. The obtained data on the 5S rDNA organization and molecular dynamics in greater duckweed will further stimulate research and discussions on the evolution of plant rDNA and molecular forces driving homogenization of rDNA repeats.

P.1322 Drought stress regulation in oil flax: Transcriptional differences and the impact of LusP5CS1 gene overexpression

Wei Wang1, Meilian Tan[1]

1 Chinese Academy of Agricultural Science, Oil Crops Research Institute, Wuhan, China.

Oil flax (*Linum usitatissimum* L.) is an exceptionally drought-tolerant oil crop, whose regulatory mechanisms under different drought stresses, such as persistent and repeated droughts, remain elusive. To address this, we employed single molecule real-time sequencing technology (SMRT) to analyze the transcriptomes of drought-tolerant and drought-sensitive flax varieties under both drought stress and repeated drought stress conditions. Our findings indicate that oil flax responds differently to different drought stresses. Specifically, when exposed to drought stress for the first time, it primarily relies on transcriptional regulation. However, under repeated drought stress, it employs both transcriptional and alternative splicing mechanisms simultaneously. The *LusP5CS1* gene serves as a typical example of this phenomenon. Our previous experimental results in *Arabidopsis thaliana* and oil flax demonstrate that overexpression of the *LusP5CS1* gene significantly enhances drought tolerance and yield in both species. Under drought stress, the average seed weight per plant of *Arabidopsis thaliana* and oil flax overexpressing *LusP5CS1* increased by 47% and 20%, respectively, compared to wild type and control varieties. Under non-drought stress conditions, *Arabidopsis thaliana* and oil flax overexpressing the *LusP5CS1* gene also exhibit a more significant fitness advantage over wild type and control varieties, with average plant yield increasing by 40% and 22%, respectively, compared to wild type and control varieties.

S.147. SUSTAINABLE USE, TRADE AND CONSERVATION OF FRANKINCENSE (BOSWELLIA SPP.)

P.1323 The online marketing of Mexican arboreal cacti

Susana López-Torralba[1], Cecilia Leonor Jiménez-Sierra[2], José Alejandro Zavala-Hurtado[2], María Loraine Matias-Palafox[3]

1 Universidad Autónoma Metropolitana-Iztapalapa, Ciudad de México, México. 2 Departamento de Biología, Universidad Autónoma Metropolitana-Iztapalapa, Ciudad de México, México. 3 Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, CONABIO, Ciudad de México, México.

The cactus trade has increased with the use of digital media. We present an analysis of the online marketing (2022-2023) of seven species of arboreal cacti from Mexico: *Cephalocereus senilis* (old man; Threatened Species, A); *C. tetetzo* (roof); *Lophocereus marginatus* (organ); *Myrtillocactus geometrizans* (garambullo); *Pachycereus militaris* (Species in Special Protection; Pr), *Pachycereus pringlei* (cardón) and *Stenocereus queretaroensis* (pitaya queretana), as well as an estimate of illegal collection in Mexico through confiscations data. Cactus sales sites were found on: Amazon, eBay, Etsy, Mercado Libre, Sodimac and Plantadecor (total N = 652 promotional). The most offered plants are: *M. geometrizans* (34.2%) > *L. marginatus* (17.5%) > *P. pringlei* (15.8%) > *C. senilis* (14.6%) > *S. queretaroensis* (10.7%) > *C. tetetzo* (6.7%) > *P. militaris* (0.5%). In addition to specimens, seeds (32%) and cuttings (29%) are sold. Only 43% of the sites are from Mexico and the rest are foreign: USA (18.9%), followed by Spain (6.6%) and Australia (6.0%). Between 1997 and 2022 in Mexico, 6,811 specimens were confiscated: 79% were *M. geometrizans*; 11% *L. marginatus*; 8% of *C. senilis* and in smaller quantities *S. queretaroensis* and *P. militaris*. The supply of arboreal cacti is permanent and generally the origin of the specimens (wild or cultivated) or compliance with national and international commercial regulations is not indicated, so it is necessary to develop mechanisms to comply with the laws and ensure the conservation of these species. In Mexico, complying with regulations for the cultivation of at-risk species is complicated, which explains the low legal supply of these plants. This puts natural populations at risk due to clandestine extraction of individuals and at the same time this does not favor the natural commercial vocation of Mexico, which has the appropriate climatic conditions for the cultivation of these plants.

S.148. SYNANTHEROLOGY RELOADED: RECENT ADVANCES AND THE FUTURE OF EVOLUTIONARY STUDIES IN COMPOSITAE

P.1325 Genetic diversity and structure of three annual autogamous species that constitute the Filago-LGC clade (Gnaphalieae, Asteraceae)

Santiago Andrés-Sánchez[1], Daniel Pinto-Carrasco[2], Javier Marcos Walias[1], Diego Sánchez Ganfornina[1], Enrique Rico[1], Catarina Siopa[3], João Loureiro[3], M. Montserrat Martínez-Ortega[1]

1 University of Salamanca, Salamanca, Spain. 2 University of Leon, Leon, Spain. 3 University of Coimbra, Coimbra, Portugal.

Connectivity and gene flow among populations are forces that shape plant genetic structure. Additionally, gene flow is modulated by several factors (i.e. geographic distance and barriers, ability to colonize new areas, specific biological properties of the species or environmental factors), which interrupt or allow different levels of genetic exchange among populations. However, the impact that some of them can have may be uneven. In this work, we contrast the structure of genetic diversity of three annual autogamous species of *Filago* (Gnaphalieae, Asteraceae) that form the monophyletic "LGC clade" (*F. lusitanica*, *F. gaditana* and *F. carpetana*). These species are distributed in the Western Mediterranean region. AFLP (Amplified Fragment Length Polymorphisms) markers were obtained for 524 individuals from 61 populations. Our results confirmed the current taxonomic status of the three species and allowed us to evaluate the role that the Strait of Gibraltar and the Spanish Central System range have played as barriers against gene flow, as well as the different degrees of their permeability for each species. The Strait of Gibraltar acts as a permeable barrier in the case of *F. lusitanica*, but it is very effective against gene flow in *F. gaditana*. The genetic variability of *F. carpetana* is structured into two groups determined by the effect of the Central System range, which exhibits a more substantial effect than that of the Strait of Gibraltar over the other two species. The observed differences in the effect of these geographical barriers on the studied species could be due to their biological characteristics. This study demonstrates that the same geographical barrier can exhibit varying levels of permeability depending on other factors affecting a particular species.

P.1327 The architectural analysis in Lychnophorinae (Asteraceae): a key method for facilitating giant clades taxonomy

Khalil Boughalmi[1,2], Benoit Loeuille[3], Artémis Anest[1]

1 AMAP, Univ Montpellier, Montpellier, France. 2 Université Grenoble Alpes, Grenoble, France. 3 Royal Botanic Gardens, Kew, Richmond, United Kingdom.

The family Asteraceae is the most diversified angiosperm family with approximately 30,000 species. Due to its diversity, it consists of a taxonomic challenge, especially at the specific level. While these species are distributed on all vegetated continents and occupy very distinct biomes along a significant climatic and altitudinal gradient, some taxa show a high level of endemism with species sometimes displaying high degree of microendemism. This is the case for the subtribe Lychnophorinae: with 19 genera and 119 species, this clade has almost all species endemic to the Espinhaço region, east of Brazil. In addition to a characteristic distribution area, these species also display characteristic structures with several genera containing arborescent species. This treelike habit, often considered anecdotal within Asteraceae, could indicate a strong selection for arborescent development in this environment. Morpho-anatomical peculiarities also seem to suggest a strong selection pressure by disturbances in this environment. The objective of this study was to gather all known taxonomic, structural, anatomical, and biogeographical knowledge of Lychnophorinae. Subsequently, a preliminary architectural analysis (sensu Hallé et al., 1978) has been conducted to determine the structural traits, over time and space, of these species. Finally, additional environmental data have been acquired via online databases to more precisely define the major ecological factors of the environment where these species grow. The final objective of this study has been to identify the key elements necessary to conduct a comprehensive study of the evolutionary history of Lychnophorinae in relation to environmental factors. In addition to showing the potential of the architectural analysis to improve the precision of the Asteraceae taxonomy, this study highlights the importance of understanding the evolutionary history of plant clades to proposing conservation plans for any plant species and clade.

7.01328 Exploring the biotic connections between southern South America and its neighboring islands with Lagenophora Cass. (Asteraceae)

Gisela Sancho[1], Rosa A. Scherson[2], Jessica N. Viera Barreto[1], Mariano Donato[3], José M. Bonifacino[4], J. Gordon Burleigh[5]

1 Museo de La Plata, FCNYM, UNLP, Buenos Aires, Argentina. 2 Universidad de Chile, Santiago, Chile. 3 ILPLA, Instituto de Limnología, FCNYM, UNLP and CONICET, Buenos Aires, Argentina. 4 Universidad de la República, Montevideo, Uruguay. 5 University of Florida, Gainesville, USA.

Lagenophora (Asteraceae) has drawn researchers' attention due to its austral, transpacific distribution and the absence of the family's typical dispersal mechanism, the pappus. Its sticky fruits seemly serve as an efficient dispersal mechanism involving several potential dispersal vectors, such as birds. Alternatively, successful over-water dispersal events may be aided by the oily fruit cover. *Lagenophora* is found in Australia, New Zealand, SE Asia, and southern South America. The three South American species are monophyletic and occur in Andean Argentina and Chile, usually as elements of the understory and gaps of southern beech forests. Two of these species extend to nearby islands, such as Tierra del Fuego and State Island, and more distant archipelagos like Malvinas/Falkland Islands, Gough and Tristan da Cunha islands, and Juan Fernandez Archipelago. Previous studies provided evidence that Antarctica played a key role in the connections of Lagenophora between New Zealand and South America. The objective of this study is to reconstruct the biogeographic history of the South American species of *Lagenophora*. Through this research, we aim to understand the impact of Quaternary climatic changes on the distribution of the southernmost South American biota. We generated nuclear sequence data using target enrichment sequencing with the GoFlag angiosperm 408 probe set to create phylogenetic trees that included individuals of South American *Lagenophora* species from continental and island populations throughout the whole distributional range. We also conducted distributional modelling for different past climate scenarios, ancestral area reconstruction, and climatic space comparisons. Phylogenetic results show that the ancestors of *Lagenophora* in South America were probably settled in the Andes. Relatively early-branching clades colonized the extreme South of Chile, i.e., islands by the Cape Horn, the Malvinas/Falklands archipelago, State Island, and Juan Fernández Archipelago. Populations of State Island are, apparently, a result of more than one colonization event.

P.1329 Hyb-Seq insights into Helichrysum and related genera (Gnaphalieae, Compositae): implications in systematics and generic delimitation

Òscar Castillo[1], Carme Blanco-Gavaldà[2], Santiago Andrés-Sánchez[3], Randall J. Bayer[4], Nicola Bergh[5], Juan Antonio Calleja Alarcón[6], Pau Carnicero[7], Glynis V. Cron[8], Susana E. Freire[9], Kazumi Fujikawa[10], Rokiman Letsara[11], Lucía D. Moreyra[1], Genís Puig-Surroca[2], Sylvain G. Razafimandimbison[12], Cristina Roquet[2], Rob D. Smissen[13], Alfonso Susanna[2], Mercè Galbany-Casals[2]

1 Botanical Institute of Barcelona, Barcelona, Spain. 2 Systematics and Evolution of Vascular Plants UAB – IBB CSIC, Bellaterra, Spain. 3 University of Salamanca, Salamanca, Spain. 4 University of Memphis, Memphis, USA. 5 South African National Biodiversity Institute, Cape Town, South Africa. 6 Autonomous University of Madrid, Madrid, Spain. 7 University of Innsbruck, Innsbruck, Austria. 8 University of Witwatersrand, Johannesburg, South Africa. 9 Museo Argentino de Ciencias Naturales, Buenos Aires, Argentina. 10 Makino Botanical Garden, Kochi, Japan. 11 Herbarium of the Parc Botanique et Zoologique of Tsimbazaza, Antananarivo, Madagascar. 12 Swedish Museum of Natural History, Stockholm, Sweden. 13 Landcare Research, Christchurch, New Zealand.

The systematics of the tribe Gnaphalieae (Compositae) has long presented challenges, particularly concerning the HAP (*Helichrysum-Anaphalis-Pseudognaphalium*) clade, which globally contains ca. 850 species. Its main component is *Helichrysum*, with ca. 600 species, identified as paraphyletic in previous phylogenies, having several genera being embedded within it. The existence of polyploidy and hybridisation, which might cause of phylogenetic incongruence and low support values in phylogenies, has further complicated our understanding of the evolutionary history of the clade. Additionally, a considerable morphological variation and the lack of synapomorphies for each clade add other layers of complexity to providing a satisfactory generic classification. The advent of high-throughput DNA sequencing methods has fostered significant advancements in plant systematics. The substantial increase in the number of markers sequenced enhances the robustness of phylogenetic reconstructions. We applied a target capture approach that resulted in the obtention of sequences for hundreds of exons. We then analysed them with ParalogWizard pipeline, which facilitates the separation of paralog sequences and the creation of orthologous alignments. Building on such large molecular dataset, we inferred the most comprehensive phylogeny to date for the HAP clade, with a total of 560 samples, including representatives of eight additional genera known to be part of it. Our phylogenetic tree recovers *Helichrysum* as a paraphyletic genus, with eight additional genera embedded in its main clade. The results obtained evidence the need of a generic recircumscription, and several options are presented considering current available data on chromosome numbers, biogeography and morphology.

P.1330 Out-of-the-Andes: molecular phylogenetics and historical biogeography of Ecliptinae (Heliantheae)

Rafael Felipe de Almeida[1,2], Maria Alves[3], João Bringel Jr.[4], Cássio van den Berg[3], Morgan R. Gostel[5], Nádia Roque[3,6]

1 Universidade Estadual de Goiás, Quirinópolis, Goiás, Brazil. 2 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 3 Universidade Estadual de Feira de Santana, Feira de Santana, Bahia, Brazil. 4 Empresa Brasileira de Pesquisa Agropecuária, Brasília, Distrito Federal, Brazil. 5 Botanical Research Institute of Texas, Fort Worth, Texas, United States of America. 6 Universidade Federal da Bahia, Salvador, Bahia, Brazil.

Ecliptinae is one of the 14 subtribes within tribe Heliantheae (Asteraceae), comprising 54 genera and ca. 570 species distributed worldwide. Even though these subtribes have been the subject of several molecular phylogenetic studies throughout the last two decades, several still show problematic circumscriptions due to large polyphyletic genera such as *Melanthera* and *Wedelia*. The latter comprises ca. 200 spp. with a very confusing taxonomic delimitation due to conflicting circumscriptions proposed by several authors around the world. In order to understand the relationship of species of the polyphyletic *Wedelia* in Ecliptinae, we ran a maximum likelihood combined analysis using RAxML based on two nuclear (ITS and ETS) and three plastid (*matK*, *psbA-trnH*, and *trnQ-rps16*) markers. The resulting tree was used to estimate a calibrated molecular clock using BEAST to generate a dated phylogenetic tree. Additionally, ancestral range reconstruction was run in BioGeoBEARS with the dated phylogeny for biome and continental ranges. Our results show that *Wedelia*, *Aspilia*, *Lundellianthus*, *Oyedaea*, *Steiractinia*, and *Zexmenia* comprise a single well-supported clade (89% bootstrap support) that we refer to as *Wedelia* s.l. The Antillean *Wedelia reticulata* was recovered as sister to *Baltimora* and *Tilesia*, rendering *Wedelia* s.l. paraphyletic. The dated phylogeny recovered the most recent common ancestor of Ecliptinae originated approximately 8.16 Mya in dry/rainforests of the Andes in South America. A single dispersal event led to the radiation of most lineages of Ecliptinae in dry forests of Central America, approximately 7.6-4.32 Mya. Several lineages of Ecliptinae reached South American dry forests a second time from 4.85-4.0 Mya via three different dispersal events (*Wedelia* s.l., *Dimerostemma* and *Echinocephalum* clades). Two lineages (*Elaphandra* and *Riencourtia*) radiated in South American savannas between 2.95-1.65 Mya.Finally, four lineages reached and radiated in old-world dry forests from 2.73-1.5 Mya.

P.1331 Achene and pollen morphology in the genus Psephellus Cass. (Asteraceae) in Turkey

Kuddisi Ertuğrul[1], Tuna Uysal[1], Meryem Bozkurt[1], Nur M. Pınar[2]

1 Department of Biology, Faculty of Science, Selçuk University, Konya, Turkey. 2 Department of Biology, Faculty of Science, Ankara University, Ankara, Turkey.

The genus *Psephellus* Cass. is represented by approximately 100 species in the world and has a distribution centered mainly in Turkey, the Caucasus and Northwest Iran. The genus is represented by 37 taxa in Turkey, and it has a distribution area centered mainly in Central and Eastern Anatolia. Additionally, a small number of species are found in the Southern, Southeastern and Northeastern Anatolia regions. 28 of these taxa are endemic to Turkey. In this study, achene and pollen characteristics of *Psephellus* taxa in Turkey were determined by light and scanning electron microscopy and data on many characters related to these two structures were obtained. A dendogram was created with the obtained data with the PRIMER program. The relationship among *Psephellus* taxa were revealed by evaluating the obtained dendrogram. Pollen and achene characteristics could be important in distinguishing the taxa of the genus. **Acknowledgements:** We are also grateful to the foundation TUBITAK (Project Number: 109T958) and S.U.BAP (Project Number: 17401028) for financial support.

P.1332 Chemophenetic significance of phenolic compounds of the Balkan Amphoricarpos Vis. taxa (Compositae)

Pedja Janaćković[1], Milan Gavrilović[1], Uroš Gašić[2], Dušanka Milojković Opsenica[3], Alfonso Susanna[4]

1 University of Belgrade, Faculty of Biology, Belgrade, Serbia. 2 University of Belgrade, Institute for Biological Research "Siniša Stanković", National Institute of Republic of Serbia, Department of Plant Physiology, Belgrade, Serbia. 3 University of Belgrade,Faculty of Chemistry, Belgrade, Serbia. 4 Botanic Institute of Barcelona (IBB, CSIC-ICUB), Barcelona, Spain.

The genus *Amphoricarpos* Vis. (Compositae-Cardueae-Xerantheminae) represents a natural group, well characterized on molecular and morphological features. *Amphoricarpos* species are heterocarpic perennial chasmophytic plants, mountain endemics in the eastern Mediterranean (the Balkans, Anatolia and the Caucasus). Taxonomy of the genus *Amphoricarpos* is complex and ambiguous. Traditionally, Blečić and Mayer recognized three taxa distributed on the Balkan Peninsula: *A. neumayerianus* (Vis.) Greuter (*A. neumayeri* Vis.), *A. autariatus* ssp. *autariatus* Blečić & Mayer and *A. autariatus* ssp. *bertisceus* Blečić & Mayer. Caković et al. (2015) treated all Balkan populations as a single species – *A. neumayerianus* (Vis.) Greuter. Latest view separated *A. neumayerianus* into three subspecies: *neumayerianus* (ANN), *autariatus* (ANA) and *murbeckii* (ANM) (Niketić, Gavrilović and Janaćković 2022). In this work, we analyzed, for the first time, phenolic compounds of the leaf extracts of the three Balkan *Amphoricarpos* taxa using HPLC-LTQ Orbitrap-MS[4]. It was shown that phenolic profiles were not identical. A total of 30 phenolic compounds were identified (27 in ANA, 26 in ANM and 25 in ANN), of which 22 were found in traces. Out of 30 compounds, 11 compounds belong to the group of phenolic acids and derivatives, seven compounds belong to the group of flavonoid glycosides, 11 compounds belong to the group of flavones, and one compound belongs to the group of flavanones. The dominant compound in ANA and ANM was 5-O-caffeoylquinic acid (6.566 mg/L and 6.715 mg/L, respectively), while the dominant compound in ANN was chrysoeriol (4.216 mg/L). In addition, five compounds, which were found in the extracts of ANM and ANA, were not detected in ANN extract, while one compound was detected only in ANN extract. These differences support segregation of the type subspecies from the other taxa of the complex.

P.1333 New Compositae specific probe set reduces paralogs in complex systems

Erika R. Moore-Pollard[1], Daniel S. Jones[2], Jennifer R. Mandel[1]

1 Department of Biological Sciences, University of Memphis, Memphis, USA. 2 Department of Biological Sciences, Auburn University, Auburn, USA.

Probe sets have been designed to broadly target gymnosperms, angiosperms, or specific plant families (i.e., Asteraceae, Fabaceae, Ochnaceae, etc.), enabling great advances in our understanding of evolutionary relationships in large plant groups. The Asteraceae specific probe set, Compositae-1061, is popular among researchers studying members of Asteraceae, and has paved the way for investigations at lower taxonomic levels and non-model organisms. Though Compositae-1061 has shown to be highly efficient at higher- and some lower-taxonomic levels within the family, it generally lacks resolution at the genus to species level, especially in groups with complex evolutionary histories including polyploidy and hybridization. In this study, we developed a new Hyb-Seq probe set, Compositae-ParaLoss-1272, designed to target known single-copy orthologous loci in Asteraceae family members. We tested its efficiency across the family by simulating target-enrichment sequencing in-silico. Additionally, we tested its effectiveness at lower taxonomic levels in the genus Packera, which has a complex evolutionary and taxonomic history. We performed Hyb-Seq with Compositae-ParaLoss-1272 for 19 taxa which were previously studied using the Compositae-1061 probe set. Sequences from both probe sets, along with a double-capture approach, were used to generate phylogenies, compare topologies, and assess node support. We found that the newer probe set captured loci across all tested Asteraceae members. Additionally, Compositae-ParaLoss-1272 recovered drastically less paralogous sequences than Compositae-1061, with only ~5% of the recovered loci reporting as paralogous with the new probe set, and 59% with the Compositae-1061 probe set. Additionally, we found that discordance was lower and species relationships more closely followed previous studies when utilizing the new probe set. Given the complexity of plant evolutionary histories, assigning orthology for phylogenomic analyses will continue to be challenging. However, we anticipate this new probe set will provide improved resolution and utility for studies at lower-taxonomic levels and complex groups in the sunflower family.

P.1334 Morphological differentiation of taxa of the Centaurea calocephala complex from the Dinaric Alps (SE Europe)

Jelica Novaković[1,*], Bojan Zlatković[2], Dmitar Lakušić[1], Nemanja Rajčević[1], Petar D. Marin[1], Pedja Janaćković[1]

*1 University of Belgrade, Faculty of Biology, Institute of Botany and Botanical Garden "Jevremovac", Belgrade, Serbia. 2 University of Niš, Faculty of Science and Mathematics, Department of Biology and Ecology, Niš, Serbia. *jelica@bio.bg.ac.rs*

The *Centaurea calocephala* complex belongs to the subgenus *Acrocentron*, subtribe Cardueae (Asteraceae). The species of this complex are characterised by large capitula, ovate to oblong involucral bracts with decurrent appendages covering the bracts. The appendages are black, brown or yellow, mucronulate to shortly spiny at the apex, and fimbriate at margins. The complex has a Carpathian-Balkan distribution, with several species inhabiting open grasslands on the mountains of the Carpathian, Dinaric, Balkan, Rhodope, and Skardo-Pindian mountain range. The largest species richness of this complex was registered in the mountains of the Dinaric system (Dinaric Alps), where the following species were registered *C. calocephala* Willd., *C. zlatiborensis* Zlatković, Novaković and Janaćković, *C. melanocephala* Pančić, *C. murbeckii* Hayek, *C. kotschyana* Heuffel ex Koch, *C. crnogorica* Rohlena, and *C. gjurasinii* Bošnjak. The aim was to present the results of the morphometric study on the morphological characteristics of the investigated taxa from the Dinaric Alps. The measurements included 140 individuals and 47 traits (morphometric, meristic, and qualitative traits) that we analysed. A canonical discriminant analysis of the *a priori* defined groups was performed. The first canonical discriminant analysis, which included all Dinaric taxa, showed a clear differentiation of *C. melanocephala* in the positive part of the first and second axes and in the negative part of the third axis. *C. kotschiana* and *C. murbeckii* formed a group in the negative part of the first and second axes, but these two taxa are morphologically well differentiated. The other taxa are morphologically close to each other and form the *Calocephala* group. The next canonical discriminant analysis included taxa that formed the *Calocephala* group in the previous analysis. The results showed a clear differentiation between the studied Dinaric taxa.

P.1335 Pollen morphology of Senecio sect. Crociseris (Compositae, Senecioneae) from Iberian Peninsula and its taxonomical implications

Rafael Pérez-Romero[1], Carmen Pérez Morales[2], Rosa M. Valencia Barrera[2], Sara del Río González[2] , Ángel Penas[2]

1 Department of Biology and Geology, IES Los Sauces, Benavente, Spain. 2 Department of Biodiversity and Environment Management, University of León, León, Spain.

This investigation focuses on the palynological examination of *Senecio* L. sect. *Crociseris* (Rchb.) Boiss., specifically on the Iberian Peninsula, and extends its comparison to closely related species within *Senecio* and *Doronicum*. The study analyzes the pollen morphology of eight species and five subspecies from the *Crociseris* section found in the Iberian Peninsula. The pollen was examined using both light microscopy and scanning electron microscopy (SEM) to capture detailed morphological features. To further discern the relationships and distinctive palynological characteristics that could aid in differentiating the studied taxa, a suite of statistical analyses was performed, including Principal Component Analysis (PCA), Discriminant Analysis (DA), Multidimensional Scaling (MDS), and Hierarchical Cluster Analysis (HCA). The research found that the pollen grains are isopolar, exhibit radial symmetry, tricolporate, and possess an echinate surface. The shape of the pollen varied from prolate-spheroidal to spheroidal, with significant differences observed primarily in the size and ornamentation of the spines. Through PCA, DA, MDS, and HCA, three well-defined groups within the *Senecio* sect. *Crociseris* were identified. These findings are instrumental in understanding the relationships among the *Senecio* taxa and provide valuable insights for future taxonomic investigations within this group.

P.1336 Systematics and evolution of Madagascan montane ericoid Helichrysum (Compositae) based on Hyb-Seq and morphometric analyses

Genís Puig-Surroca[1], Mercè Galbany-Casals[1], Carme Blanco-Gavaldà[1], Òscar Castillo[2], Rokiman Letsara[3], Lucía D. Moreyra[2], Sylvain G. Razafimandimbison[4], Cristina Roquet[1], Alfonso Susanna[1], Santiago Andrés-Sánchez[5]

1 Systematics and Evolution of Vascular Plants (UAB) – Associated Unit to CSIC, Bellaterra, Spain. 2 Botanical Institute of Barcelona, Barcelona, Spain. 3 Herbarium of the Parc Botanique et Zoologique of Tsimbazaza, Antananarivo, Madagascar. 4 Swedish Museum of Natural History, Stockholm, Sweden. 5 University of Salamanca, Salamanca, Spain.

Madagascar is one of Earth's biodiversity hotspots, with high species richness and exceptional levels of endemism. Despite this, there is an evident lack of knowledge on taxonomy and evolution, particularly on its mountains' flora. Given the current biodiversity crises, it is imperative to improve our understanding of species delimitation and evolutionary processes (plant diversification and speciation) in these areas. The genus *Helichrysum* Mill. (Compositae, Gnaphalieae) constitutes an interesting case-study to address these knowledge gaps. With 111 species in Madagascar, all but one endemic, and more than 40% found in montane habitats, including some exclusive to mountain summits, it offers valuable insights into these topics. This work focuses on a group of endemic Madagascan montane *Helichrysum* composed of 25 taxa, all of them ericoid subshrubs, the Madagascan Montane Ericoid *Helichrysum* clade. They have different habitat preferences and varied distribution patterns, providing contrasting examples of plant evolution. Additionally, many of these taxa are rare and probably threatened by human activities, but conservation assessment is lacking for most of them. The main objective of this study is to provide insights into the current status, systematics and evolution of the group, through a multidisciplinary approach. We made morphometric analyses and a chorological study of all taxa based on herbarium material, as well as own field collections and observations. Furthermore, we used a Hyb-Seq methodology targeting 1061 nuclear conserved ortholog loci designed for Compositae to infer a phylogeny of this group, including most taxa and several specimens of each taxon when available. We provide preliminary hypotheses on the phylogenetic relationships and diversification patterns of this group in Madagascar mountains. All data point out to the need of a comprehensive taxonomic revision of the whole group and the urgency of a conservation assessment for most of the species.

P.1337 The taxonomic importance of glandular-hairy phyllaries in Cichorium intybus (Asteraceae)

Nilay Şen[1], Aslı Doğru-Koca[1]

1 Department of Biology, Faculty of Science, Hacettepe University, Ankara, Turkey.

The genus *Cichorium* L. is distributed worldwide with seven species. Among them, the species *C. intybus* L., *C. spinosum* L., *C. pumilum* Jacq., *C. glandulosum* Boiss. & A.Huet grow naturally in Turkey. *C. endivia* L. is cultivated in Istanbul and Europe. *C. bottae* Deflers and *C. calvum* Sch. Bip. are endemic to Saudi Arabia-Yemen and Ethiopia respectively. It has been noticed that in different herbarium samples of *Cichorium intybus* collected from the coastal localities of the Black Sea region, there are glandular hairs on their phyllaries, although there are no glandular hairs in other populations all over Turkey. Twenty-five populations were collected from the entire Black Sea coast. These and previously collected samples from all over Turkey were examined in detail morphologically, and evolutionary relationships were revealed using Bayesian and Maximum Likelihood analyses based on sequences of ribosomal DNA (ITS1-5.8S-ITS2) and combined chloroplast DNA (trnL, trnL-trnF, psbA-trnH, rpl32, rpl16, matK, ndhF, rpoC1, rbcL, rps16, trnK, trnQ).According to the chloroplast phylogeny tree, four populations with glandular hairs and four populations with non-glandular hairs are placed in two separate monophyletic clades. However, the populations from the Western Black Sea (Akçakoca) and the Central Black Sea (Kastamonu) belonged to opposite lineages. According to the ribosomal phylogeny, *C. endivia* was nested within *C. pumilum*. Similarly, *C. spinosum*was nested in the *C. intybus* clade. The glandular-hairy populations of *C. intybus* did not generate a monophyletic clade according to ITS. As a result, the glandular-hairy populations could be evaluated as a new variety of *C. intybus* based on the combined phylogenetic result and morphological data.

P.1338 Helichrysum Mill. on Balkans – a review of current taxonomy

Milica Trajković[1], Milan Gavrilović[1], Alfonso Susanna[2], Peđa Janaćković[1]

1 Department of Morphology and Systematic of Plants, University of Belgrade, Faculty of Biology, Belgrade, Serbia. 2 Botanic Institute of Barcelona (IBB, CSIC-ICUB), Barcelona, Spain.

Helichrysum Mill. (HAP clade-Gnaphaliinae-Gnaphalieae) comprises 500-600 species. In the central Balkan region (Serbia, Croatia and Montenegro) there are four species of *Helichrysum*, *H. arenarium* (L.) Moench in Serbia, Croatia and Montenegro, *H. stoechas* (L.) Moench and *H. litoreum* Guss. in Croatia, and *H. italicum* (Roth) G. Don with two subspecies *H. italicum* subsp. *italicum* in Croatia and Montenegro and *H. italicum* subsp. *microphyllum* (Willd.) Nyman in Croatia. *Helichrysum italicum* complex comprises three species sharing two morphological characters: cylindrical to cylindrical-campanulate capitula and outermost involucral bracts partially or completely herbaceous and covered with a dense indumentum. These species are *Helichrysum serotinum* (DC.) Boiss., found in Spain, Portugal, France and Algeria with two subspecies *H. serotinum* subsp. *serotinum* and *H. serotinum* subsp. *picardii* (Boiss. & Reut.) Galbany, L. Sáez & Benedí, *H. litoreum* Guss. found in Italy and Croatia and *H. italicum* spread across the whole Mediterranean. According to Galbany-Casals et al. (2006) three subspecies are recognized within *H. italicum*, *H. italicum* subsp. *italicum* (widespread in Italy, Croatia, eastern Mediterranean coast of France and Corsica, Bosnia and Herzegovina, Greece – mainly Aegan islands and Cyprus), *H. italicum* subsp. *microphyllum* (endemic to Crete) and *H. italicum* subsp. *siculum* (Jord. & Fourr.) Galbany, L. Sáez & Benedí (endemic to Sicily). Herrando-Moraira et al. (2016) provided a taxonomic revision of the whole *H. italicum* complex. The Majorcan mountain populations of *H. italicum* subsp. *microphyllum* is considered as *H. massanellanum* Herrando, J. M. Blanco, L. Sáez & Galbany, *H. italicum* subsp. *tyrrhenicum* (Bacch., Brullo & Giusso) Herrando, J.M.Blanco, L.Sáez & Galbany, comprises populations from Corsica, Sardinia, Majorca coastline and Dragonera islet, while subsp. *microphyllum* is restricted to the island of Crete. These observations indicate an ambiguous relationship within the *H. italicum* complex which needs to be reexamined.

P.1339 Phylogeography of Schlechtendalia luzulifolia, a member of the basal subfamily Barnadesioideae (Asteraceae)

Klusch M. Celeste[1], Salariato Diego L. [1], Stuessy Tod F. [2], Nicola Marcela V. [1], Bonifacino Mauricio J.[3], Freire Susana E. [4], Delfini Carolina[1], Urtubey Estrella[1]

1 Instituto de Botánica Darwinion, San Isidro, Argentina. 2 The Ohio State University, Columbus, United States of America. 3 Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay. 4 Museo Argentino de Ciencias Naturales, Ciudad de Buenos Aires, Argentina.

Schlechtendalia luzulifolia Less. belongs to the basal South American subfamily Barnadesioideae (Asteraceae). It is a perennial herb that diverges morphologically, geographically and ecologically from the other nine barnadesioid genera. This monospecific genus is mainly distributed across the ecoregions of eastern Argentina, Uruguay and southern Brazil (Rio Grande do Sul and Paraná). The objective of this study is to understand the evolutionary history and genetic diversity and structure of this taxon. We have conducted phylogeographic studies based on a wide populational sampling, using nuclear and plastid markers for analysing genetic spatial distribution, diversity and structure, test for range expansion, and reconstruct ancestral areas. In addition, climatic niches of the main phylogeographic groups were studied and compared using multivariate techniques in environmental space. Our results reveal two main haplogroups associated with: (1) savannas (Argentina and Uruguay) and grasslands (Uruguay and Rio Grande do Sul, Brazil); and (2) grasslands of the northern portion of the Araucaria moist forest (Paraná, Brazil). Likewise, ecological niche comparisons in n-dimensional space showed that populations belonging to these two phylogeographic groups differ not only in the ecoregions where they are distributed, but also in the climatic niches they occupy. These results evidence a major genetic and ecological differentiation for *Schlechtendalia* populations into two main phylogroups, which suggest historical processes that may have influenced divergence of these two metapopulations. Furthermore, results emphasize that for this species, which grows in grasslands strongly threatened by human activity, not only should conservation of the species itself be proposed, but also of its main phylogeographic groups.

S.149. SYSTEMATICS AND EVOLUTION OF EUPHORBIACEAE

P.1340 Afrotropical Euphorbiaceae genera on the EDGE: singular and endangered species

Ángela Aguado-Lara[1*]; Paloma Ruiz de Diego[1]; Irene Villa-Machío[1,2]; Patricia Barberá[2]; Ricarda Riina[1], Isabel Sanmartín[1]

1 Real Jardín Botánico, CSIC, Madrid, Spain. 2 Missouri Botanical Garden, St. Louis, Missouri, USA.

Despite being larger in size than South America, Africa hosts a lower number of vascular plant species (47% less than the Neotropics), a difference termed the "Odd-Man-Out" pattern. The family Euphorbiaceae is a clear example of this disparity in species richness (1014 in Africa vs. 2548 in the Neotropics). Even more striking is the ratio species/genera: c. 80% of African genera comprise less than 10 described species; some of the remaining genera include hyper-diverse genera that are also present in other tropical regions (e.g., *Croton*). The drivers behind this pattern are still debated, fueled by a knowledge gap on alpha taxonomy, phylogenetic relationships, and species distribution ranges in comparison with the better-studied Neotropical flora. An ongoing study on Afrotropical Euphorbiaceae revealed that some of these species-poor genera originated in the Paleogene. We suggestthat high-extinction rates associated to an increase in aridification arebehind species depauperation in these genera, and that these lineages fit the "dead clade walking" concept, i.e., formerly diverse groups bottlenecked by an extinctionevent without subsequent recovery. Here, we focus on 70 Afrotropical genera, summing over 288 species, of which 22 genera are monotypic. We reconstruct phylogenetic relationships and divergence times for each genus, based on molecular data obtained with a target sequencing approach (Hyb-Seq), and use these reconstructions to estimate rates of diversification, background extinction, and migration among biomes. Afrotropical Euphorbiaceae occurs on a variety of bioregions, being the tropical rainforest the most threatened by climate change and human activities. Using the information generated above, and conservation assessments, we aim to identify EDGE (Evolutionary Distinct and Globally Endangered) taxa among Afrotropical Euphorbiaceae. We present our preliminary results based on molecular data for 157 species and 144 assessments for the IUCN (ca. 55% and 51% sampling).

P.1341 From morphology to phylogenomics: a hidden adaptive radiation of Malagasy Alchornea with seven new species

Patricia Barberá[1], Armand Randrianasolo[1], Olivier Lachenaud[2,3], Irene Villa-Machío[1], Peter B. Phillipson[1,4], Alexander G. Linan[1], Joan Garcia-Porta[5]

1 Missouri Botanical Garden, St. Louis, Missouri, USA. 2 Meise Botanic Garden, Meise, Belgium. 3 Université Libre de Bruxelles, Brussels, Belgium. 4 Muséum National d'Histoire Naturelle, Paris, France. 5 Complutense University of Madrid, Madrid, Spain.

Madagascar stands as a significant biodiversity hotspot, with more than 9,000 species of endemic plants. At the same time, many of these species face substantial threats and remain poorly known, emphasizing the need for biodiversity exploration and species discovery on the island. Here we address this challenge, by establishing an integrated taxonomic framework, incorporating evidence from morphology, distributions, climatic niche, and phylogenomics, to produce a taxonomic revision of the genus *Alchornea* in Madagascar and the Comoros. Before the present study, only three species were documented in the region; however, our study revealed that this previously known diversity was greatly underestimated. Our findings include the description of seven new species, significantly expanding the eco-morphological species diversity within *Alchornea* in Madagascar. Through the morphometric comparison of the 13 Malagasy-Comoran species with their continental relatives, we observe a notable and rapid expansion of morphospace of island endemic lineages, consistent with the existence of adaptive radiation. This study underscores the power of integrating multiple sources of evidence, not only for the discovery of new species but also for identifying remarkable diversification patterns. Strikingly, four of the newly described species were assessed as threatened, stressing even more the urgency for biodiversity discovery and conservation in Madagascar.

P.1342 Origin and evolution of tropical plant lineages of economic interest: integrated studies on the megadiverse genus Acalypha

José María Cardiel[1], Iris Montero Muñoz[2], Emma Ortúñez Rubio[1], Roberto Gamarra Gamarra[1], Francisco Pando de la Hoz[2], Patricia Barberá[3], Geoffrey Levin[4], Leopoldo Medina Domingo[2,5], Lucía Villaescusa González[5], Pablo Muñoz-Rodríguez[5]

1 Universidad Autónoma de Madrid, Madrid, Spain. 2 Real Jardín Botánico-CSIC, Madrid, Spain. 3 Missouri Botanical Garden, Saint Louis, USA. 4 Canadian Museum of Nature, Ottawa, Canada. 5 Universidad Complutense de Madrid, Madrid, Spain.

Big tropical genera host a large part of the world's plant diversity. These genera often have a pantropical distribution and include species of economic interest. *Acalypha*, the third largest genus in Euphorbiaceae, is one such example, with *ca.* 500 described species present in all tropical and subtropical regions of the world. Around a third of *Acalypha* species have been reported to produce metabolites of pharmacological or chemical interest. Despite its relevance and potential economic importance, most *Acalypha* species remain poorly known, and new species are still described regularly. In this context, we need to accelerate the pace at which biodiversity studies are done. This, in turn, requires a good taxonomic and biogeographic knowledge of the group, which is missing for most species. Understanding the origin and evolution of *Acalypha* species requires a comprehensive approach to the whole genus and not only the species of economic importance. In this talk, we will present ACALPHARMA, an ongoing project to study the taxonomy and evolution of the genus *Acalypha* worldwide with a focus on the species of continental Africa and Madagascar, where the genus likely originated, and where more species with medicinal properties are known. Our project integrates herbarium-based morphological studies and field work with molecular sequence data and global biodiversity databases to study the genus *Acalypha* at a global scale. Our aim is to produce comprehensive molecular phylogenies, taxonomic monographs, and identification tools that enable subsequent studies at both global and local scales. In addition, we also aim to study how *Acalypha* originated and diversified throughout history, and to better understand the chemical and pharmacological diversity existing in the genus and its potential applications.

P.1343 Ewangoa cardiophora, a new genus and species of Euphorbiaceae from the Democratic Republic of Congo

Olivier Lachenaud[1,2], Paloma Ruiz de Diego[3], Ricarda Riina[3], Patricia Barberá[4]

1 Meise Botanic Garden, Meise, Belgium. 2 Université Libre de Bruxelles, Brussels, Belgium. 3 Real Jardín Botánico, CSIC, Madrid, Spain. 4 Missouri Botanical Garden, St. Louis, USA.

Euphorbiaceae are a very diverse family with about 230 genera and more than 6,300 species worldwide, most of which occur in tropical areas. They are not very well-known in the Congo Basin, both due to the generally low density of botanical collections in the area, and to the relative rarity of recent taxonomic studies. An enigmatic undescribed taxon of Euphorbiaceae from the Democratic Republic of the Congo, represented by four relatively recent (1983-2015) herbarium collections, has been investigated. Molecular phylogenetic analyses based on *trnL-F* and *rbcL* markers confirmed that this taxon represents a new genus and species, *Ewangoa cardiophora*, which belongs to the informal 'alchorneoids clade' of Acalyphoideae, and appears as sister to a group composed by the Malagasy genus *Amyrea* and the two African genera *Discoglypremna* and *Cyttaranthus*. *Ewangoa* is easily separated from all other genera in the family by its leaf-opposed inflorescences surrounded by a single cordiform involucral bract. Male and female inflorescences are similar, but due to the paucity of flowering material, it is unclear whether the species is dioecious or monoecious. The new taxon occurs in undergrowth lowland rainforest, from 300 to 480 m in elevation, and is known from three widely distant localities in the central Congo Basin depression (the area known as "cuvette congolaise"). It appears to be the only genus of Angiosperms endemic to this region, which has a lower level of plant endemism compared to the more elevated areas to the east and west. It is assessed as Endangered according to IUCN criteria.

P.1344 Taxonomic and phylogenetic updates of Euphorbia section Anisophyllum for the Iberian Flora

Martín-Muñoz Juan[1,2], Montero Muñoz Iris[1], Riina Ricarda[1]

1 Real Jardín Botánico, CSIC, Madrid, Spain. 2 Departamento de Botánica y Fisiología Vegetal, Universidad de Salamanca, Salamanca, Spain.

Euphorbia section *Anysophyllum* is a monophyletic lineage within the hyperdiverse genus *Euphorbia*. The section is distributed worldwide and includes numerous weedy plants that are mostly herbs and occasionally subshrubs or trees. Due to its marked morphological differences from other groups of *Euphorbia* such as opposite, usually basally asymmetric leaves, interpetiolar stipules, petiolar nectary appendages and C_4 photosynthesis in most of the species, this section was previously classified as genus *Chamaesyce*, but molecular phylogenetic evidence places this group well embedded within *Euphorbia*, as one of the major subclades of subgenus *Chamaesyce*. The section comprises about 350 species, of which nine are included in *Flora iberica* (treated as genus *Chamaesyce*). Our goal with this study is to update the systematic knowledge of this group for the Iberian Peninsula by revising the herbarium specimens accumulated after the publication of *Flora iberica* in 1997, documenting recently introduced or previously unrecorded species, and providing a phylogenetic framework using multiple samples per species and universal genetic markers used in previous *Euphorbia* studies. We will also update the identification key and include additional tools for specimen identification.

P.1345 Taxonomic revision of the genus Tragia (Euphorbiaceae) in Gabon

Iris Montero Muñoz[1], Patricia Barberá[2]

1 Real Jardín Botánico de Madrid, CSIC, Madrid, Spain. 2 Missouri Botanical Garden, Saint Louis, USA.

Gabon, including more than 7,000 plant species, is one of the most diverse countries in tropical Africa. Despite its high levels of biodiversity, extensive areas remain either completely unexplored or insufficiently studied, leaving significant gaps in the knowledge of many of the plant groups existing in the region. This is the case for the genus *Tragia*, the sixth largest genus within the Euphorbiaceae family (tribe Plukenetiae). This pantropical genus of c. 150 nettle-like species comprises twining, scandent, or erect herbs or subshrubs that are mainly distributed in dry habitats. It includes c. 40-50 species in sub-Saharan Africa, but they are relatively difficult to identify due to their variability in some morphological characters (female flower and fruit bracts, bracteoles, and calyx) and by the absence of a recent comprehensive taxonomic treatment. In the *Checklist of Gabonese Vascular Plants*, published in 2006, five species of *Tragia* were included. After revising all the material collected in Gabon and adjacent countries for the treatment of the flora, we recognize six species for the country. This includesthe description of a new one and the exclusion of two previously cited in Gabon. We also recover one name previously cited as a synonym.

P.1346 Solving the puzzle: systematics and biogeography of Acalypha (Euphorbiaceae) of the Western Indian Ocean Region

Iris Montero Muñoz[1], Patricia Barberá[2], José María Cardiel[3], Ricarda Riina[1]

1 Real Jardín Botánico de Madrid, CSIC, Madrid, Spain. 2 Missouri Botanical Garden, Saint Louis, USA. 3 Universidad Autónoma de Madrid, Madrid, Spain.

Acalypha is one of the biggest genera in the Euphorbiaceae family, after *Euphorbia* and *Croton*, and is present in all tropical and subtropical regions of the world. It comprises mainly small trees and shrubs, but also herbs. Species range from tropical humid forests to sub-desertic areas, and from sea level to about 4000m in tropical mountains. The greatest diversity is found in tropical America, with c. 250 species, followed by continental Africa, with c. 80 species, and the Western Indian Ocean Region (WIOR), with c. 51 species. WIOR is one of the world's biodiversity hotspots and is especially interesting in the case of *Acalypha* because three of the four subgenera are present and includes a high number of endemic species, being one of the main centers of diversity in the paleotropics. Recently a monograph of *Acalypha* of the WIOR has been published, which is the starting point of our phylogenetic study. We have sampled 100% of the species including more than one sample per species when available. We also complement the genus-wide sampling of the last phylogeny published in 2022. We sequenced one nuclear region (ITS) and three plastid regions (*trnLF*, *ndhF*, *psbA*). This comprehensive phylogenetic framework allows us to understand processes of diversification and speciation in the focal WIOR clades, as well as the main biogeographic patterns and the identification of high-diversity areas within the WIOR.

P.1348 Unraveling the sticky clade of Croton (Euphorbiaceae): phylogenetics and classification update of subsection Medea

Amanda da Paixão Noronha Pereira[1], Ricarda Riina[2], Maria Beatriz Rossi Caruzo[1,3]

1 Programa de Pós-graduação em Biodiversidade Vegetal e Meio Ambiente, Instituto de Pesquisas Ambientais – Unidade Jardim Botânico, São Paulo, Brazil. 2 Real Jardín Botánico, Madrid, Spain. 3 Universidade Federal de São Paulo - Unifesp. Instituto de Ciências Ambientais, Químicas e Farmacêuticas, Departamento de Ecologia e Biologia Evolutiva, Diadema, Brazil.

Croton is a megadiverse genus, with more than 1,200 species widespread mainly in tropical regions worldwide. Currently, 31 sections are recognized for the genus in the New World. Among these sections, *C.* sect. *Barhamia* stands out as one of the three largest in species number. *Croton* sect. *Barhamia* was divided into 5 subsections, and the most diverse one is the *C.* subsect. *Medea*. Species of subsection Medea share a set of diagnostic characters, such as indumentum with often stellate or lepidote trichomes, reduplicate-valvate pistillate sepals, tetrafid to multifid styles, and stand out by its stipules, bracts, and sepals with glands (colleters). We provide a revised assessment of *Croton* subsect. *Medea* based on molecular data. We used nuclear ITS and chloroplast *(trnL-F, trnT-L)* data to generate a phylogenetic hypothesis to confirm the correct phylogenetic placement of the species previously included in the subsection based on morphology only. Our sampling included 82 species (115 specimens): 31 species (49 specimens) from C. subsect. Medea; 23 species (36 specimens) from other subsections of sect. *Barhamia*; and 28 species (30 specimens) from other *Croton* clades as outgroups. Our results allow us to recircumscribe the subsection *Medea* with 38 species ranging across South America, with the highest diversity in Brazil. We also provide a morphological description and geographic range updated of the subsection *Medea*, and a list of currently accepted species names in the group.

P.1349 An updated list of Croton subsect. Barhamia (Euphorbiaceae) for Neotropical region

Nicolas G. Burilli[1], Amanda P. N. Pereira[2], Maria B. R. Caruzo[1,2]

1 Universidade Federal de São Paulo, Unifesp. Instituto de Ciências Ambientais, Químicas e Farmacêuticas, Departamento de Ecologia e Biologia Evolutiva, São Paulo, Brazil. 2 Instituto de Pesquisas Ambientais, Unidade Jardim Botânico, São Paulo, Brazil.

Croton L. (Euphorbiaceae) is a megadiverse genus with approximately 1200 species distributed mainly in tropical regions worldwide. The genus is divided into four subgenera and 31 sections for the New World, with Barhamia standing out with about 80 species. The section is an exclusively Neotropical group, from open and dry vegetation, which can be recognized by a set of characters including leaf blade serrate to dentate, trichomes stellate, stipules glandular, sepals valvate, some species with bracts glandular and pistillate sepals often glandular. The section *Barhamia* is currently divided into 5 subsections (*Astraeopsis*, *Barhamia*, *Medea*, *Micranthi* and *Sellowiorum*). Considering its high morphological diversity, and scarce studies, we focus on subsection *Barhamia*, where we identified a gap in knowledge. This study focused on survey and update the species belonging to *Croton* subsection *Barhamia*, which previously included 19 species. Recent studies have removed species from the subsection, in response, our work proposes an updated list of species, as well as an identification key for them and comments on their geographic distribution. The taxonomy study was based mainly on the analysis of herbaria materials, original protologues, and photographs of the type specimens. Moreover, the observation of species in the field, in the states of Bahia and Minas Gerais, was a complement for understanding the morphological variation of some species. Our results pointed out an increase for 20 species belonging to the subsection, besides a better understanding of taxonomic delimitation and extend of geographical range of each species. This study expects to determine new morphological characters for species circumscription and increase knowledge about *Croton* in the neotropical region.

P.1350 Relationships among the Euphorbiaceae illuminated by high-throughput sequencing data: first steps towards a new classification

Otávio Luis M. da Silva[1,2], Kenneth J. Wurdack[3], Ricarda Riina[4], Inês Cordeiro[1], Federico Fabriani[5], Olivier Maurin[5], Sue Zmarzty[5], Alexandre Zuntini[5], Felix Forest[5], William Baker[5]

1 Núcleo de Pesquisa Conservação da Biodiversidade, Instituto de Pesquisas Ambientais, São Paulo, Brazil. 2 Departamento de Botânica, Universidade de São Paulo, São Paulo, Brazil. 3 National Museum of Natural History, Smithsonian Institution, Washington, USA. 4 Real Jardín Botánico, CSIC, Madrid, Spain. 5 Royal Botanic Gardens, Kew, Richmond, United Kingdom.

Resolving relationships among Euphorbiaceae are challenging due to the family's diversity, age, and wide geographical distribution. Molecular studies from early 2000's indicated the paraphyly of Acalyphoideae and Crotonoideae, as well of many tribes and subtribes, and poorly supported relationships among the seven major lineages within the family. Based on genomic data generated by the Plant and Fungal Trees of Life (PAFTOL) project for 150 of the ca. 230 genera of Euphorbiaceae, we corroborated the inclusion of Erismantheae as the first diverging lineage in Acalyphoideae, and therefore the monophyly of this subfamily. The sister relationship between Acalyphoideae and Euphorbioideae is indicated, but with low support. On the other hand, the monophyly of Crotonoideae is strongly supported, with the articulated crotonoids as early diverging within the subfamily, followed by a clade comprising Gelonieae and Adenoclineae, excluding *Klaineanthus*, which was recovered as sister to the inaperturate crotonoids. Within the inaperturate crotonoids, our data present advances on the relationships among the C2 clade, recovering two large clades, one uniting genera mostly from Africa, and the other with genera from Asia, Australasia and Pacific. However, some internal clades present low support and notably indicate paraphyletic Aleuritideae and Codiaeae. Within the Euphorbioideae, Hippomaneae represents a gap in our taxonomic sampling, with only nine of the nearly 40 genera sampled. Advances presented here represent first steps towards a well-resolved generic phylogeny that would underly a new classification for the Euphorbiaceae and support future studies concerning the evolution of the astonishing morphological diversity of the family and its biogeographic history.

S.150. SYSTEMATICS AND EVOLUTION OF LAMIALES

P.1351 Biogeography of the genus Lamium (Lamiaceae) based on the most comprehensive phylogenetic analysis

Ferhat Celep[1], Fergan Karaer[2], Aslı Yılmaz[3], Jeff Rose[4], Bryan Drew[4]

1 Department of Biology, Kırıkkale University, Kırıkkale, Turkey. 2 Department of Mats and Science, Ondokuz Mayıs University, Samsun, Turkey. 3 Department of Molecular Biology and Genetics, Ataturk University, Erzurum, Turkey. 4 Department of Biology, University of Nebraska-Kearney, Kearney, USA.

Lamium L., the type genus of the Lamiaceae, comprises 16–40 species, depending on the circumscription of the genus. Recent morphological and molecular phylogenetic studies shown that taxonomy and phylogeny of the genus needs extensive revision particularly on infrageneric and species delimitations. In this study, all known *Lamium* species were used for phylogenetic analysis with 2 nuclear (*ITS* and *ETS*) and 4 chloroplast regions (*matK*, *rpoA*, *ycf1* and *psba-trnH*). *ETS* and *ycf1* regions were used for the first time in this study. We estimated divergence times using the software BEAST. There were some incongruences between the nuclear and chloroplast phylogenies. Based on the analysis, nrDNA regions provided better results when comparing the morphology and taxonomy. Based on nrDNA phylogeny and fossil records, we found ancestral areas and biogeographic pattern of the genus using BioGeoBEARS. According to the results, the genus naturally originated in mostly crossroad of the Mediterranean, Euro-Siberian and Irano-Turanian phytogeographic regions in Miocene (16-24 mya). Turkey is the center of the diversity of the genus. Although some species are specialized in one phytogeographic region, some other species are distributed in three phytogeographic regions. For example, *L. galeobdolon, L. maculatum* and *L. ponticum* are only grow in Euro-Siberian phytogeographic region, on the other hand, *L. garganicum* complex, *L. flexuosum, L. eriocephalum, L. gevorense* and *L. bifidum* are grow in Mediterranean region and *L. tomentosum, L. iranicum, L. orientale, L. multifidum* and *L. aleppicum* are grow in Irano-Turanian phytogeographic region. *Lamium amplexicaule, L. purpureum* and *L. album* are grown in two or three phytogeographic regions.

P.1352 Systematics and biogeography of *Cyrtandra* (Gesneriaceae) in Sumatra, Indonesia

Syadwina H. Dalimunthe[1,2,4], Catherine Kidner[1,2], Hannah J. Atkins[2], Gemma L. C. Bramley[3], Flávia Fonseca Pezzini[2], Abdulrokhman Kartonegoro[4]

1 Institute of Molecular Plant Sciences, The University of Edinburgh, Edinburgh, UK. 2 Royal Botanic Garden Edinburgh, Edinburgh, UK. 3 Royal Botanic Garden Kew, Richmond, UK. 4 Research Center for Biosystematics and Evolution (BRIN), West Java, Indonesia.

Cyrtandra is the largest genus in the Gesneriaceae family and has more than 800 species distributed across Asia and the Pacific. It is a common element in tropical Southeast Asian forests, including in Sumatra, Indonesia. Sumatra is the third largest island in the Malesian region and has been recognized for its high plant species richness, yet it lacks a comprehensive taxonomic treatment. Diversity in Sumatra is poorly known due to low collecting density on the island. An updated taxonomic revision of *Cyrtandra* in Sumatra and a well-sampled, robust phylogeny will be an important contribution to our understanding of the evolution and biogeography of Southeast Asian plant groups. The results of preliminary systematic and biogeography analysis are presented.

P.1353 Unraveling the phylogeny and morphological evolution of the Neotropical genus *Cuspidaria* DC. (Bignoniaeae, Bignoniaceae)

Jéssica N. C. Francisco1, Luiz H. M. Fonseca2, Lúcia G. Lohmann1,3

1 Department of Botany, Universidade de São Paulo, São Paulo, Brazil. 2 Systematic and Evolutionary Botany Lab, Ghent University, Ghent, Belgium. 3 Department of Integrative Biology, University of California, Berkeley, USA.

In this study, we integrated High Throughput Sequencing (HTS) data with targeted loci to reconstruct a robust phylogeny of *Cuspidaria* DC. (Bignonieae, Bignoniaceae), a diverse clade of lianas and shrubs in South American wet and dry forests. We used HTS to sequence the chloroplast genome of seven *Cuspidaria* individuals, encompassing all main clades of the genus, and used this data to reconstruct relationships at the phylogeny's deepest nodes (backbone). Sanger sequences of chloroplast (*ndh*F and *rpl*32-*trn*L) and nuclear (*Pep*C) markers from 64 individuals representing 18 of the 21 recognized *Cuspidaria* species were then used to test individual species' monophyly and reconstruct interspecific relationships. Maximum likelihood and Bayesian inferences of the combined datasets, including 64 *Cuspidaria* individuals and 22 outgroup taxa, reconstructed a monophyletic *Cuspidaria*, excluding *C. bracteata,* placed within the outgroup. Ancestral state reconstructions for selected characters identified 10 putative morphological synapomorphies across different *Cuspidaria* lineages. For example, anther curvature emerged as a putative synapomorphy for the entire *Cuspidaria* clade, while features like gland fields, leaf morphology, venation patterns, and certain fruit characteristics served as putative synapomorphies for specific clades within *Cuspidaria*. This study demonstrates that even limited chloroplast genomic data, combined with extensive Sanger data, can provide a robust understanding of phylogenetic relationships. It contributes valuable insights into *Cuspidaria*'s phylogenetic relationships, enhancing our understanding of taxonomy, evolutionary history, and morphological evolution within the group.

P.1354 Building bridges and growing genomes: an awards program to support international collections and genomics infrastructure

Morgan R. Gostel[1,2], Ray Mims[3], Patricia Malcolm[4], Charlotte Ely[4], Raakel Toppila[5], Elizabeth Thomas[6], Devin Dotson[3], Abby Meyer[5]

1 Fort Worth Botanic Garden, Fort Worth, USA. 2 National Museum of Natural History, Smithsonian Institution, Washington, USA. 3 United States Botanic Garden, Washington, USA. 4 Botanic Gardens Conservation International, Richmond, UK. 5 Botanic Gardens Conservation International US, San Marino, USA. 6 University of Georgia, Athens, USA.

Access to high-quality tissue samples is a limiting factor for plant genomics research in the 21st Century. Recognizing this need, the Global Genome Initiative for Gardens (GGI-Gardens) was founded in 2015 for the purpose of collecting and preserving genome quality tissues for all species of plants on Earth. Since this time, GGI-Gardens has grown to an international partnership of more than 50 botanic gardens that has supported the collection of more than 15,000 herbarium and genomic vouchers and over 3,000 vascular plant genera. The partnership is rooted in building capacity to support collections at botanic gardens and foster collaboration with the genomics community. Botanic gardens are home to a remarkable proportion of plant biodiversity and work on the front lines of plant conservation, which makes them ideally suited to support the rapidly expanding opportunities for plant genomics research. In 2017, GGI-Gardens started the GGI-Gardens Partner Award program in collaboration with the United States Botanic Garden and Botanic Gardens Conservation International. To date, this award program has supported 36 botanic garden programs from 31 partners in 21 countries. This poster highlights our plan for strategic success of this program that is driven by a perspective focused on outcomes for our partners. We highlight statistics from these awards that reflect the success of this collections program and our partners as well as statistics that demonstrate the relative impact of this award and the effectiveness of our strategic sampling approach that focuses on current taxonomic gaps in existing collections.

P.1355 Abundant incongruence in a clade endemic to a biodiversity hotspot: Phylogenetics of the scrub mint clade (Lamiaceae)

Andre A. Naranjo[1,2], Christine E. Edwards[3], Matthew A. Gitzendanner[4], Douglas E. Soltis[2,4],Pamela S. Soltis[2]

1 Institute of Environment Department of Biological Sciences Florida International University Miami, USA. 2 Florida Museum of Natural History University of Florida, Gainesville, USA. 3 Missouri Botanical Garden, St. Louis, USA. 4 Department of Biology University of Florida, Gainesville, USA.

The Scrub Mint clade (Lamiaceae) provides a unique system for investigating the evolutionary processes driving diversification in the North American Coastal Plain from both a systematic and biogeographic context. The clade comprises *Dicerandra, Conradina, Piloblephis, Stachydeoma,* and four species of the broadly defined genus *Clinopodium* (Mentheae; Lamiaceae), almost all of which are endemic to the North American Eastern Coastal Plain. Most species of this clade are threatened or endangered and restricted to sandhill or a mosaic of scrub habitats. We analyzed relationships in this clade to understand the evolution of the group and identify evolutionary mechanisms acting on the clade, with important implications for conservation. We used a target-capture method to sequence and analyze 238 nuclear loci across all species of scrub mints, reconstructed the phylogeny, and calculated gene tree concordance, gene tree estimation error, and reticulation indices for every node in the tree using ML methods. Phylogenetic networks were used to determine reticulation events. Our nuclear phylogenetic estimates were consistent with previous results, while greatly increasing the robustness of taxon sampling. The phylogeny resolved the full relationship between *Dicerandra* and *Conradina* and the less-studied members of the clade (*Piloblephis*, *Stachydeoma*, *Clinopodium* spp.). We found hotspots of gene tree discordance and reticulation throughout the tree, especially in perennial *Diceran-*

dra. Several instances of reticulation events were uncovered between annual and perennial *Dicerandra*, and within the *Conradina* + allies clade. Incomplete lineage sorting also likely contributed to phylogenetic discordance. These results clarify phylogenetic relationships in the clade and provide insight on important evolutionary drivers in the clade, such as hybridization. General relationships in the group were confirmed, while the large amount of gene tree discordance is likely due to reticulation across the phylogeny.

P.1356 The trichome diversity in genus Clinopodium L. from the Balkans with emphasis on the transferred genus Acinos Mill.

Janković Smiljana[1], Rajčević Nemanja[1], Novaković Jelica[1], Marin D. Petar[1], Alimpić Aradski Ana[1]

1 University of Belgrade, Faculty of Biology, Belgrade, Serbia, jelica@bio.bg.ac.rs.

The genus *Clinopodium* L. comprises 186 accepted species, distributed in Europe, Asia, Indomalasia, the New World and Africa. Through great taxonomic revisions, inter alia, the complete genus *Acinos* Mill. has been transferred to *Clinopodium*. The taxa from the former genus *Acinos* exhibit great morphological variability, and various transitional forms between taxa are noticed. This study aims to provide insight into the micromorphological pattern of variability in a group of former *Acinos* taxa and to examine whether these characters could be useful for the taxa delimitation. Additionally, more detailed knowledge of the micromorphological patterns of this group may be useful for understanding the diversity in the genus *Clinopodium*. This study includes five taxa (15 populations) collected in Serbia and Northern Macedonia: *C. acinos* (L.) Kuntze (AC), *C. alpinum* subsp. *alpinum* (L.) Kuntze (AL), *C. alpinum* subsp. *hungaricum* (Simonk.) Govaerts (ALH), *C. alpinum* subsp. *albanicum* (Kümmerle & Jáv.) Govaerts (ALA), and *C. suaveolens* (Sm.) Kuntze (SU). The middle leaves of each population were selected, air-dried, and analysed from both sides under a scanning electron microscope. All populations showed peltate, capitate and non-glandular trichomes. The great diversity is noticed in the morphology of the capitate trichomes, which have as many as nine subtypes. However, all studied taxa exhibit interpopulation variability in the presence of different capitate trichomes and general micromorphological appearance. In some cases, the indumentum of populations belonging to different taxa was identical (e.g., AC and ALH, AC and ALA). Bearing in mind previous research on this issue in the family Lamiaceae, these results suggest that micromorphological characters may be useful features for delimiting taxa in some groups and not in others. However, such a complex relationship between taxa in the structure of the indumentum indicates a very complex biology of *Acinos* taxa, and broader sampling may facilitate this taxonomic problem.

P.1357 Phylogenetic investigation of Justicia (Acanthaceae) using molecular, morphological and micromorphological data

P. Soumya[1], Y. Deng[2], P. Sunojkumar[3], S.S. Dash[4]

1 Central National Herbarium, Botanical Survey of India, Howrah, West Bengal, India. 2 South China Botanical Garden, Chinese Academy of Sciences, Guangzhou, People's Republic of China. 3 University of Calicut, Malappuram District, Kerala, India. 4 Botanical Survey of India, Salt Lake, Kolkata, West Bengal, India.

Justicia L. is the most species-rich and taxonomically complex genus within the tribe Justicieae (Acanthaceae) comprising 700 species worldwide (Kiel *et al.*, 2017). It is mainly distributed in the tropical and subtropical regions, extending into warm temperate zones in Europe, Asia and North America (Graham, 1988). Due to its extensive distribution, the taxonomic identity of *Justicia* has long been debated among researchers, ultimately leading to the recognition of numerous infrageneric groups within the genus. In India, the genus is represented by approximately 51 species and 5 varieties (Karthikeyan *et al.*, 2009), exhibiting high endemism. However, adequately assessing the identity of all these entities is challenging due to the extreme phenotypic plasticity exhibited by this group. The latest infrageneric classification of *Justicia* by Graham (1988) was exclusively based on morphological characters, but many Indian species did not fit well into any of these sectional treatments with morphological characters sometimes overlapping across sections. Furthermore, previous phylogenetic studies by Kiel *et al.* (2017) have suggested the polyphyletic nature of the genus, emphasizing the need for increased sampling from old-world countries to trace its evolutionary origins. Even though India represents one of the largest species diversity countries in the world, poor representation of Indian endemic forms in such wide studies causes controversy regarding the generic delineation of Indian *Justicia.* Similarly, the placement of *Rungia* within *Justicia* is also uncertain due to unclear relationships and the insufficient representation of Indian taxa. Therefore, the present study focuses on: 1) conducting a well-sampled phylogenetic study of the genus *Justicia* in India; 2) re-evaluating the infrageneric groups present in Indian *Justicia* through an integrated approach involving morphological, micromorphological and molecular data; 3) determining whether Indian *Rungia* species belong to *Justicia* or not?

P.1358 First steps towards the conservation of endemic Italian Salvia through population genomics

Chiara Paleni[1], Cristina Puricelli[1], Camilla Pieri[1], Silvia Manrique[2], Larissa De Paola[1], Aureliano Bombarely[3], Martin M. Kater[1], Carla Lambertini[1]

1 Università degli Studi di Milano, Milan, Italy. 2 Universitat Politècnica de València, Valencia, Spain. 3 Instituto de Biologia Molecular y Celular de Plantas (CSIC-UPV), Valencia, Spain.

Salvia is a common taxon in the collections of botanical gardens due to its long history of medicinal and culinary use across the world. Twenty-five species can be found in the wild in Italy; *S. pratensis* is one of the most common and is closely related to some endemic taxa with debated species rank, defined by some authors as the *S. pratensis* species complex (*S. ceratophylloides, S. saccardiana, S. pratensis* subsp. *haematodes, S. pratensis* subsp. *bertolonii*). We are interested in studying the distribution of genetic diversity in wild populations of *Salvia pratensis* and related taxa to inform species delimitation and define a conservation strategy that can be applied by botanical gardens to conserve genetic variation and resources of, potentially, any *ex-situ* collection. We are characterizing a collection of samples from wild populations of *Salvia* in Italy with Genotyping-By-Sequencing (GBS) to obtain genetic variation data. Thanks to a network of collaborators, this collection spans a large portion of the Italian territory and 15 *Salvia* taxa. We analysed the genomic variation by combining a population structure approach with phylogenomic analysis to assess whether there is divergence between *S. pratensis* populations that may support speciation of different endemic taxa. Moreover, we have sequenced and assembled the genome of *S. pratensis* to use as reference for GBS. We are also annotating the genes related to pollination syndromes to assess the role of plant-pollinator interaction in *S. pratensis* diversification. In the future, we are going to integrate the collection with a wider sampling range, potentially including samples from outside of Italy. As a final goal, we would like to identify markers from GBS to barcode species and phylogeographic variation that can be easily produced with Sanger sequencing to better develop *ex situ* collections.

P.1359 A study of phylogeny and biogeography of the genus Scutellaria (Lamiaceae)

Rashad A. Salimov[1], Gerald Parolly[2], Thomas Borsch[2]

1 Faculty of Natural Sciences, Sumgayit State University, Sumgayit, Azerbaijan. 2 Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, Berlin, Germany.

Scutellaria L. (*Scutellarioideae*) is the second largest genus of the *Lamiaceae* with a nearly worldwide distribution. The species numbers range from 360 species estimated by Paton and Harley to 617 accepted names in the World Flora Online. Most species occur mainly in mountain regions of the Caucasus and the wider Irano-Turanian region, particularly Central Asia and Afghanistan, many of them considered endemic. However, temperate region of the Eastern Mediterranean and in the tropics mountain regions of the Andes represents the second centers of its speciation. Because of the highly variable morphology of the many species and treatments in different Floras, *Scutellaria* is one of the most difficult genera taxonomically. Several species complexes need study. Our studies were carried out in nature and herbarium materials of the *Scutellaria* in 2016-2020. Herbarium specimens deposited at the herbarium of BAK, B, NY, MO, LE, TBI, MSKU, MSKH, MSK-V, MARK as well as other available Flora accounts and the results of monitoring carried out by authors in nature were analyzed. Based on fast-evolving DNA regions in the chloroplast genome (*matK-trnK*, *rpl16*, *trnL-F*), we reconstructed the phylogenetics relationship of *Scutellaria* using 76 taxa representing most infrageneric entities recognised by Paton and nearly all subgenera, sections or series accepted by Juzepczuk and main geographical areas in the previous classifications of the genus. In light of molecular and morphological evidence, an infrageneric classification with three major clades or subgenera of *Scutellaria* is proposed. Currently accepted subgenus *Scutellaria* is paraphyletic to subgenus *Apeltanthus*. The detailed infrageneric classification of Juzepczuk mostly does not reflect natural groups. Ancestral states of 12 morphological characters frequently used as diagnostic from subgenus to species level were reconstructed with Bayes Traits.

P.1360 Taxonomy, Nomenclature and Bioecology of Lamiaceae L. species in Azerbaijan

Rashad A. Salimov[1], Sabina F. Hajiyeva[2], Lala Z. Isgandarova[2], Ulkar E. Ibrahimzada[2]

1 Faculty of Science, Sumgayit State University, Sumgayit, Azerbaijan. 2 Institute of Botany, The Ministry of Science and Education Republic of Azerbaijan, Baku, Azerbaijan.

Azerbaijan is part of the Caucasus, which is one of the 36 biodiversity hotspots in the world and possesses a unique phytogeographic region within the South Caucasus. Azerbaijan consists of about 5,000 species of vascular plants that represent ~79% of the total species known for the Caucasus region. By species count, *Lamiaceae* is the fourth plant family with greater diversity in Azerbaijan flora. Based on the field investigations, ongoing molecular systematic studies, clarification and re-identification of herbarium specimens lead to taxonomical and nomenclatural disputable issues regarding generic, infrageneric, specific, and infraspecific classifications. The family is represented by 37 genera, 241 taxa (204 (native and introduced) species, and 37 subspecies) of which 19 taxa are endemics. 4,638 herbarium specimens of BAK and 1,245 specimens from various virtual herbaria have been analyzed. 46 new taxa were added as a supplementary to the VII volume Flora of Azerbaijan after its publication. The largest three genera according to taxon number are ***Salvia*** L. (38 taxa), ***Nepeta*** L. (30 taxa), and ***Stachys*** L. (25 taxa). Mountain part of Nakhchivan (62 taxa), Diabar (58), Guba part of the Greater Caucasus (37) are the most species-rich and genera-rich botanical-geographical regions. The phytogeographic regions with the highest taxon number are Irano-Turanian (88 taxa (37%)), Euro-Siberian (42 taxa (18%) and Caucasian (39 taxa (16%)) regions.12 taxa are in threatened categories (CR-4, EN1, and VU-7) and 12 are near threatened (NT) according to IUCN. 7 species are listed in the 2nd edition of Red Book of Azerbaijan. After current nomenclatural updates, the result proved that Azerbaijan with its landscape and habitat diversity plays a significant role in speciation of the *Lamiaceae* family in the Caucasus.

P.1362 Phylogenetic relationships within Phlomoides (Lamioideae: Lamiaceae): new insights from nuclear and plastid DNA sequence data

Yasaman Salmaki[1], Maryam Almasi[1], Zohreh Pourghorban[1], Maximilian Weigend[2]

1 Department of Plant Science, University of Tehran, Tehran, Iran. 2 Bonn Institute of Organismic Biology, University of Bonn, Bonn, Germany.

The genus *Phlomoides*, comprising approximately 150–170 species, is the second-largest and taxonomically most challenging genus in subfamily Lamioideae (Lamiaceae). Recent molecular phylogenetic studies have led to the inclusion of a range of former segregate genera - *Eremostachys*, *Lamiophlomis*, *Metastachydium*, *Notochaete*, *Paraeremostachys*, *Pseuderemostachys*, and *Pseudomarrubium* - into *Phlomoides*. This reassignment has rendered *Phlomoides* one of the most heterogeneous genera of Lamiaceae. *Phlomoides* is very widespread from the central Mediterranean to NE Asia with centres of diversity across mountainous and arid regions across Central Asia, Iran, and China. However, its phylogeny and evolution remain are poorly understood. Here, we present the phylogeny of *Phlomoides* utilizing nuclear (ITS) and chloroplast (*trnT-A*, *trnK*) regions, with an expanded range of taxa and across its range. Based on Bayesian Inference and maximum likelihood approaches, the monophyly of the expanded *Phlomoides* is strongly supported in both the nuclear and plastid phylogenies. At the same time, most previously defined infrageneric classifications were found to be non-monophyletic. In our study five main clades were retrieved as consecutive sister clades: Clade I include "*Notochaete*" and "*Lamiophlomis*", along with the core group of Chinese *Phlo-*

moides (*P.* sect. *Phlomoides*). Clades II, III, and IV consist of species distributed across both East and Central Asia. Clade II and III, comprise five resp. three species of sect. *Phlomoides*. Clade IV includes monotypic "*Metastachydium*", along with *P. tuberosa*, *P. puberula* and *P. adylovii*. Clade V predominantly comprises Central and southwestern Asian species, mostly from "*Eremostachys*". The diversification of extant *Phlomoides* lineages is suggested to have originated from an early diversification in Eastern and Central Asia, with subsequent dispersal towards the west.

P.1363 Proposal to conserve the name Thymus marschallianus (Lamiaceae)

Vladimir M. Vasjukov1

1 Institute of Ecology of the Volga river basin of the Russian Academy of Science.

Thymus marschallianus Willd., Sp. Pl. 3: 141. 1800 [Angiosp.: *Lab.*]. The species was described from the former Taurida province (Russia). Lectotypus (Vasjukov in Novosti Sist. Vyssh. Rast. 45: 117. 2014): "ex Herb. Willdenow" (B barcode B-W 11029-02 0). *Thymus marschallianus* is a species of forest–steppe and steppe zone of Eastern Europe, Western Siberia and Central Asia (from the Southern Bug to the Irtysh): Russia, Kazakhstan, Kyrgyzstan, China (Xinjiang), Ukraine. The indications for Central Europe relate to other, albeit similar species or hybridogenic complexes of different origins. Jalas (in Bot. J. Linn. Soc. 64: 259. 1971; Auct. Syn. Meth. Stirp. Hort. Regii Taur.: 6. 1773) reduces *T. marschallianus* to synonyms with the Central European *T. pannonicus* All. We insist on the independence of *T. marschallianus* relative to *T. pannonicus*, taking into account the differences in life form (*T. pannonicus* is capable of vegetative reproduction, with the formation of large curtains, while *T. marschallianus* is not). The life form is important in the taxonomy of thyme and it is not entirely clear why this feature is ignored. Nachychko & Sosnovsky (in Taxon 70(2): 439-440. 2021) even suggest rejecting the name *T. marschallianus*. We have shown (Vasjukov in Novosti Sist. Higher. Rest. 45:117. 2014), that the sample previously selected as the lectotype of the name *T. marschallianus* in the Herbarium of the Martin-Luther-Universität in Halle (Schmidt in Feddes Repert. 83:666. 1973; HAL barcode HAL 0014427; isolectotypus: B barcode B-W 11029-01 0) does not correspond to either the description of the species or the modern idea of this taxon (and actually belongs to *T. callieri* Borbás ex Velen.), therefore cannot be accepted as a lectotype. We propose to keep the name *T. marschallianus* with the selected lectotype from the original material for its traditional use.

S.151. SYSTEMATICS, BIOGEOGRAPHY, ADAPTATION AND UTILIZATION OF THE GRAPE FAMILY VITACEAE

P.1364 Unveiling the evolutionary and pantropical biogeographic history of Cissus, the largest genus of the grape family Vitaceae

Alberto J. Coello[1, 2],Gabriel Johnson[1], Jun Wen[1]

1 National Museum of Natural History, Smithsonian Institution, Washington DC, United States. 2 Universidad Autónoma de Madrid, Madrid, Spain.

Pantropical disjunction is a major biogeographic pattern often attributed to the break-up of Gondwana, but vicariance is not the mechanism for this disjunction in many plant groups. One of the plant genera with a pantropical disjunction is *Cissus*, the largest genus of Vitaceae (c. 300 species). Currently, two main clades have been recognized in *Cissus* s.l.: the *Cissus antarctica* – *C. trianae* clade and the core *Cissus* clade. The *Cissus antarctica* – *C. trianae* has only eight species in Australasia and the Americas and has been recently segregated as a new genus *Apocissus*. The core *Cissus* is widely distributed in the Southern Hemisphere and tropical regions of the Northern Hemisphere. A possible hybrid origin for the smaller *Cissus ant-*

arctica – *C. trianae* clade has been suggested that involved the stem lineage of *Cissus* and the tropical ancestral lineage of *Ampelocissus* – *Vitis*. Additionally, within the core *Cissus* there are two major biogeographic patterns: a disjunction pattern between Africa and Asia, and radiation in the Neotropics. Therefore, we propose to unveil the phylogenetic relationships of *Cissus* s.l. and untangle the pantropical biogeographic patterns using *Cissus* as a model. In particular, in this project we propose to: (i) test the hybrid origin of the *Cissus antarctica* – *C. trianae* clade (*Apocissus*), (ii) explore the *Cissus* radiation in the Neotropics, and (iii) study the African – Asian disjunction of the core *Cissus*. To achieve these goals, we employ the target-enrichment Hyb-Seq approach for c. 200 specimens of *Cissus* and analyze the phylogenomic data together with morphological data in an integrative temporal and spatial framework. The results will shed light on the assembly and development of tropical forests through time and across spaces and contribute to the understanding of major pantropical biogeographic patterns.

P.1365 Resolving the Vitis arizonica complex and the Occidentales group of Vitis in North America

Stefanie M. Ickert-Bond[1], Alicia Talavera[2], Gabriel Johnson[2], Zelong Nie[3], Jun Wen[2]

1 UA Museum of the North Herbarium and Department of Biology and Wildlife, University of Alaska Fairbanks, Fairbanks, USA. 2 Department of Botany, National Museum of Natural History, Smithsonian Institution, Washington DC, USA. 3 College of Biology and Environmental Sciences, Jishou University, Jishou, Hunan, China.

The grape genus *Vitis* L. has received considerable attention from viticulturists, plant biologists, and geneticists. Recent molecular sequencing efforts have supported several novel relationships in the genus in North America. Included was a monophyletic clade corresponding to the Occidentales group of subgenus *Vitis,* but only few samples from the highly variable *Vitis arizonica* complex (the canyon grape and its close allies) were included. Species of the Occidentales group have leaves with small stipules (1-3 mm long), small fruits (4-11 mm in diameter) that ripe late, including *V. arizonica, V. girdiana, V. acerifolia, V. riparia, V. rupestris*, *V. treleasei*, and several species from Central and Western Mexico, including *V. blancoi* Munson, *V. bloodworthiana*, *V. jaegeriana*, and *V. peninsularis*. Here we included a geographically and morphologically broad range of representative populations of the Occidentales group and conducted phylogenomic analyses using a bait set of 1013 genes. ASTRAL was used to infer a Maximum Quartet Support Species Tree, which resolved *V. californica* as sister to the moderately supported Occidentales group. Within the Occidentales group, *Vitis arizonica* did not form a monophyletic group. Two samples of *V. arizonica* from western Texas and Mexico are sister to a clade composed of four subclades. The earliest diverging clade is highly supported representing samples of the California and Baja California endemic *V. girdiana*, which in turn is sister to an unambiguously supported clade of three subclades of *V. arizonica*. We recovered one weakly supported clade (PP 0.38) of *Vitis arizonica* from Northern Arizona, sister to a weakly supported clade with several well-supported subclades. The easternmost population of *V. arizonica* from Kimble Co., Texas was resolved to be closely related to the *V. cinerea* complex. The phylogenomic results call for reassessment of species delimitations in the *V. arizonica* complex.

P.1366 The genus Cyphostemma (Vitaceae) in Gabon, with one new species

Olivier Lachenaud[1,2]

1 Meise Botanic Garden, Meise, Belgium. 2 Université Libre de Bruxelles, Brussels, Belgium.

Cyphostemma is the second largest genus of Vitaceae with around 200 species, forming three major clades, one in Asia, one in Madagascar, and the third mostly in continental Africa, with a few species in Madagascar and the Comoros. The genus is especially diverse in dry areas of eastern and southern Africa, with a markedly lower diversity in the Guineo-Congolian rainforest zone, of which Gabon is part. Only three *Cyphostemma* species have so far been recorded from Gabon: *C. adenocaule*, *C. adenopodum*, and *C. ukerewense*. A new species, *C. trigonospermum*, is here recognized based on one recent collection by the author in the Mayombe range, in the extreme south of the country; it is easily recognized by its very characteristic seed shape. An examination of historical herbarium specimens also revealed the occurrence in Gabon of *C. perforatum*, previously considered endemic to the Democratic Republic of Congo. As a result, five species of *Cyphostemma* are now known from Gabon, one of which is so far only known from the country.

S.152. SYSTEMATICS, EVOLUTION AND DIVERSIFICATION OF MAGNOLIALES (ANNONACEAE, EUPOMATIACEAE, MAGNOLIACEAE, MYRISTICACEAE)

P.1367 What happened in the tropical rain forests of Africa during the last 25 Myr? Insights from the Monodoreae tribe (Annonaceae).

Léo-Paul M. J. Dagallier[1,2], Fabien L. Condamine[3], Thomas L.P. Couvreur[1]

1 DIADE, Univ Montpellier, IRD, CIRAD, Montpellier, France. 2 New York Botanical Garden, Bronx, USA. 3 CNRS, Institut des Sciences de l'Evolution de Montpellier, Université de Montpellier, Montpellier, France.

Throughout the Cenozoic, Africa underwent several climatic and geological changes impacting the evolution of tropical rainforests (TRF). African TRF are thought to have extended from East to West in a 'pan-African' TRF, followed by several events of fragmentation during drier climate periods. During the Miocene, climate cooling and mountain uplift led to the aridification of tropical Africa and open habitats expanded at the expense of TRF, which likely experienced local extinctions. However, in plants, these drivers were previously inferred using limited taxonomic and molecular data. Here, we tested the impact of climate and geological changes on diversification within the diverse clade Monodoreae (Annonaceae) composed of 90 tree species restricted to African TRF. We reconstructed a near complete phylogenetic tree, based on 32 nuclear genes, and dated using relaxed clocks and fossil calibrations in a Bayesian framework. We inferred the biogeographic history and the diversification dynamics of the clade using multiple birth-death models. Monodoreae originated in East African TRF ca. 25 million years ago (Ma) and expanded toward Central Africa during the Miocene. We inferred range contractions during the middle Miocene and documented important connections between East and West African TRF after 15–13 Ma. Our results indicated a sudden extinction event during the late Miocene, followed by an increase in speciation rates. Birth-death models suggested that African elevation change (orogeny) is positively linked to speciation in this clade. East Africa is inferred as an important source of Monodoreae species, and possibly for African plant diversity in general. Our results support a scenario where increased aridification triggered extinction of TRF species in Monodoreae. This was quickly followed by rainforest fragmentation, subsequently enhancing lagged speciation resulting from vicariance and improved climate conditions. The uplift of East Africa is also shown to have played a positive role in Monodoreae diversification.

S.153. SYSTEMATICS, FLORISTICS, AND CONSERVATION: FACILITATING DATA INTEGRATION TO PROMOTE SOUND SCIENCE

P.1368 Extinction risk assessment of vascular plant species in Latvia: first results

Liene Auniņa[1], Valda Baroniņa[5], Rūta Katrīna Berga[3], Aiva Bojāre[2], Gunta Evarte-Bundere[2], Pēteris Evarts-Bunders[2], Iluta Dauškane[3], Dzirkstīte Gritāne[5], Laura Grīnberga[1], Sandra Ikauniece[4], Ivars Kabucis[5], Julita Kluša[5], Dace Kļaviņa[6], Dana Krasnopoļska[2], Ilze Kukāre[5], Brigita Laime[3], Otars Opermanis[4], Ansis Opmanis[1], Agnese Priede[4], Sanita Putna[5], Ieva Roze[1], Nora Rustanoviča[5], Uvis Suško[5], Inita Svilāne[2], Lilita Svirževska[5], Linda Uzule[4], Gunta Čekstere[1]

1 Institute of Biology, University of Latvia, Riga, Latvia. 2 Institute of Life Sciences and Technology, Daugavpils University, Daugavpils, Latvia. 3 Faculty of Biology, University of Latvia, Riga, Latvia .4 Nature Conservation Agency, Sigulda, Latvia. 5 Society of Botanists of Latvia, Ilgas, Latvia 6 National Botanical Garden, Salaspils, Latvia.

For the first time, the extinction risk assessment according to the IUCN criteria and categories has been carried out in Latvia (2021-2023). We studied 345 vascular plant taxons: legally protected, included in the previous Red Data Book of Latvia (2003), species discovered after 1999 in Latvia, and other species considered rare and endangered in the region. The majority of the taxons met the criteria for EN (164), less for VU (52), CR (47), LC (32), NT (22), RE (16), and DD (12). The B criterion was the most common criterion applied followed by criterion D. Mainly vascular plant species, included in Annex II of the Habitats Directive, are regularly monitored in Latvia. Regarding the habitats, about half of the critically endangered species were semi-natural grassland species, but in categories EN and VU, also species of old-growth forests, clear-water lakes, mires, coastal habitats as well as outcrops were well represented. There are eight endemic taxons of the Baltic Sea region in Latvia, such as *Taraxacum lissocarpum, T. balticum, T. suecicum, Tragopogon heterospermus, Saussurea esthonica, Linaria loeselii, Anthyllis maritima, Dianthus arenarius* subsp. *arenarius,* and one endemic species of the Eastern Baltic region – *Corispermum intermedium*, we assessed. Still, there are 50-100 species, for which extinction risk assessment is urgent, e.g., habitat specialists of semi-natural grasslands, and under-recorded species. Further studies dealing with various aspects of plant species protection are necessary. Taxonomy, distribution, and population size studies as well as studies on appropriate management practices and habitat requirements we consider a priority.

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P.1369 A taxonomic approach to species conservation: the case of a Brazilian regional red list

Mayara Krasinki Caddah[1], Daniele R. Drischel[1], Ana Flávia Augustin[1], Gabriela M. Cardoso[1], Gabriela Goebel[1], Okesanna E. Puhale[1], Duane F. Lima[1]

1 Federal University of Santa Catarina, Florianopolis, Brazil.

Poor taxonomy has hampered biodiversity conservation worldwide. Red lists (RL) of threatened species are among the main legal tools for species conservation. Brazil has one of the richest floras in the world and, considering its size, regional lists are important strategies for conservation policy and management. However, Brazilian regional lists are usually taxonomically outdated, and have traditionally been prepared without clear methods, raising doubts on its effectiveness for conservation. Ca. 5300 native species of vascular plants are currently registered in the state of Santa Catarina, southern Brazil, including 125 Melastomataceae and 185 Myrtaceae. The official RL of the state lists 314 taxa of vascular plants, with only five Melastomataceae and four Myrtaceae. To shed light on the problems of Brazilian regional RL we analyzed the current taxonomic status of all species names of the RL of plants of the state of Santa Catarina. Moreover, we are currently reassessing the extinction risk of Myrtales species, following the IUCN criteria and current taxonomy knowledge. For the taxonomic update of the RL, we used mainly the Flora & Funga of Brazil online database. We have found, so far, that 55% of all the species names of the RL of Santa Catarina are problematic, being either misspelled, synonyms or applied to species considered exotic, compromising the RL application. For the Myrtales reassessments, we have so far evaluated 48 species (28 Myrtaceae; 20 Melastomataceae), and found that at least 25 of them are in some level of threat. Up to now, our results have suggested that a careful taxonomic approach can reveal the threatened status of numerous species that currently have no legal protection, which severely compromises their conservation. This study highlights the value of taxonomic knowledge when assessing extinction risk and compiling RL, especially regional lists, in which several conservation plans rely on.

P.1370 Phylogenetic and trait-based correlates of extinction risk in Italian flowering plants

Angelino Carta[1], Simone Orsenigo[2], Elena Zappa[3], Mariacristina Villani[4], Simonetta Bagella[5], Sara Magrini[6], Annalisa Santangelo[7], Emmanuele Farris[5], Giulia Calderisi[8], Donatella Cogoni[8], Maria Silvia Pinna[8], Gianpietro Giusso del Galdo[9], Saverio Sciandrello[9], Gianmarco Tavilla[9], Gianmaria Bonari[10], Lorenzo Pinzani[11], Silvia Assini[2], Domenico Gargano[12], Giuseppe Fenu[8]

1 Department of Biology, University of Pisa, Pisa, Italy. 2 Department of Earth and Environmental Sciences, University of Pavia, Pavia, Italy. 3 Hanbury Botanic Gardens, University of Genoa, Ventimiglia, Italy. 4 Botanical Garden, University of Padua, Padua, Italy. 5 Department of Chemical, Physical, Mathematical and Natural Sciences, University of Sassari, Sassari, Italy. 6 Department of Ecological and Biological Sciences, University of Tuscia, Viterbo, Italy. 7 Department of Biology, University of Naples Federico II, Napoli, Italy. 8 Department of Life and Environmental Sciences, University of Cagliari, Cagliari, Italy. 9 Department of Biological, Geological and Environmental Sciences, University of Catania, Catania, Italy. 10 Faculty of Agricultural, Environmental and Food Sciences, Free University of Bozen-Bolzano, Bozen-Bolzano, Italy. 11 Department of Science, University of Roma Tre, Rome, Italy. 12Department of Biology, Ecology and Earth Sciences, University of Calabria, Rende, Italy.

Plants differ in their biological susceptibility to extinction. However, it is yet unclear which patterns are common across lineages or ecosystems, and which are taxon-specific or restricted to specific context, with consequences to conservation practice. Moreover, whilst extinction risk is not a heritable trait, there is emerging evidence that it is not randomly distributed across the tree of life, likely because extinction-proneness is shared among closely related species. Here, we investigated the contribution of spatial predictors, adult traits, reproductive traits, and habitat type on the extinction risk of Italian flowering plants using phylogenetic generalized linear mixed models accounting for the shared evolutionary history among species. Specifically, we collected Red List categories of the Italian vascular flora compiled by the working group for Nature Conservation of the Italian Botanical Society for 472 angiosperm species. Overall, extinction risk in the Italian flora affects all species living in fragile and threatened habitats regardless of their reproductive or vegetative traits but with similar susceptibility to extinction among phylogenetically related species and with restricted ranges and habitat breath. Not surprisingly, extrinsic predictors of extinction risk (habitat type as a proxy of human footprint) indicate that habitat degradation is one main threat to plant species. However, in light of the phylogenetic clustering in extinction risk, we also show that extinction-proneness is shared among closely related species likely because similar species share intrinsic biological features. We conclude that whilst extrinsic and spatial predictors undoubtedly explain extinction risk, it is still not entirely clear which intrinsic plant traits could explain phylogenetic clustering of susceptibility to extinction. The integration of evolutionary and biological data would thus facilitate more effective conservation and management strategies.

P.1371 Cyperaceae of Ukraine - diversity and current classification

Ivan M. Danylyk[1]

[1] Institute of Ecology of the Carpathians National Academy of Sciences of UKraine, Lviv, Ukraine.

The family Cyperaceae Juss. is one of the largest vascular plant families in Ukraine and within the class Liliopsida Batsch it is the third species-rich, after Poaceae Barnhart and Orchidaceae Juss. According to our preliminary data, the family Cyperaceae contains one typical subfamily, 8 tribes, 19 genera, and 153 species in Ukraine (Danylyk 2012). The development of molecular taxonomy in more recent time has led to new insights and changes in the nomenclature and taxonomy of the Cyperaceae (Starr & Ford 2009, Larridon et al. 2011-2021, Hayasaka 2012, Shiels et al. 2014, Verloove et al. 2016, Reid et al. 2017, Villaverde et al. 2020). Based on the results of these recent data, we have revised the taxonomic diversity of the family Cyperaceae in Ukraine, now including one subfamily, 13 tribes, 16 genera, and 148 species (Danylyk & Koopman 2023). A particular number of changes has been recorded in the genus spectrum, for example, we have accepted the genera *Schoenoplectus* (Rchb.) Palla and *Schoenoplectiella* Lye are listed by us as recognised taxa. On the other hand, we consider formerly separate genera like *Juncellus* (Griseb.) Clarke, *Mariscus* Vahl, *Pycreus* P.Beauv., and *Torulinium* (M.Bieb.) S.S.Hooper in synonymy of the genus *Cyperus* L. Significant changes in the classification of the genus *Carex* L., in particular its intrageneric taxa – 4 subgenera and 42 sections are taken into account. Subgenus *Psyllophorae* (Degl.) Peterm. now includes only one species (*Carex curvula* All.), and the species previously included in this subgenus (Sosnovska et al. 2013) are now placed in the subgenus *Euthyceras* Peterm. (sections *Leucoglochin* Dumort. and *Rupestres* Fr.) and subgenus *Vignea* (P.Beauv. ex T.Lestib.) Heer (section *Physoglochin* Necker ex Dumort.). Thus, the Cyperaceae family in the flora of Ukraine reflects its current state both in terms of number and placement of tribes, genera, intrageneric taxa.

P.1372 Plant fibres for basketry from the Andean region of Colombia

Galvis R. Manuel1

1 Facultad de Ciencias de la Educación, Jardín Botánico, Universidad Uptc- Tunja, Boyacá Colombia.

For years, palms, trees, vines, reeds, grasses and some aquatic plants have offered artisans a wide variety of soft and hard fibres, extracted from buds, leaves, inflorescences, stems and roots, woven by women and men. The objects were registered and inventoried, with the elaboration of ethnobotanical data sheets, from tours and visits to artisans in marketplaces in three Andean departments: Boyacá, Cundinamarca and Santander. As a result, 48 botanical families were identified among 142 fibre-producing species, including plants from the following families: Arecaceae, Araceae, Cyperaceae, Cyclanthaceae, Cucurbitaceae, Clusiacea, Dioscoreaceae, Smilacaceae, Juncaceae, Malvaceae, Marantaceae, Meliaceae, Amnonaceae, Musaceae, Poaceae, Polypodiaceae, Cyatheaceae and Thyphaceae. Artisans make a wide range of utilitarian and decorative objects, in multiple shapes and designs, sizes and colours: weavings, ropes, hats, masks, paper, dresses, baskets, mats, packaging, bags, ornaments, backpacks, nets, belts, bracelets, fans, among others. Fibres can be classified into systems according to their use, such as for example textile fibres that are long, resistant, fibres for making brushes and brooms, rigid and resistant, where Iraca stands out. Fibres for braided fabrics are the most widely used in the region. These are divided into three types of fibres: fibres for hats such as iraca (*Carludovica palmata*), palmicho (*Sphaeradenia laucheana*), caña brava (*Gynerium sagittatum*), cañuela (*Arthrostylidium* sp.), enea (*Typha latifolia*). Matting fibres such as rush (*Juncus bufonius*), esparto (*Juncus ramboi*), fique (*Furcraea hexapetala*). Fibres for basketry such as chin (*Arundo donax*), bijao (*Calathea lutea)*, fern (*Cyathea caracasana*), gaques (*Clusia multiflora*) and estropajo (*Luffa cylindrica*). It is concluded that there is a need to elaborate conservation and development strategies in cultivar protocols, one of the challenges, and how to meet the demand for future fibres and non-forest products without harming the ecosystem resource and socio-cultural environment.

Note: This abstract was translated with AI.

P.1373 Exploring the Brassicaceae Tree of Life online

Kasper P. Hendriks[1], Brianne de Deugd[2], Robin Dekker[2], Roosmarijn Hoekstra[2], Frederic Lens[1]

1 Naturalis Biodiversity Center, Leiden, The Netherlands. 2 Amsterdam University of Applied Sciences, Amsterdam, The Netherlands.

The mustard family (Brassicaceae) is one of the most studied plant families in the world. It contains many model species, including *Arabidopsis thaliana*, as well as important crop species, such as cabbage, canola, and mustard. In light of global climate change and associated agricultural and conservational challenges, the role of this family as a model in plant science is expected to increase even further. Therefore, a solid understanding of the family's history, including knowledge of the relationships among species and trait evolution, is essential. Great progress was recently made by publications of comprehensive family-wide phylogenies, indeed facilitating the dissemination of crucial insights. However, the sheer size of these phylogenetic reconstructions now presents a new challenge, as it becomes increasingly difficult to distil the wealth of information contained within these gigantic network graphs. Here, we present a brand-new interactive online tool, the Brassicaceae Tree of Life (brassitol.vercel.app). While a work in progress, the first version already assists both students and scientists in studying the family's evolution, relationships, taxonomy, distribution, and a first set of traits. Various intuitive filters allow swift selection of the taxa of interest at different taxonomic ranks. The tool combines valuable resources easily and effectively, including a calibrated 297-nuclear gene phylogeny representing 92% of the family's genera (Hendriks et al. 2023), the most recent taxonomic decisions (German et al. 2023), distribution, habitat, and growth form data (World Checklist of Vascular Plants), and appealing images (iNaturalist). Future versions will include more complete phylogenies, further filtering options, details of the specimens that represent each species, and options to export details in tabular format. We believe that our new, user-friendly tool to explore mustard family evolution was long overdue and will serve a wide range of Brassicaceae students and scientists for years to come.

P.1374 The botany at GBIF Spain

Gloria Martínez-Sagarra[1,2], Katia Cezón[1], Francisco Pando de la Hoz[1]

1 GBIF Spain, Real Jardín Botánico, CSIC, Madrid, Spain. 2 Department of Botany, Ecology and Plant Physiology, University of Córdoba, Spain.

GBIF Spain (GBIF.ES) is not a team, it is a robust network currently comprising 117 entities (including research institutes, collections, projects, public agencies, associations, private companies…) actively engaged in mobilizing, publishing, and using biodiversity data. The glue in this endeavor is the "GBIF.ES Coordination Unit" (UdC, from its Spanish name). Since the inception of GBIF.ES UdC in 2003, its main goal has been supporting the involvement of the Spanish biodiversity community within the GBIF network. This is achieved by providing the following services, adjusted based on the current needs: 1) training workshops, 2) publishing services, 3) portal data and specific data hubs, 4) ICT tools and biodiversity information standards, and 5) supporting citizen science through Natusfera (iNaturalist in Spain). These components are intended to work together in an "organic" way, creating an interconnected framework where the outcomes of each service contribute collaboratively to the success of the others. The Spanish botanical community activity in GBIF is strong: currently publishing over 16 million records through 189 datasets contributed by 72 institutions (as of January 2024). And just as significant is the utilization of this data by the scientific community: the number of citations of these datasets in peer-reviewed journals is 37,605, representing 67.6% of the total citations gathered by datasets from Spanish entities. We have learnt many lessons along the way. Two to emphasize here: 1) Training serves as an open door to the outside world, initiating numerous collaborations and partnerships. In them, GBIF gets known at its best: partnership, data sharing and capacity building in action, and direct contact with participants gives us excellent feedback and ideas. 2) Looking just after data does not work. The key to GBIF's success lies in motivating and providing skills to biodiversity researchers and data contributors to disseminate their data.

P.1375 Selective-OCR protocol for the mass digitization of herbarium specimen labels

Miguel Murguía-Romero[1], Diana G. Flores-Camargo[2]

1 Unidad de Informática para la Biodiversidad, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, Mexico. 2 Jardín Botánico, Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad de México, Mexico.

The herbarium specimens' information contained in databases has been very useful for understanding the world's biodiversity. However, the information on a high percentage of specimens still needs to be incorporated into public databases in a more expedited way. In this work, a protocol is proposed for the massive digitization of specimen label information using Optical Character Recognition (OCR). Its efficiency was evaluated using a set of herbarium specimens. A selective-OCR protocol was applied to identify information from only five fields including taxonomy and collecting site classes. 1) OCR was applied to 8,451 herbarium labels of specimens housed at the National Herbarium of Mexico (MEXU), integrating all identified lines of text into a working database. 2) Lines containing information on five target fields were identified: family, genus, species, country, and state. 3) The identified information was cleaned using taxonomic catalogs (Kew's World Checklist of Vascular Plants) and geographic catalogs (including the Getty Thesaurus of Geographic Names). 4) The number of successful cases was quantified. 5) The information on the specimens properly identified and their associated images were integrated into the public database of the National Herbarium of Mexico (www.ibdata.ib.unam.mx). With the selective-OCR protocol applied, the information contained in the five target fields was successfully identified in 5392 (63.8%) specimens, in one to four of the target fields 2515 (29.8%) specimens, and only in 544 (6.4%) none could be identified. With selective-OCR it is not possible to automatically digitize all the information on the herbarium specimen labels; however, for the information on the most consulted fields (e.g., species and state), automatic identification is possible. Therefore, applying the selective-ORC protocol will accelerate the integration of herbarium information into public databases and manage capture efforts toward particular objectives.

P.1376 Preliminary survey of Asteraceae in the municipality of Petrolina, Pernambuco, Brazil

Edilton V. de Oliveira-Neto[1], Joesili C. P. Oliveira[1]

1 Universidade Federal Rural de Pernambuco, Recife, Brazil.

Petrolina is a municipality located in the semi-arid region of the state of Pernambuco, Brazil. It was founded in 1870 and covers an area of 4,561.87 km² within the Caatinga biome, being considered one of the largest fruit-growing centers in the country. It is irrigated by the São Francisco River Basin and has vegetation classified as Semideciduous Seasonal Forest, from which part of the population derives its livelihood through extractivism. The landscape is softly undulating, and the climate is hot and dry, with the rainy season from November to April. The aim of the present work was to carry out a preliminary survey of Asteraceae in the municipality of Petrolina. The survey was conducted on the SpeciesLink online platform (www.specieslink.net), where the species of the mentioned family that have already been collected in the area were summarized, except those cultivated. Asteraceae is represented in Petrolina, in principle, by 41 genera and 50 species, deposited in 22 different herbaria. The genus that stood out the most was *Bidens* L., with three species, followed by *Acanthospermum* Schrank, *Acmella* Rich. ex Pers., *Conyza* Less., *Emilia* (Cass.) Cass., *Lepidaploa* (Cass.) Cass., *Mikania* Willd., and *Praxelis* Cass., with two species each. Eleven tribes were recorded, with an emphasis on Heliantheae (11 spp.), Eupatorieae (8 spp.), Vernonieae (8 spp.), and Astereae (5 spp.). Of the total species, six are considered endemic to Northeast Brazil: *Chresta martii* (DC.) H. Rob., *Conocliniopsis prasiifolia* (DC.) R. M. King & H. Rob., *Isocarpha megacephala* Mattf., *Lepidaploa chalybaea* (Mart. Ex DC.) H. Rob., *Stilpnopappus pratensis* Mart. ex DC., and *Trichogonia heringeri* R. M. King & H. Rob. As for the growth habit, the herbaceous habit stood out (28 spp.), followed by subshrub (17 spp.), shrub (2 spp.), scandent (2 spp.), and arboreal (1 spp.).

P.1377 Quantitative analysis of leaf shape variation in Ipomoea: insights from geometric morphometrics

Kavi K. Oza[1], Vinay M. Raole[1]

1 Department of Botany, Faculty of Science, The Maharaja Sayajirao University of Baroda, Vadodara, Gujarat, India.

Leaves are one of the most significant organs for plant identification due to their variability across different taxonomic groups. Leaf morphology provides distinguishing features which help in the discernment of plant species. Traditional morphometrics has contributed greatly to reducing the problems of plant identification and morphology-based species delimitation. Image analysis and digital morphometrics have made it easy to detect more characters to complement existing leaf data sets in recent years. This study aimed to investigate leaf shape variation between some species of the genus *Ipomoea* L. using the geometric morphometric method (GMM). We have examined leaves from different species of *Ipomoea* using morphometric techniques. We identified different shape variations due to the result of differing length-to-width ratios, shape, and size changes. The variations were mainly due to changes in the leaf blade ratio, size, and shape of the posterior lobes of leaves and anterior lobes differentiation. Obtained results suggest that the leaf blade ratio was highly correlated with the first principal component (PC1) of morphometric variation calculated using elliptic Fourier Descriptors (EFDs). Subsequent PCs corresponded to complex shape variation which cannot be captured by traditional linear measurements. ANOVA showed a significant difference (p = P.01159) among the analyzed species of the *Ipomoea* genus. Based on the results obtained, we can suggest that the geometric morphometric of leaf shape is effective in interspecific discrimination within members of the genus *Ipomoea*. Further morphometric studies of leaf shape involving a larger number of samples especially in the study of intergeneric and inter-specific variation are suggested.

P.1378 Beyond the digitization project: using digitized specimen data to inform collections management of an aggregated herbarium

Tiana F. Rehman[1]

1 Botanical Research Institute of Texas, Fort Worth, USA.

Specimen digitization expands the possibilities of research by increasing access to critical data from natural history collections across the globe in a standardized format. Beyond access for researchers, this trove of data can be mined by collections management professionals to manage strategic growth of their repositories as they face restrictions on space, staffing, and other resources necessary to safely house specimens. For those repositories representing aggregated collections, the ability to use digitized specimen data to inform the integration of their holdings cannot be overstated. The Philecology Herbarium of the Botanical Research Institute of Texas at the Fort Worth Botanic Garden was established in 1987 and is an aggregate composed of four separately recognized herbarium collections totaling approximately 1.4 million specimens. These collections are in various stages of inter-filing, and there is known duplication of specimens (collector name and number matches) across as many as three of the collections. As a result of previously funded United States National Science Foundation grants, certain geographic areas and taxonomic groups have been digitized in their entirety. We present the preliminary results of the use of these digitized data to inform collections management decisions to more efficiently manage space and increase physical access to specimens through duplicate distribution to other herbaria.

P.1379 Taxonomic revision of Serpocaulon (Polypodiaceae)

David Sanín[1,2], Alexandre Salino[3] & Alan R. Smith[4]

1 Herbario UIS, Universidad Industrial de Santander, Santander, Colombia. 2 Jardín Botánico del Magdalena, Caldas, Colombia. 3 Herbário BHCB, Instituto de Ciências Biológicas, Minas Gerais, Brasil. 4 University Herbarium, University of California, Berkeley, USA.

We present a taxonomic revision of *Serpocaulon* (Polypodiaceae), a tropical American fern genus. Our work is based on a morphological analysis of 56 characters recorded from 2167 specimens deposited in 41 herbaria. Field trips were carried out in Argentina, Bolivia, Brazil, Colombia, Costa Rica, Ecuador, Panama, and Peru, where observations on the habit and habitat of several species were made. Digital images were also consulted. A total of 260 names were found and their nomenclatural types were studied, resulting in the lectotypification of 47 names (first step 30, second step 17 names). We recognize 37 species and five hybrids in *Serpocaulon*; one of the hybrids is given a new status (*S.* ×*semipinnatifidum* (Fée) A.R. Sm.) and another one is described (*S.* ×*tabuleirense* D. Sanín & Salino). Moreover, 19 names are newly synonymized, five species are excluded, 18 names are considered as of uncertain application, and five as *nomina nuda*. We document for 22 species a total of 63 chorological novelties in different countries. The elevational range of the genus is 0 to 4200 m. The Andes of Ecuador and Colombia are the main center of diversity and endemism; secondarily, the Atlantic Rain Forest of Brazil has five endemic species. We provide a taxonomic key, descriptions, discussions, local names, uses, illustrations, photographs of the plants in the field, micro-photographs of the rhizome scales and the spores, and distribution maps of all species.

P.1380 Passiflora of the Caatinga, Brazil: richness, distribution and endemism

Glaucia Silva[1], Leonardo M. Versieux[2], Ana C. Mezzonato-Pires[3]

1 Department of Botany and Zoology, Federal University of Rio Grande do Norte, Natal, Brazil. 2 Department of Botany and Zoology, Herbarium UFRN, Federal University of Rio Grande do Norte, Natal, Brazil. 3 Department of Botany, Federal University of Goiás, Goiânia, Brazil.

Passiflora L. is the richest genus of the Passifloraceae *sensu stricto*, comprising 525 pantropical species. These species include herbaceous or woody vines, rarely shrubs and trees. *Passiflora*'s fruits are known as passion fruit, "maracujá" (Brazilian portuguese) and "maracuyá" (Spanish) in Latin America. In Brazil, there are currently listed 157 species of *Passiflora*, occurring in all phytogeographic domains Amazon, Atlantic Forest, Caatinga, Cerrado, Pampa, and Pantanal. The Caatinga - Dry Woodlands has species with unique morphological adaptations, carrying ecological, economic, and medical importance. Although its importance for biodiversity, Caatinga is still poorly known scientifically, the third most deforested, and it has the third lowest overall number in angiosperms richness among the domains. Research regarding *Passiflora* in this region are still missing. Thus, the purpose of this study was to identify *Passiflora* species that occur in Caatinga, verify its distribution and endemism. Our results show that i) Caatinga has 65 species of *Passiflora*, becoming the third richest domain for passion fruit species in Brazil; ii) *P. cincinnata*, *P. edmundoi*, *P. foetida*, *P. recurva*, and *P. setacea* have wide distribution; iii) *P. porophylla*, *P. quadriglandulosa*, *P. racemosa*, *P. riparia*, and *P. trifasciata* have restricted distribution and iv) *P. bahiensis*, *P. mucugeana*, and *P. jiboiaensis* are the only endemic species to Caatinga. These results indicate the taxonomical potential of the Caatinga, and the importance of conducting more herbaria and field work research in such domain, increasing the knowledge of the Flora of Brazil. It also provides new and updated data to justify the creation and maintenance of reserves, and development of public strategies for conservation.

P.1381 Passiflora natalensis, a new light purple species of Passiflora (Passifloraceae s.s.) from Brazil

Glaucia Silva[1], Alan A. Roque[2,3], Rubens Queiroz[4], Ana C. Mezzonato-Pires[5]

1 Department of Botany and Zoology, Federal University of Rio Grande do Norte, Natal, Brazil. 2 Institute for the Environment and Sustainable Development, Natal, Brazil. 3 Herbarium RN - Natal Dunes State Park, Natal, Brazil. 4 Department of Systematics and Ecology, Federal University of Paraíba, João Pessoa, Brazil. 5 Department of Botany, Federal University of Goiás, Goiânia, Brazil.

In this study we present a new species of *Passiflora*, the most representative genus of vines and lianas in the Neotropics. Such distinctive new species was identified during fieldwork in the Atlantic Forest, for the project Flora of Rio Grande do Norte state, Brazil, and is supported by robust morphological characterization, such as i) the presence of two to three smooth and lustrous glands in the base of the petiole; ii) always 5- lobed leaves, with the presence of one or two pairs of horizontal slits in the leaf blade's central lobe, iii) none, one or two pairs of horizontal slits in the adjacent lobe, iv) absence of the operculum, and v) a sparsely pubescent ovary. This *Passiflora* is endemic to coastal sand plain vegetation (restinga), an ecosystem of the Brazilian Atlantic Rainforest, a hotspot for biodiversity and a conservation priority. Rio Grande do Norte state has more than 22 Conservation Units but this new species is protected by only one Conservation Unit: Natal Dunes State Park, that has tourism activities allowed in some areas. We also provide a conservation assessment for the newly recognized *Passiflora*, indicated as Critically Endangered. This work is also part of a project that aims to describe the biodiversity of a poorly inventoried state and highlights the potential of floristic investigations in this priority area, as an effort to direct public policies for conservation in these regions, which harbors narrowly endemic and severely threatened species.

P.1382 Hope for Aristolochia hypoglauca (Aristolochiaceae, Magnoliidae): new occurrences and conservation actions for the rare tropical plant

André V. Suzuki[1], Joelcio Freitas[2], Patricia da Rosa[3], Danilo A Zavatin[4], Elton J. de Lírio[1,4]

1 Universidade Federal do ABC, Santo André, Brazil. 2 Instituto Nacional da Mata Atlântica, Santa Teresa, Brazil. 3 Universidade Estadual do Rio de Janeiro, Rio de Janeiro, Brazil. 4 Universidade de São Paulo, São Paulo, Brazil.

Aristolochia hypoglauca Kuhlm. was described in 1936 based on collections carried out on the banks of the Rio Doce, in Espírito Santo state (ES), Brazil. The species was considered extinct in 2007, as only the type was known. New records were discovered in the mountainous region of ES, which allowed the species to be evaluated in 2013 as Endangered (EN). Until then, 6 localities of occurrence and 11 mature individuals were known, with occurrence only for ES. After the investment of the CEAMA project it was possible to expand knowledge of its geographic distribution, we increased the total number of subpopulations to 17 and the number of individuals to 43. Only three subpopulations of *A. hypoglauca* occur in protected areas. The EOO was less than 5,000 km^2, now includes the states of Rio de Janeiro and Bahia, increasing to 228,604 km^2 and AOO 96,000 km^2, but maintaining the species as EN following the EN B2ab(ii, iii) + C2 a(i) from IUCN, because populations are fragmented and there has been an observed decline in habitat quality. Conservation actions for formal and non-formal environmental education were carried out in schools and with the community in general in the ES (where most populations of the species occur). We offered participatory lectures and publicized the project through posters, social media and by developing a species identification guide in the local language. As for ex situ conservation, the seeds are included in the germplasm bank from botanical garden of Rio de Janeiro and also germinated at the National Institute of the Atlantic Forest (INMA). The germination rate was 68% under natural conditions using local soil. Seeds from two subpopulations in Espírito Santo were collected to carry out experiments under controlled conditions. To date, there are 18 seedlings, which will be reintroduced into their natural range.

P.1383 Characteristics of plastomes of Papaver (Papaveraceae)

Zhiyun Yang[1,2], Hongtao Li[1], Jie Cai[1], Siyun Chen[1], Dezhu li[1*], Tingshuang Yi,[1*] Junbo Yang[1*]

1 Germplasm Bank of Wild Species, Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, Yunnan, China.

Papaver L. (Papaveraceae) contains ca. 80 annual, biennial and perennial herbaceous species widely distributed in temperate and cold regions of Eurasia, Africa and North America. The only molecular phylogenetic study on the whole genus applied two molecular loci using 25 *Papaver* species. It is urgent to develop highly informative molecular markers to resolve the intrageneric relationships. In this study, we newly sequenced 18 complete plastomes and downloaded 5 plastomes of *Papaver* from NCBI, and 5 related genera as outgroup. These 23 plastomes of *Papaver* have typical quadripartite structures, which include a large single copy (LSC), two inverted repeats (IR) and a small single copy (SSC) region. Each *Papaver* plastome contained 114 unique genes, including 80 protein-coding genes 30 transfer RNAs (tRNAs), 4 ribosomal RNAs (rRNAs). The genome sized were ranged from 152,448 to 153,921bp, with IRs of 25,672 – 25,990 bp, LSCs of 82,703 – 83,634 bp, SSCs of 17,926 – 18,954 bp. The overall GC content of these 23 plastomes was 38.64 – 38.91%. The IR regions exhibited higher GC contents from 43.03 to 43.30% than the LSC regions from 37.12 to 37.49%, and the SSC regions from 33.12 to 33.89%. We found higher variable loci (Pi > P.5) among 21 *Papaver* species and 2 subspecies, one coding gene and thirteen intergeneric regions genes, which could be used to resolve the interspecific relationship and identify species of *Papaver*. *Papaver* s.s. is not a monophyletic with the nesting of three related genera (*Roemeria*, *Meconopsis* and *Stylophorum*), and was identified two clades (I and II) and the clade I comprises the *Meconopsis* subclade and the sect. *Meconella* subclade, with the later subclade comprising *Stylophorum*. The clade II comprises sects. *Rhoeadium*, *Papaver*, *Oxytona* and *Argemonidium*, with *Roemeria* nesting within sect. *Argemonidium*.

P.1384 Cacti of Eastern Brazil: twenty years on

Daniela C. Zappi[1], Nigel P. Taylor[2], Sinzinando Albuquerque-Lima[3], Lidyanne S. Aona[4], Fernando F. Franco[2], Milena Telhe[2], Monique Romeiro-Brito[2], Evandro M. Moraes[2]

1 Department of Botany, University of Brasília, Brasilia, Brazil. 2 Departament of Biology, Federal University of São Carlos, Sorocaba, Brazil. 3 Laboratory of Floral and Reproductive Biology, Federal University of Pernambuco, Recife, Brazil. 4 Centro de Ciências Agrárias, Ambientais e Biológicas, Univ. Federal do Recôncavo da Bahia, Cruz das Almas, Brazil.

Eastern Brazil is home to the third diversity centre of Cactaceae, with a high number of endemic and microendemic species found throughout three biomes (Caatinga, Atlantic Rain Forest and Cerrado). Varied in habit, habitat and survival strategy, these species are predominantly bat and hummingbird pollinated, however hawkmoth and bees play an important role in their floral biology. Initially 30 genera and 130 species were treated in the 2004 book, however, over the last 20 years, new phylogenies reduced the number of genera to 24, while at least 15 new species have been described. The Chapada Diamantina and Southern Espinhaço *campo rupestre* provinces are home to some of the most enigmatic species of cacti, and continue to yield new discoveries. In terms of classification, an integrated sequence data approach using public gene and genomic databases with new target sequences (generated using the customized Cactaceae591 probe set) across representatives of tribe Cereeae led to new and revised subtribes. Within Cactoideae, only *Strophocactus brasiliensis* and epiphytic tribes Rhipsalideae and Hylocereeae are not included in Cereeae. The phytogeographic significance of cactus endemism in river basins has also been explored and we seek opportunities to test a dryland refugia hypothesis for the area. The significance of cephalia in pollination orientation is under research, together with novel cues such as flower odour. Increasing threats from habitat destruction caused by human activities (agrobusiness, mining, urban development) have led us to list a large proportion of Eastern Brazilian cacti as endangered. Research on the distribution pattern of Caatinga cacti predicts a retraction of areas of environmental suitability, with more restricted woody species occupying marginal habitats at greater risk of extinction. Conservation actions such as new and extended protected areas, seed collection and *ex situ* propagation and seed production are needed if we are to ensure the survival of these species.

S.154. SYSTEMATICS, PHYLOGENETICS, BIOGEOGRAPHY AND EVOLUTION OF MELASTOMATACEAE

P.1385 The role of phylogenetic niche conservatism and climatic niche divergence in ecologically diverse Andean Miconia (Melastomataceae)

Juan C. Angulo[1, 2], Léo-Paul M. J. Dagallier[1], Lucas F. Bacci[3, 4], Lucas C. Majure[3, 4], Fabián A. Michelangeli[1]

1 New York Botanical Garden, New York, USA. 2 The Graduate Center, City University of New York, New York, USA. 3 University of Florida, Florida USA 4 Florida Museum of Natural History, Florida, USA.

The tropical Andes is a biodiversity hotspot, harboring a diverse flora along steep elevational and ecological gradients. Species are not distributed evenly within these mountains and are ecologically constrained by the environmental conditions in which a species can persist, or its climatic niche. As a lineage diversifies species can continue to retain their ancestral climatic niche through phylogenetic niche conservatism (PNC) or diverge from it, particularly when presented with ecological opportunity. Both PNC and niche divergence have played roles in

Andean species assembly, either through migration from temperate lineages into high elevation habitats (PNC) or colonization of lineages with Amazonian origins by way of niche divergence. However, we still lack insight into what role these processes play in structuring the distribution of lineages that have successfully diversified across the Andean ecological gradient from warm lowlands to cold sub-alpine ecosystems. The genus *Miconia* (Melastomataceae) contains an Andean centered clade (~500 sp) in which species are narrowly endemic to elevational bands, but as a whole the group can be found from sea level to 3500m. We generate a new phylogeny of the group and use distribution and environmental data to reconstruct the dynamics of niche evolution as the lineage diversified. We hypothesize that PNC has constrained diversification largely within climatic regimes, but that niche shifts have allowed for successional tracking of low to high elevation Andean habitats. We predict that some aspects of the niche, such as precipitation related variables, are conserved, while others have shifted with more frequency, such as temperature. Our study contributes to the understanding of the biogeographical patterns of Andean plant diversity and the processes that generate it.

P.1386 Phylogeny and biogeographic history of the fleshy-fruited Sonerileae (Melastomataceae)

Luo Chen[1], J. Peter Quakenbush[2], Darin S. Penneys[3], Deepthi Yakandawala[4], Marie-Claire Veranso-Libalah[1], Gudrun Kadereit[1,5]

1 Prinzessin Therese von Bayern-Lehrstuhl für Systematik, Biodiversität & Evolution der Pflanzen, Ludwig-Maximilians-Universität München, Munich, Germany. 2 Department of Biological Sciences, Western Michigan University, Kalamazoo, USA. 3 Department of Biology and Marine Biology, University of North Carolina Wilmington, Wilmington, USA. 4 Department of Botany, University of Peradeniya, Peradeniya, Sri Lanka. 5 Staatliche Naturwissenschaftliche Sammlungen Bayerns: Botanische Staatssammlung München, Botanischer Garten München-Nymphenburg, Munich, Germany.

In this study, we investigated the phylogenetic relationships of the fleshy-fruited Sonerileae, the second largest tribe in Melastomataceae, which comprises approximately 1080 species and is predominantly found in Southeast Asia and Madagascar. Despite its diversity, the evolutionary history of Sonerileae, particularly among the fleshy-fruited genera (*Catanthera*, *Heteroblemma*, *Kendrickia*, *Medinilla*, *Pachycentria*, and *Plethiandra*), remained poorly understood due to limited phylogenetic sampling. Utilizing nuclear and plastid loci obtained through target capture and genome skimming, our analysis revealed that fleshy-fruited Sonerileae are not monophyletic but instead fall into three distinct lineages. We found that *Kendrickia* is closely related to an Afrotropical endemic clade, while *Heteroblemma* and *Catanthera* form a second clade with certain *Phyllagathis* and *Driessenia* species. *Medinilla*, along with *Pachycentria* and *Plethiandra*, constitutes a separate lineage. This study also examined cyto-nuclear discordances, shedding light on the complex evolutionary relationships within these taxa. Through molecular dating and biogeographic analysis, we explored the temporal and spatial patterns of diversification, offering new insights into the biogeographic and evolutionary processes that have shaped the current distribution and diversity of the fleshy-fruited Sonerileae.

P.1387 Current state of knowledge of the family Melastomataceae in the department of Huila, Colombia

Mariano Cortés[1], Hilda Dueñas[2]

1 Applied Biology, Universidad Surcolombiana, Huila, Colombia. 2 SURCO Herbarium, Universidad Surcolombiana, Huila, Colombia.

For the department of Huila, studies on the Melastomataceae family are incipient despite the evident biological, ecosystem, biogeographic diversity and protected natural areas of regional and national interest. The objective of this study was to recognize the current state of knowledge of the Melastomataceae family for the department of Huila, Colombia, through physical and virtual consultation of Herbaria collections (SURCO, COL, UDBC and MO) and the GBIF database, with data between the years 1905 to 2022. To this end, a database was organized with botanical records, including information on growth habit, locality, year of collection, national distribution, conservation status and endemism. 1728 Records were analyzed, corresponding to 191 species and 25 genera, with *Miconia* (119), *Blakea* (15), *Meriania* (12), *Chaetogastra* (7) and

Monochaetum (6) being the most species-rich genera. For Huila, there is at least one specimen in 33 of the 37 municipalities, with Palestine (67), Neiva (55), La Plata (53) and San Agustín (45) being those with the highest number of collections. Additionally, 71 species are reported as Least Concern, 7 as Near Threatened, 6 as Vulnerable, and 2 as Endangered. Finally, this review allowed us to have an approach to the current status of the Melastomataceae family for Huila, which contains 19% of the species and 42% of the genera for Colombia. Furthermore, it was evident that 4 municipalities do not have any reports of the Melastomataceae family in the herbaria and that the sampling has been concentrated in some particular localities.

P.1388 Sundry sonication: bee diversity across three buzz-pollinated Melastomataceae communities.

Ash M. Kerber[1], Benjamin S. Lazarus[2], Agnes S. Dellinger[2]

1 Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, USA. 2 Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria.

In the plant family *Melastomataceae*, more than 5,000 species have evolved stamens with poricidal anthers that necessitate a functionally specialized interaction with pollinators in order to release pollen: buzz-pollination. Bees are the only group of pollinators capable of applying vibrations of the required frequency, amplitude and duration to flowers so that pollen is expelled in clouds from the stamens. However, not all bees are capable of sonicating flowers, but at least 74 recognized genera are. How these bees ration floral resources is unclear. It is possible that bee size and morphology may influence the frequency and amplitude of their vibrations. In this poster, we aim to explore whether buzz pollinating bees share or partition floral resources across three communities of co-flowering *Melastomataceae*. Through observational studies, video data and field experiments, we measure pollinator composition, behavior, and visitation rates across three different ecosystems in the campo rupestre of Brazil, the cloud forests of Ecuador and the pine savannas of Florida, USA. While we see substantial pollinator overlap in the *Melastomataceae* community in Florida, certain bee behaviors indicate pollination niche partitioning and specialization in the tropical communities. Some of our data suggests that larger bees visit larger flowers while smaller bees may be less picky about flower size. By investigating the pollinator composition of distinct *Melastomataceae* communities with different floral phenotypes, we hope to contribute to a more realistic understanding of the evolutionary processes underlying the diversification of flower phenotypes sharing the same functionally specialized pollination strategy.

P.1389 Towards a next-generation field guide to and systematics of the Philippine Astronia

Jeffrey P. Mancera[1], Darin S. Penneys[2]

1 University of the Philippines Manila, Manila, Philippines. 2 University of North Carolina Wilmington, Wilmington, USA.

Astronia is an Asia-Pacific genus of shrubs and trees in the Melastomataceae whose center of endemism includes the Philippines. Twenty of its 58 species, all except one endemic to the country, and 12 varieties are common components of lowland to lower and upper montane rainforests. Despite its frequency in the wild, most *Astronia* are known only from the type or very old and few herbarium collections, or are seldom reproductive when sighted, making accurate species-level identification in the field very challenging. Moreover, a genus-level systematic study has yet to be conducted since its last taxonomic treatment from over 30 years ago. This presentation outlines the ongoing steps being taken for the creation of a reliable, public-friendly, and accessible field guide to, as well as preliminary systematics of, the Philippine *Astronia*. A total of 194 herbarium vouchers from eight local and international herbaria with significant holdings of Philippine flora, recent spirit collections, and photographs from seven expeditions conducted between 2011-2023, and 52 protologues of accepted names as well as their synonyms were examined. Comparative morphological examination was conducted using 205 discrete and continuous characters to produce a draft dichotomous key and visual guide, as well as a cladogram of putative evolutionary groups. Local non-specialist plant taxonomists and forest-based laypersons will be interviewed to test and improve the effectiveness of the field guide. Wide access and regular updates will be ensured through a community-shared digital platform. This endeavor puts forward an expedition- and citizen science-based approach in creating modern and effective field guides and updated phylogenies for Philippine flora.

P.1390 Taxonomic revision of Miconia albicans (Sw.) Steud. clade (Melastomataceae, Miconieae)

Julia Meirelles[1], Mayara Krasinki Caddah[2], Renato Goldenberg[3]

1 Instituto Nacional da Mata Atlântica, Santa Teresa, Brazil. 2 Universidade Federal de Santa Catarina, Florianópolis, Santa Catarina, Brazil 3 Universidade Federal do Paraná, Curitiba, Brazil.

With more than a thousand species, ***Miconia*** is one of the largest neotropical plant genera. However, recent phylogenetic analyses have shown the genus is artificial, as well as its sections and subsections, which corroborates the necessity of a new taxonomic delimitation for the tribe Miconieae. This work presents a taxonomic treatment of the 18 species in the albicans clade, characterized by their shrubby to treelet habit, discolorous leaves with abaxial surface covered by amorphous trichomes and inflorescences with secundiflorous and scorpioid branches. These species are either widely distributed from Mexico to Paraguay, or endemic to the Amazon. For this monograph, more than 2,500 herbarium sheets were analyzed from 18 herbaria in Brazil and abroad (BR, G, G-DC, HUEFS, IAN, INPA, JOI, K, M, MBM, MG, NY, P, RB, UEC, UPCB, US, W). Five new species were discovered (*M. astrocalyx*, *M. macuxi*, *M. suberosa*, *M. waimiri-atroari*) and the status of M. *argyrophylla* subsp. *gracilis* is changed and a new name for this taxon (*M. mayarae*) is proposed. Two new synonyms were established, *M. cinerea* under *M. stenostachya* and *M. nambyquarae* under *M. herpetica*. This work also provides an identification key to the species, descriptions, a complete list of examined material, distribution maps, illustrations, images, comments about the species and lectotypifications.

P.1391 The diversity, endemism and conservation of Melastomataceae in Idukki district, Kerala state, India

Vishnu Mohan[1], Santhosh Nampy[1]

1 Floristics and Angiosperm Taxonomy Division, Department of Botany, University of Calicut, Malappuram, Kerala, India.

Idukki, the largest district in Kerala state, is part of the southern Western Ghats. The area is unique in having an abundance of habitats that attribute rich vegetation and a high degree of plant diversity. The vegetation comprises evergreen, moist deciduous, dry deciduous, temperate forests, scrub jungles, and grasslands. Melastomataceae are among the top ten families of flowering plants consisting of about 170 genera and *ca.* 5,100 species worldwide. The family comprises of herbs, shrubs, trees, or woody climbers and is widely distributed in tropical and subtropical regions. The present study documented 34 species of Melastomataceae belonging to six genera, of which 24 are endemic to South India, including four species endemic to Kerala. *Memecylon idukkianum* and *Sonerila roxburghi* are recently described species that are exclusively endemic to the study area. *Miconia crenata* is the only invasive species recorded. The endemism pattern highlights an urgent need for their conservation. The present study discusses the diversity, endemism and conservation of Melastomataceae of Idukki district in Kerala.

P.1392 Exploring the evolutionary complexity of Chaetogastra within the Andean Clade

Malu Ore-Rengifo[1,2], Fabian Michelangeli[3], Nico Cellinese[2,4], Lucas C. Majure[1]

1 University of Florida Herbarium, Florida Museum of Natural History, Gainesville, Florida, USA. 2 Department of Biology, University of Florida, Gainesville, Florida, USA. 3 Institute of Systematic Botany, The New York Botanical Garden, New York, USA. 4 Florida Museum of Natural History, Gainesville, Florida, USA.

This research focuses on the Andean clade of the genus *Chaetogastra* DC. (Melastomataceae). *Chaetogastra* was originally described by de Candolle (1828) and circumscribed into multiple sections. Subsequent phylogenetic research revealed misclassifications with species assigned to genera closely related (*Tibouchina, Andesanthus, Brachyotum,* and *Pleroma*), as well as distantly related genera (*Desmoscelis, Meriania, Pterogastra, Pterolepis,* Rhexia). Thus, the taxonomy of *Chaetogastra* has evolved greatly since its original conception. *Chaetogastra* s.s. of ca. 117 recognized species is distributed throughout the Neotropics, with centers of diversity in the Andean mountains and the Atlantic Forest of Brazil. Despite high species richness, the Andean clade, consisting of approximately 60 species, remains understudied, presenting numerous taxonomic complexities and potential hybridization scenarios. This research aims to explore the evolutionary complexity within the Andean clade of *Chaetogastra*, focusing on phylogenomic reconstruction, hybridization scenarios, and whole-genome duplication (WGD) events. 90 species were sequenced using genome skimming and custom probe data sets, with subsequent mapping of raw plastid reads to a previously published plastome publicly available in Genbank. We conducted phylogenetic analyses using Maximum likelihood and Bayesian methods for plastome data, complemented by pseudo-coalescence using ASTRAL for nuclear data, to address gene tree incongruence and incomplete lineage sorting. The aim was to compare phylogenetic signals in nuclear and chloroplast genomes. Preliminary findings suggest incongruence among those datasets within the Andean clade of *Chaetogastra*, suggesting potential hybridization events and shedding light on evolutionary dynamics. Furthermore, the inferred ploidy across phylogeny suggests signatures of whole genome duplication events, as inferred from both genomic data and chromosome number information available for certain species. This highlights the evolutionary complexity within the Andean clade and provides an opportunity to validate predicted polyploid events. Further investigations are encouraged to reconcile these findings and provide deeper insights into its evolutionary history.

P.1393 A comparative approach for investigating biogeographic patterns and processes in Southeast Asian Melastomataceae

Linde N. Wieringa[1], Marie-Claire Veranso-Libalah[1], Elizabeth Joyce[1], Gudrun Kadereit[1,2]

1 Prinzessin Therese von Bayern Lehrstuhl für Systematik, Biodiversität & Evolution der Pflanzen Ludwig-Maximilians Universität München, München, Germany. 2 Botanischer Garten München-Nymphenburg, Botanische Staatssammlung München, Staatliche Naturwissenschaftliche Sammlungen Bayerns, München, Germany.

Melastomataceae is a mega-diverse, pantropical flowering plant family, consisting of an estimated 172 genera and 5858 species. In terms of species diversity, the neotropics take the lead, followed by Asia and then Africa. To date, research on melastomes have focused mainly on New World and African lineages, while Asia lineages remain critically understudied. Generating phylogenies for various Southeast Asian Melastomataceae will provide unique opportunities for exploring how the dynamic paleogeographic history of the region has shaped the diversification and biogeography of Southeast Asian flora. Using a comparative phylogenetic approach we intend to explore the patterns and processes shaping the diversity and biogeography of three Southeast Asian Melastomataceae lineages: (1) *Dissochaeteae* (6 gen./c. 90 spp.),a tribe with interesting variation in fruit morphology, showing a pattern of decreasing diversity from west to east across the region; (2) *Melastoma*, a genus consisting of c. 80 species, of which many are narrowly endemic and a few widespread species, like the morphologically diverse *M. malabathricum*; and (3) *Astronieae* (4 gen./c. 136 spp.), an early-diverging tribe within *Melastomatoideae*, with a trans-Atlantic distribution and centre of diversity in New Guinea. Using phylogenomic (target capture and whole genome skimming) data, we will reconstruct a phylogeny for each lineage, and use these phylogenies as a framework for diversification, ancestral area and ancestral trait analyses. Through these analyses we aim to identify the underlying processes that have led to the stark contrasts in diversity patterns of these lineages, to ultimately gain further insights into the processes that shape the floristic diversity of this unique region

S.155. TAXONOMY AND EVOLUTION OF BAMBOOS IN THE PHYLOGENOMIC ERA

P.1394 The phylogeny and evolution of the paleotropical woody bamboos (Poaceae: Bambusoideae)

Jing-Xia Liu[1], Cen Guo[1,2], Peng-Fei Ma[1], Meng-Yuan Zhou[1], Ya-Huang Luo[1], Guang-Fu Zhu[1], Zu-ChangXu[1], Richard I. Milne[3], Maria S. Vorontsova[4], De-Zhu Li[1]

1 Kunming Institute of Botany, Chinese Academy of Sciences, Kunming, China. 2 Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun, China. 3 University of Edinburgh, Edinburgh, UK. 4 Royal Botanic Gardens Kew, Richmond, UK.

The evolutionary lability of morphological characters has been hypothesized to have been driven by multiple factors, but few studies have synthesized morphological data with phylogenetic frameworks to elucidate broader patterns of character evolution. The paleotropical woody bamboos (PWB) are distinct hexaploidy with complex evolutionary history and remarkably diverse morphology, making it an ideal clade to investigate the factors underlying morphological evolution in bamboos. We generated a robust and time-calibrated phylogeny of the PWB using SNPs retrieved from *Mi* ddRAD-seq data, reconstructed ancestral characters with rates of transition, and explored associations between environmental variables and key morphological characters. The PWB started to diverse across the Oligocene/Miocene boundary and formed four major clades including Melocanninae, Racemobambosinae, Hickeliinae and Bambusinae corresponding to recognized subtribes. The ancestor of PWB was reconstructed as having erect habit, indeterminate inflorescence and nucoid caryopsis. However, the evolution of all three traits was correlated with, and hence likely influenced by, aspects of climate, topography, and soil in general, leading to homoplasy across the PWB. Our results synthesized here provide an example of how morphological characters under environmental selection can show homoplasy and hence must be used with caution at generic and higher taxonomic levels, with novel perspectives on morphological evolution of the woody bamboos.

P.1395 National collection of native bamboos of Mexico: taxonomy, conservation, propagation and uses

Teresa Mejia-Saulés[1]

1 Red de Biología Evolutiva, Instituto de Ecología, Xalapa, Mexico.

The Institute of Ecology, A.C., the Bamboo of the Americas-American Bamboo Society and the Technological Institute of Chetumal in 2003 began the formation of the National collection of native bamboos of Mexico to represent the 36 species recorded this year. The main objectives were: 1) to contribute to the knowledge of the national bamboos and its *ex situ* conservation, 2) to select species with potential use for their propagation and sustainable management, 3) to know the species with some degree of vulnerability and 4) training of human resources. To this, a literature review was carried out; field collections were made; identification of the collected material and the herbarium; establishment and propagation of promising species such as the vegetative propagation of *Rhipidocladum racemiflorum* and germination of seeds of *Otatea acuminata*. As a result, the bamboo collection was inaugurated and opened to the public in 2005. With taxonomic identification, new species are delimited and discovered, resulting in 63 species, of which 42 are endemic and 24 new species were described. In terms of uses, the Florentine Codex (1577) records that the ohtlatl, acatl or otate (*Otatea acuminata*), widely distributed in Mexico, has been used since pre-Hispanic times in the elaboration of chimallis (shields), bahareque (walls), plumes and icpalli (seats). The current uses of bamboo are diverse: as a form of furniture, housing, farm tools and handicrafts. This collection has been the basis for studies on: molecular phylogeny, barcoding, propagation, sustainable management, conservation, uses, physical and mechanical properties, associated insects, etc. With undergraduate and postgraduate theses, as well as the teaching of courses and workshops, the training of human resources has been promoted. The results have been published in scientific journals, magazines and in National and International Congresses.

P.1396 Bamboos from Brazil: what do we know and what do we still need to know?

Reyjane P. Oliveira[1], Iasmin L. C. Oliveira[1], Maria Luiza S. Carvalho[2], Alessandra S. Schnadelbach[2], Fabrício M. Ferreira[3], Cassiano A. D. Welker[3], João P. S. Vieira[1], Marcos C. Dórea[1], Kaio V. A. Vidal[1], Evandro P. Machado[1], Pedro L. Viana[4], Edgar A. L. Afonso[5], Aline C. Mota[6], Ana Paula S. Gonçalves[7], Lynn G. Clark[8]

1 Universidade Estadual de Feira de Santana, Bahia, Brazil. 2 Universidade Federal da Bahia, Salvador, Brazil. 3 Universidade Federal de Uberlândia, Minas Gerais, Brazil. 4 Instituto Nacional da Mata Atlântica, Espírito Santo, Brazil. 5 Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 6 Universidade de Pernambuco, Pernambuco, Brazil. 7 Universidade Federal de Viçosa, Minas Gerais, Brazil. 8 Dept. of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, USA.

Bamboos are easily distinguishable within Poaceae and widely distributed wordwide, with several groups taxonomically complex and intriguing for science. Brazil has the world's largest diversity of plant species and a high known richness of bamboos, with many floras still underexplored and potentially rich in members of this group, as well as species supposedly useful for humans. However, the exact number of genera and species of bamboos in Brazil remains uncertain. For these reasons, there has been an increasing investment in research projects and human resource training on bamboos in the country. Our studies have involved fieldwork and plant collections in all Brazilian regions, ranging from classic taxonomic methods to more modern and integrative approaches in a network including several institutions and post-graduate programs. We prioritized efforts to study groups with great taxonomic complexity, members of the tribes Bambuseae and Olyreae. Taxonomic studies are supported by phylogenies, resulting in the description of five new bamboo genera in the last decade, four of them endemic to the Atlantic Forest and mainly belonging to the tribe Olyreae. Additionally, over 30 new species have been described, mainly in genera such as *Eremitis*, *Piresia*, *Chusquea*, *Guadua* and *Merostachys*. Several of them are rare, endemic to Brazil and often threatened with extinction. Our results have been crucial for updating monographs on the Flora e Funga do Brasil and to deepen studies on taxa with confusing boundaries and poor known phylogenetic relationships (i.e. *Olyra*, *Pariana*, *Aulonemia*), as well as the processes that have acted in their evolution and diversification. Currently, we are actively engaged in a deep international collaborative project (Bamboo phylogeny Group II), including Brazilian bamboo species on a global scenario to better unravel the diversity of this group in both the New and Old worlds, using phylogenomic information.

S.156. TAXONOMY AS OPEN SCIENCE: TOOL SUPPORT TO FACILITATE DATA USE FOR HANDSON PRACTITIONERS

P.1397 Chemotaxonomic study of ten species of Ficus from Nigeria

Abdullahi A. AbdulRahaman[1], Abdulquadri Sagaya[1]

1 Department of Plant Biology, University of Ilorin, Ilorin, Nigeria.

Ficus is one of the most diverse groups of flowering plants with a great complexity which needs a proper classification. Several studies have shown the differences and similarities among this genus but little have been done on the chemical composition to delimit the taxa. GC-MS analysis was carried out on ten different species using standard procedure. The results reveal 195 compounds belonging to 17 functional groups. Carboxylic acids were the most prominent groups follow by alcohol, ketone, aldehyde and ester among others. *F. thonningi* and *F. platyphylla* are more related among the ten species while *F. vogelii* is the most distance species in terms of the metabolite concentration. The percentage similarity among the ten species was very high between *F. mucuso* and *F. asperifolia* (94.84%) while the lowest was between *F. capensis* and *F. vogelii* (81.17%). The GC-MS analysis of the *Ficus* could provide useful information to the understanding of species variability and therefore, the distribution of the phytocompound of *Ficus* can be used as chemotaxonomic character in explaining the relationship among the various species.

P.1398 Looking for efficiency when creating scientific labels and certificates? labeleR package is the answer!

Julia G. de Aledo[1,2,3], Francisco Rodríguez-Sánchez[4], Jimena Mateo-Martín[1], Ignacio Ramos[1,3]

1 Departamento de Biología, Universidad Autónoma de Madrid, Madrid, Spain. 2 Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos, Madrid, Spain. 3 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid. Madrid, Spain. 4 Departamento de Biología Vegetal y Ecología, Universidad de Sevilla, Sevilla, Spain.

A comprehensive R package, labeleR, has been developed to streamline the generation of labels for herbarium specimens and other scientific collections, attendance certificates, meeting identification badges, and labels related to other scientific needs. This highly accessible tool enables automatic label and document renderization from extensive databases, optimizing typically lengthy and repetitive processes. This package stands as an accessible choice to other frequently used alternatives, such as the mail merge function between Microsoft Excel and Word, Microsoft Access functions, or alternative computer programs that are often expensive and require previous expertise. In contrast, the labeleR package can be used under an open-source license, allowing it to be freely downloaded from the CRAN repository or GitHub (detailed tutorial is accessible online at https://ecologyr.github.io/labeleR/). Users can easily choose their source database, input QR codes and logos, customize content according to specific needs and even create their own custom templates. The package has six main functions, three of them focused on the management of scientific collections (herbarium labels, collection labels, and a smaller version called "tinylabels"), and another three functions on the organization of scientific events (event badges, attendance certificates, and participation certificates). LabeleR turns a tedious process into a quick activity to obtain labels and/or certificates in PDF format for easy printing or distribution. We believe that this versatile tool contributes to scientific efficiency by simplifying complex, time-demanding labelling and organization processes.

P.1399 American Ternstroemia: a state of the art

José R. Grande A.[1], Andrés Fonseca-Cortés[2], Fernanda Nunes Cabral[3], Yeni C. Barrios O.[4], Thiago Mouzinho[5], Leslie G. Castillo R.[6], Rosana Y. Gutiérrez A.[7]. Leysi Martínez[8]

1 Departamento de Botánica, Facultad de Ciencias, Universidad de Granada, Granada, Spain. 2 Departamento de Ciências Biológicas, Universidade Estadual Feira de Santana, Feira de Santana, Brazil. 3 Instituto Federal de Minas Gerais, Minas Gerais, Brazil. 4 Instituto Jardín Botánico de Mérida, Facultad de Ciencias, Universidad de Los Andes, Mérida, Venezuela. 5 Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil. 6 Facultad de Farmacia y Bioanálisis, Universidad de Los Andes, Mérida, Venezuela. 7 Facultad de Farmacia y Bioanálisis, Universidad de Los Andes, Mérida, Venezuela. 8 Facultad de Farmacia y Bioanálisis, Universidad de Los Andes, Mérida, Venezuela.

Genus **Ternstroemia** has been, historically, one of the less studied Pantropical genera. In the last few decades, however, a wealth of contributions ranging from classical alpha-taxonomy to molecular systematics, biogeography, conservation, and ethnopharmacology, has expanded our understanding of it. In the present contribution we show, as a first step towards a monographic treatment of the genus, a synthetic approach to the current state of knowledge of the genus **Ternstroemia** in the Americas. To date, Venezuela, Brazil, Colombia, Panama, Central America, and Mexico have more or less updated knowledge, remaining most of the Andes and Insular Caribbean to be properly reviewed. Guayana Shield, Insular Caribbean, and northern Andes are the three main distribution and endemism centers. We introduce an updated species list, including synonyms, and geographic distributions for all the species. After the present revision, it is known that the New World harbors ca. 88 species (ca.

87 native, 1 introduced), 62% of the World total (ca. 141): 7 from the Brazilian Shield, 9 from North America and Panama, 21 from tropical Andes, Chocó, and Venezuelan Coastal Cordillera, ca. 24 from Insular Caribbean, and 29 from the Guayana Shield and Amazonia. Most diverse countries are Venezuela (28 spp.), Brazil (24 spp.), and Colombia (20 spp.). After a preliminary conservation assessment, near 1/3 of the known species are to be considered as endangered. A synoptic table is included giving gross information for each country, biogeographic area, and major ecosystem type. Recent phytochemical screening confirms phenolic compounds and sterols in two additional species, and new pharmacological studies expand our knowledge on sedative effects and antibiotic properties.

P.1400 Taxonomical studies on leaves of Butea monosperma (Lam.) Taub., Dalbergia sissoo Roxb., Phaseolus vulgaris L. and Pisum sativum L.

Jessica Rene Hansdah[1], Ajay Kumar Srivastava[2]

1 Dept. of Botany, Ranchi University, Ranchi, India. 2 Dept. of Botany, St. Xavier's College, Ranchi, India.

Plant taxonomy is a branch of botany that deals with identification, classification and nomenclature of plants. All the four genera discussed in this paper belong to subfamily Faboideae according to the APG IV classification. Most of the taxonomic keys that are available for Family Fabaceae Lindl. are based on floral characters for which plants will have to be in their reproductive phase. Flowering phase for most members of the concerned family lasts for a maximum of four months, therefore the plant is mostly found in its vegetative phase and lack of a taxonomic key solely based on vegetative characters can delay the identification process. The solution to this could be achieved by developing a valid taxonomic key using leaf morphological characters. Studies incorporating the varied and unique architecture of each leaf or leaflet may prove to be an important breakthrough to help identify plants in any season and help pace up the related research works. These can also provide adequate information in paleobotanical fields concerning fossils discovered in the form of leaves. Comparison of tree constructed based on the phenetics with the molecular key may help validate the results.

P.1401 Development of an AI-powered herbarium image pre-identification system in Violaceae: focusing on Korean species

Hyeonji Moon[1], Su-Jeong Han[2], Jaesung Lee[2], Sangtae Kim[1]*

1 Sungshin Women's University, Seoul, Republic of Korea. 2 Chung-Ang University, Seoul, Republic of Korea.

An herbarium sheet is a record of temporal, geographical, morphological, and genetic information of a species. In recent years, the major herbaria in the world have rapidly digitized the labels and images of their collections and made them available online. It promotes traditional specimen-based taxonomic, evolutionary, and ecological studies, as well as AI-driven fields of biodiversity loss and climate change. Although accurate species identification is critical to specimen-based botanical research, large herbaria still contain many misidentified specimens that take taxon-specific experts considerable time and effort to re-identify. In recent years, the application of deep learning to species identification in herbarium sheets has been growing, driven by the growth of digital specimen data, improvements in GPU performance, and the development of convolutional neural networks (CNNs) that are adept at image identification. *Viola* (Violaceae) are distributed in *ca.* 660 taxa worldwide (*ca.* 40 in Korea). Their specimens in Korea have high misidentification rates due to 1) morphological similarity among species and 2) seasonal or environmental variation within species. In this study, we developed an automated pre-identification system using a CNN with a curated dataset for fast and efficient re-identification of herbarium data, focusing on Violaceae distributed in Korea. We collected and re-identified herbarium data from major herbaria in Korea. After preprocessing to remove non-plant specimen components in the images, the entire dataset was split into a training set, validation set, and test sets. The CNN models were evaluated based on accuracy, F1-score, and confusion matrix. This preliminary study, focusing on a specific taxon with a high misidentification rate, will contribute to improving the accuracy of future automated models for identifying Korean flora.

P.1402 The death of taxonomy: Comments on the digitization of Natural History Collections

Evgeny V. Mavrodiev[1], Manuel B. Crespo[2], David M. Williams[3]

1 Florida Museum of Natural History, University of Florida, Gainesville, USA. 2 Department of Environmental Sciences and Natural Resources (Botany), University of Alicante, Alicante, Spain. 3 Department of Life Sciences, the Natural History Museum, London, UK.

The digitization of natural history collections has become a priority in many museums and botanic gardens to document the specimens acquired. Some issues have yet to receive appropriate attention. Consider one such potential problem: after digitization, there will be limited opportunity for taxonomists to propose new conclusions from these gigantic digital databases. This may lead to the permanent inclusion of images of individuals from multiple *aphyletic* groups – that is homonyms (in a broad application of this term) and non-monophyletic taxa and to their wide usage in future "global" bioinformatic studies. Any expectation that Artificial Intelligence (AI) will help resolve this issue and eventually replace human-based taxonomy results from a lack of understanding of what taxonomy involves and what it is. The massive digitization of natural history collections biases reliable taxonomic practices with respect to identifying living organisms. The small number of remaining experts-taxonomists worldwide, and the rare involvement of the latter in the machine learning process, provide no warranty even from the elementary mistakes in the automatic AI's identification of the images of digital collections. The architecture of massive digitization ignores the potential of a positive relationship between taxonomy and digitization. Because of this, the science of traditional taxonomy cannot effectively survive within the current digital reality. Taxonomy is the foundation of any biological systematic knowledge, and the destruction of taxonomy is nothing but a detachment from biological reality. However, because giant digitization is irreversible, it is critical to establish a new semantic framework for future studies based on massive, digitized collections. The philosophical heritage of Jean Baudrillard, one of the most prominent figures in European Postmodernism of the 20th century, is the best candidate for this role.

P.1403 European taxonomy in profile: a data-driven approach

Sofie Meeus[1], Melanie De Nolf[1], David Fichtmüller[2], Kennet Lundin[3], Laura Tilley[4], Quentin Groom[1]

1 Meise Botanic Garden, Meise, Belgium. 2 Botanic Garden and Botanical Museum Berlin, Freie Universität Berlin, Berlin, Germany. 3 Gothenburg Natural History Museum, Gothenburg, Sweden. 4 Consortium of European Taxonomic Facilities, Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

This study examines the service aspect of taxonomy in Europe, with a specific focus on the description, identification, and nomenclature of taxa. Traditionally viewed as a research discipline primarily concerned with evolutionary aspects of biodiversity, this investigation specifically addresses the supply and demand sides of taxonomy as a critical service for European biodiversity conservation. Leveraging an automated approach facilitated by OpenAlex, an open bibliography of scholarly publications, we extract comprehensive data on taxonomists, their affiliated institutions, and their areas of expertise. This method ensures thorough coverage across all taxa while mitigating potential biases associated with self-reported questionnaires. In addition to analyzing the current availability of taxonomic expertise (supply side), our study delves into evaluating expertise gaps by examining significant taxa from both research and policy perspectives (demand side). By drawing upon datasets such as the list of invasive species on the horizon for Europe, Crop Wild Relatives, and the IUCN Red List of Threatened Species, we assess the relevance and demand for taxonomic expertise. By adopting a nuanced approach that considers the demand side, rather than assuming equal policy importance across all taxa, our study provides valuable insights into the contributions of taxonomists in addressing conservation and policy needs in Europe. Through highlighting impacts, challenges, and potential solutions, this research underscores the significance of taxonomy as a vital service. Our recommendations aim to prioritize taxonomy, enhance its contributions to biodiversity conservation efforts, and offer guidance to policymakers, researchers, and stakeholders invested in sustaining Europe's rich biodiversity.

P.1404 Synopsis of the genus Rhynchospora (Cyperaceae) for Paraguay

María Fátima Mereles H.[1], Ever López Grau[2,3], Pablo García Murillo[3]

1 Herbarium FCQ, Department of Botany, Faculty of Chemical Sciences, Research Directorate, Nationl University of Asunción and National Researcher Incentive Program, National Council of Science and Technology, CONACYT, Paraguay. 2 Department of Botany, Research Directorate, Faculty of Chemical Sciences, National University of Asunción, Paraguay. 3 Department of Plant Biology and Ecology, University of Seville, Seville, Spain.

The family Cyperaceae in Paraguay is one the four main ones together with the Asteraceae, Fabaceae and Poaceae, with the species of the genus *Rhynchospora* Vahl being the most abundant together with *Cyperus* L. and *Eleocharis* R.Br. The reason is that 30% of the country's surface is linked to water a preferred hábitat for species of the genus since the vast majority are in habitats with permanente and temporary wáter. The family is one of the least know, so the objective to the research is to understand the species that inhabit the environments of Paraguay. For this, studies werw carried out in National herbaria: FCQ, Herbarium FACEN and PY and in some regional ones: CTES, in addition to *in situ* colections. To date, 39 species hace been found, 25 of which are found in National herbaria: *Rhynchospora alba, R. albiceps, R. asperula, R. Barrosiana, R. brasiliensis, R. confinis, R. corymbosa, R. emaciata , R. exaltata, R. globosa, R. gollmeri, R. holoschoenoides, R. marisculus, R. megapotamica, R. pedersenii, R. polyantha, R. praecincta, R. pungens, R. riparia, R. robusta, R. rugosa, R. scutellata, R. setigera, R. tenuis, R. velutina* and others 14 species distributes in: CTES, G, MO, NY, SI, mentioned in the literature. This is a considerable number of species for a family of great importance of Paraguayan flora. Likewise, our results demonstrate that to achieve adequate knowledge of the genus, it is necessary to make an additional research effort to know more accurately other species of the genus since there are still information gaps in wetlands areas in the country, which must be investigated.

S.157. TELLING PLANT SPECIES APART WITH DNA

P.1406 The complete plastome sequences of Caroxylon Moq. (Chenopodiaceae Vent.) species from Kazakhstan

Shyryn Almerekova[1], Moldir Yermagambetova[1], Saule Abugalieva[1], Yerlan Turuspekov[1]

1 Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan.

Chenopodiaceae Vent. is one of the largest and most ancient desert families in the World. Representatives of the family take a dominating position in the flora of arid territories in Kazakhstan and are known as classical halophytes and xerophytes. The exact number of *Caroxylon* species worldwide is still ambiguous, according to various authors, the genus representatives are widely distributed in desert and semi-desert regions of Central Asia. *Caroxylon* species are known as fodder, medicinal plants, bioremediants and good sand fixators. The complete plastome genome of *Caroxylon* species from Kazakhstan were sequenced for the phylogenetic assessment. The NovaSeq 6000 Illumina system performed the plastome sequencing of *Caroxylon* species from Kazakhstan. *Caroxylon* samples from Kazakhstan and GenBank were aligned to reconstruct phylogenetic tree. In total, 133 genes, including 88 protein-coding genes, 37 transfer RNA, and 8 ribosomal RNA genes (including duplicated genes) were annotated in plastomes of *Caroxylon* species. The phylogenetic tree was reconstructed based on 78 common protein coding genes. The mononucleotide, dinucleotide, trinucleotide, tetranucleotide, pentanucleotide and hexanucleotide repeats were detected in *Caroxylon* species from Kazakhstan. By conducting a comparative analysis of plastome genome sequences in *Caroxylon* species, regions with high polymorphism were identified. These genes may serve as potential DNA barcode markers for future investigations.

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P.1407 Morphological variations in Phyllanthus genus: dilemmas in identification of the correct medicinal species

Barupal M.[1], Shani A.[2], Arora S.[3]

1 Department of Botany, Jai Narain Vyas University Jodhpur, Rajasthan, India.

Some species of the *Phyllanthus* genus are renowned for their properties as kidney stone breakers and anti-inflammatories. However, the genus *Phyllanthus* comprises approximately 1000 species, some of which are quite mysterious to identify solely through morphological descriptions found in floras. Early nomenclature and variations in naming conventions further complicate the identification of correct species, particularly for their medicinal properties. Molecular barcoding sometimes adds to the uncertainty, as species may be incorrectly annotated based on given morphology and avialable flora. In this study, we present the characterization of five species (*Phyllanthus amarus, P. niruri, P. fraternus, P. debilis, P. maderaspatensis and P. urineria*) of this genus grown locally, employing a combination of morphological analysis, anatomy of leaf and stem, and molecular barcoding. *Phyllanthus amarus* Schum and Thonn. is often mistaken for other similar species such as *P. niruri L., P. fraternus* G.L.Webster, and *P. debilis* Klein ex Willd. All five species are commonly found in monsoonal regions. However, during the winter season, a species with five tepals, typically identified as *P. amarus* in flora literature, dominates the area. Notably, winter plants exhibit smaller leaf sizes and heights but bear a greater abundance of stacked fruits compared to their summer counterparts, if we agree with the fact that both are the same species having five tepals. In most floras, these species are primarily distinguished by leaf shape and the number of tepals in the perianth. Furthermore, the evolutionary and genetic causes behind the high rate of variation in this genus we also discussed in this report.

P.1408 Phylogenetic relationships of the Campanula group Megalocalyx, and assignment of a new species from Beirut

Calvo-Heredia, L[1], Itani, M[2], Aldasoro J.[3], Alarcón M.[3], Al-Zein, MS[5], Manzano, P[2,4], Meseguer, AS[1]

1 Department of Biodiversity and Conservation. Real Jardín Botánico, CSIC, Madrid, Spain. 2 Global Change and Conservation Lab, Faculty of Biological and Environmental Sciences, University of Helsinki, Finland. 3 Instituto Botánico de Barcelona, CSIC, Barcelona, Spain. 4 Basque Centre for Climate Change, Leioa, Spain. 5 Department of Biology. Faculty of Arts and Sciences. American University of Beirut, Beirut, Lebanon.

During a thorough assessment of coastal plant diversity in Lebanon in 2012, we came across a population of *Campanula* in a restricted area (<1km²) in Beirut, the population divided into two sites by a road. Specimens from this population exhibit a close resemblance to *Campanula stellaris* Boiss., although some morphological and ecological traits, combined with a contrasted distribution, suggest that they could belong to a new species. *Campanula stellaris* has a native range stretching from southern Turkey to Israel, and western Iraq. In Lebanon this speciesis common and usually grows in rocky fields. In contrast, the Beirut population was found on a single sandstone cliff close the sea. Notable morphological differences, such as variations in calyx and calyx lobe size, style length and colour, corolla, nectary colour, and seed shape, suggest the potential existence of a distinct species tentatively named *Campanula infilicimi*. In this study, we reconstruct phylogenetic relationships among the twelve Middle Eastern and Mediterranean species comprising the *Megalocalyx* group, to which this putative species and *C. stellaris* belongs, based on nuclear and chloroplast markers. We then infer the phylogenetic position of the new specimens within this tree. We also use species delimitation approaches to define species boundaries within the *Megalocalyx* group and evaluate the tentative assignment of the Beirut specimens to a new species. Further, we discuss the conservation status of *Campanula infilicimi*, whose only known population is severely threatened by the development of a tourist resort. Parts of the lower cliff have already been lost to the development of a hotel, and the population is experiencing major fluctuations and a decreasing trend. The documentation and classification of this new species is essential to justify the protection of the area and prevent its potential extinction.

P.1409 Reversible phosphorylation of WOX5 protein controls the homeostasis of QC

Ling Chen1

1 State Key Laboratory of Hybrid Rice, Institute of Advanced Studies. Wuhan University, WuHan, China.

Fundamental questions of structural and functional homeostasis of the *Arabidopsis* QC in root stem cell niche remain elusive. WUSCHEL-RELATED HOMEOBOX 5 (WOX5) protein, which serves as a QC marker, yet the regulation of its homeostasis remains unknown. Here, we characterize a novel role of PEST domain in WOX5 protein, which stabilizes WOX5 protein by phosphorylating GSK3 Motifs (GMs). Next, we demonstrate that the subfamily II of *Arabidopsis* SHAGGY-like Kinases (AtSKs) stabilizes WOX5 protein by phosphorylating the GMs in the PEST domain and the subfamily II of the catalytic subunit of *Arabidopsis* PP2A (AtPP2A-Cs) holoenzymes destabilizes WOX5 protein by dephosphorylating the GMs. Moreover, we find both in situ overexpressed and phosphate-mimicked WOX5 protein can reduce the proliferative activity of the original stele initials (SI) and its daughter cells (SID), leading to the production of more quiescent cells. Taken together, our findings suggest that the homeostasis of WOX5 protein is modulated by reversible phosphorylation, which functionally controls the homeostasis of the QC cells' low proliferative activity. Furthermore, the subfamily II of AtPP2A-Cs structurally controls the homeostasis of one-layer QC by down-regulating WOX5 expression and destabilizing WOX5 protein in the SI and SID.

P.1410 DNA barcoding the Dutch Flora: a case study of Ficaria (Ranunculaceae)

Annabelle R. de Vries[1], Hans ter Steege[1,2], Helena Duistermaat[1,3]

1 Naturalis Biodiversity Center, Leiden, the Netherlands. 2 Quantitative Biodiversity Dynamics, Utrecht University, Utrecht, the Netherlands. 3 Institue of Biology Leiden, Leiden University, Leiden, the Netherlands.

To identify and monitor all multicellular organisms in the Netherlands, the project *Authoritative and Rapid Identification System for Essential biodiversity information* (ARISE) was set up. Within this project, the subproject "DNA barcoding the Dutch Flora" focusses on building a DNA barcoding library of the Dutch flora, which contains about 1500 vascular plant species representing 136 plant families. With this DNA library, plant DNA obtained during metabarcoding projects can be identified. However, there is not one standard DNA barcode by which all vascular plants can be identified. So far, the Internal Transcribed Spacer (*ITS*) and the chloroplast maturase K gene (*matK*) have been obtained for a large part of the Dutch Flora. For each species, three individuals from different populations have been collected, sampled and sequenced. Collecting and sampling has been carried out by volunteers coordinated by FLORON, the Dutch Floristic Research foundation. This ongoing project creates the opportunity to investigate which DNA markers give better resolution for specific plant groups. While making sure all of the Dutch vascular plants are added to the reference library. Here, we present a case study on the Dutch Ranunculaceae species testing the different markers by investigating if they show the same phylogenetic signal and species delimitation. Within *Ranunculus* subgenus *Batrachium* we expect to find incongruence caused by hybridization which complicates identification based on morphology. For the genus *Ficaria*, a new species for the Netherlands or a possible hybrid between *F. verna* and *F. ambigua*, is expected based on preliminary study of flower size, DNA weight, pollen fertility, and achenes viability. We test whether the different markers provide more insight on species delimitation or presence of a hybrid.

P.1411 Enhancing Quercus cerris identification via DNA barcoding and new PCR primers

D. Fantozzi[1], D. Trupiano[1], G.S. Scippa[1], G. Sferra[1]

1 University of Molise, Campobasso, Italy.

In an increasingly urbanised world, the importance of oak trees in urban environments is growing. Although oaks continue to provide ecological, aesthetic, and social benefits in cities, they face unique challenges due to urban environmental stressors, such as limited root space and poor-quality soils. Therefore, it is essential to understand the adaptability and resilience of oak roots since they play a crucial role in the survival trends and health states of these urban plants. Roots are crucial in resisting adverse environmental conditions since they absorb nutrients and water, as well function in tree anchoring especially in often altered urban soils. However, studying roots in urban environment represents a significant challenge due to their underground nature, which, in urban contexts, is furtherly complicated by the complexity of this environment. So, molecular techniques, such as DNA barcoding, provide new opportunities to distinguish tree species and to explore the biological diversity associated with their roots. Thus, the purpose of this study, funded by "National Biodiversity Future Center—NBFC" project (CUP: H73C22000300001) under the National Recovery and Resilience Plan (NRRP) —NextGenerationEU, Mission 4 Component 2 Investment 1.4, is to apply DNA barcoding to identify oak species and related abiotic and biotic interactors in urban contexts. In this perspective here we propose the design of PCR primers for species-specific DNA barcoding of *Quercus cerris.* The approach was based on: target sequence identification (scientific literature and sequence databases) and selection known sequences among oak genus with the highest genetic divergence, primer design and testing. Several primer pairs have been identified with the potential to distinguish *Q. cerris* from other species of the same genus and have been in silico validated. The upcoming phase includes the testing of these primers by known samples to confirm their specificity to *Q. cerris* and subsequently applying them to field samples.

P.1412 Detection of phylogenetic variability in the Hypopterygium tamarisci complex through Sanger sequencing and genetic capture

David G. del Olmo[1], Rafael Medina[2]

1 Universidad Pablo de Olavide, Sevilla, Spain. 2 Universidad Complutense de Madrid, Madrid, Spain.

Hypopterygium tamarisci (Sw.) Brid. ex Müll. Hal. is a taxon of pleurocarp mosses with a disjunct distribution in the southern hemisphere, spanning South America, Africa, Southeastern Asia, and Australasia. Bryophytes with disjunct distributions and wide morphological variability often hide cryptic diversity within despite being commonly assigned to a single species. Previous studies of *H. tamarisci* revealed substantial phylogenetic structure and some degree of biogeographic clustering, but remain inconclusive due to limited molecular variability of the sequenced loci. This study expands the exploration of traditional genomic regions by incorporating unsequenced markers from the plastid genome. Sanger sequencing is employed, and a phylogenetic reconstruction is conducted using maximum likelihood and Bayesian inference methods. Additionally, a Hyb-Seq approach using the GoFlag probe set is implemented to identify highly variable nuclear genes, design specific primers for conventional amplification, and include a new set of nuclear loci in the analysis. We discuss this combined approach as a cost-effective system to find variable sites and explore the consequences of our results for the systematics of the *H. tamarisci* complex.

P.1413 The nature of oak species

Andrew L. Hipp[1,2], Alan T. Whittemore[1]

1 Herbarium and Center for Tree Science, The Morton Arboretum, Lisle, USA. 2 Committee on Evolutionary Biology, University of Chicago, Chicago, USA.

Plant biologists have debated the nature of oak species for more than 200 years. Opinions range from the opinion that oak species hybridize relatively rarely to the view that related oaks form syngameons, near-freely interbreeding complexes of species. Understanding species boundaries and gene flow in oaks is essential to conserving the ca. 425 global oak species on which humans and hundreds to thousands of arthropod, fungus, vertebrate, and plant species depend. We review published data on oak species boundaries based on multilocus nuclear data and conclude that most traditional oak species investigated are diagnosable as genomic cluster species. Nonetheless, individual oaks demonstrate a wide range of mixed-species ancestry, with as many as 20% of individuals averaged across studies admixed at a level of 10% or higher. We also review the burgeoning oak literature investigating adaptive introgression, the incorporation of alleles from one species into another through hybridization followed by generations of natural selection and backcrossing. species. In combination, these studies suggest that introgression often plays a creative force in oaks, increasing diversity and offering a potential genetic rescue for species on the verge of extinction. Several outstanding questions demand additional research. How important is multispecies introgression in oaks, which often grow within pollination distance of a numerous reproductively compatible species? Are there conditions under which we expect genetic swamping to pose a strong risk to endangered oak species, and if so, does adaptive introgression significantly offset this risk? Does interspecific gene flow in oaks generally reflect a history of divergence with genetic exchange or secondary contact after speciation? Finally, we highlight the connections between oak introgression and introgression studies in other tree genera, the evident low prevalence of hybrid speciation in oaks compared to other tree genera, and the implications of oak introgression for the diversity of other trophic levels.

P.1414 Phylogenetic approach to the genus Breutelia (Bartramiaceae, Bryophyta).

Irene Lafuente[1], Guillermo Díez[2], Rafael Medina[3], Jesús Muñoz[1]

1 Real Jardín Botánico (CSIC), Madrid, Spain. 2 Universidad Autónoma de Madrid, Madrid, Spain. 3 Universidad Complutense de Madrid, Madrid, Spain.

Bryophytes are among organisms that make the tropical Andes one of the most diverse regions of the world. The great diversity, endemicity and the important role that bryophytes play in the ecosystem make them a key element of the region, since they account for the water and soil conservation in the Andes, especially in the wasteland, humid puna, and montane forest. *Breutelia* (Bruch & Schimp.) Schimp. is a genus of bryophytes containing about 90 species, of which about 40 are found in the Neotropics. *Breutelia* belongs to the Bartramiaceae, a little studied family where taxonomy work has focused almost exclusively on morphology, while molecular phylogenetic analyses are still missing. Although there is a global phylogeny of the family, the genus *Breutelia* is underrepresented (6 specimens of 6 different species) and there are no broader phylogenetic studies of the genus. This work constitutes the first phylogenetic approach to *Breutelia*. After DNA extraction, plastidial (*trnL-F, rpl16, atpb-rbcL, rps4* and *psbA-trnH*) and nuclear (ITS2) genetic markers were sequenced by Sanger sequencing, and phylogenetic inference was performed by Maximum Likelihood and Bayesian Inference methods. This work reflects the complex phylogenetic and taxonomic situation of the genus highlighting the existence of fast radiations and the resolution of several morphologically defined species as polyphyletic. These results show the need for further taxonomic study in this group for the proper delimitation of the species and to unravel their evolutionary history.

P.1415 Reconstructing past vegetation dynamics on the Korean peninsula using eDNA analysis

Jung A Kim[1], Yoonjee Hong[1], Hye Sook Jeon[1], Chae Eun Lim[1]

1 Climate change and environmental biology research division, National Institute of Biological Resources, South Korea.

Understanding paleoenvironmental changes can provide valuable information for predicting and preparing for future climate change. In this study, environmental DNA(eDNA) analysis was introduced as a method to understand paleoenvironmental changes. We focused on soil sediment samples from the temperate wetland region of the Korean Peninsula, which are presumed to be sensitive to climate change. As a result of eDNA analysis of soil samples from temperate wetlands on the Korean Peninsula, it was confirmed that eDNA analysis targeting plant taxa was possible in soil sediment core samples from the topsoil layer to 17m underground. A total of 25 families and 21 genera of vascular plants and 2 families of bryophytes were identified. The results of heat map analysis showed a high frequency of occurrence of the Genus Pinus and Quercus. In addition, aquatic plants, evergreen broad-leaved trees, and deciduous coniferous trees appeared over time, confirming changes in flora within the same area. In addition, flora information from the past to the present was reconstructed by combining eDNA and pollen composition results in soil samples, and past flora changes were recognized. In particular, through eDNA analysis, new taxa that were not detected in existing pollen analysis were discovered. To predict floral changes due to future climate change, we developed a prototype artificial intelligence (AI) model based on the correlation between average temperature and the taxonomic information by each era. We present a new approach to predict future biodiversity changes based on past biodiversity information using eDNA analysis and AI technology. As a result, eDNA technology is expected to not only complement existing biodiversity research methods but also become an important tool for understanding past ecosystem changes and predicting future changes. This study is expected to contribute to the development of protocols for soil eDNA analysis and environmental monitoring programs.

P.1416 Development of molecular marker for Chinese ginger identification

Kittayout Pollakhan[1], Thanaboon Wichianrat[1], Maliwan Nakkuntod[2]

1 Naresuan University secondary demonstration school, Phitsanulok, Thailand. 2 Biology Department, Naresuan University, Phitsanulok, Thailand.

Fingerroot or Krachai belonging to the Zingiberaceae family becomes a potential herb inhibiting the COVID -19 virus because of containing Panduratin A as flavonoid. In Thailand, there are three popular species of fingerroot, namely *Boesenbergia rotunda* (L.) Mansf., *B. panduratada* Roxb. and *Kaempferia parviflora* Wallich ex Baker. Due to the morphological similarities among three species, it is difficult to distinguish based on only morphology. The aim of this research was to develop SCAR markers from SRAP polymorphism to identify the species *B. rotunda* containing high potential chemicals. The results showed that SRAP markers were able to generate 2 polymorphic bands to specific to *B. rotunda*. After cloning and sequencing, the polymorphic band size of 1,000 bp was successful, which had 93.76 percent identity with be intergenic spacer between *cob* and *rps14* gene of *Haberlea rhodopensis* (MH757117). After that, the 3 forward (BoRo-F1, BoRo-F2, BoRo-F3) and 2 reverse (BoRo-R1, BoRo-R2) SCAR primers were designed and made 6 combinations for PCR testing. The results demonstrated that a combination primer (BoRo-F1R1, BoRo-F2R1, BoRo-F3R1, and BoRo-F3R2) was successfully used to identify *Boesenbergia* genus; moreover, another pair primer (BoRo-F1R2 and BoRo-F2R2) was used for the identification of the *B. rotunda* species. Therefore, these SRAP-SCAR markers are effective to identify in levels of genus and species.

P.1417 The impostor among Limonium vulgare Mill.: the Limonium case in the Azores

Guilherme Roxo[1], Ana Caperta[2], Mark Carine[3], Ann Mc Cartney[4], Maria Romeiras[2], Rúben M. C. Rego[1], Alejandra Herrezuelo[1], Pedro Talhinhas[2], Luís Silva[1], Roberto Resendes[1], Raúl Mendes[1], Elisabete Dias[1], Mónica Moura[1]

1 University of Azores, School of Sciences and Technology, Ponta Delgada, Portugal. 2 Instituto Superior de Agronomia, Universidade de Lisboa, Lisbon, Portugal. 3 Life Sciences, The Natural History Museum, London, UK. 4 Genome Institute, University of California, Santa Cruz, USA.

The Plumbaginaceae Juss. is a cosmopolitan family within which the genus *Limonium* Mill. is the richest in terms of the number of species, with estimates ranging from 300-600. The Azores archipelago consists of nine islands and is located approximately 1,300 kilometres west of mainland Portugal, 1,600 kilometres east of North America, and 800 kilometres north-west of Madeira. In the Azores, the genus is represented by one taxon. While typically referred to *Limonium vulgare* Mill, Diáz-González *et al.* (2006) suggested that Azorean individuals should be recognised as *L. diasii*. This designation, used in a book of abstracts, has yet to be validly published and there has been no morphological or molecular data to support the proposed segregation of the taxon. In this study, flow cytometry, karyotype and phylogenetic data were used to investigate the status of *L. diasii*. Preliminary results revealed a lower genome size in Azorean specimens (3.345 ± P.40 pg) compared to plants from populations from Portugal and Morocco (5.75 ± 0.10 pg, Róis *et al.*, 2018). Whereas taxa belonging to the *Limonium vulgare* complex are considered tetraploid ($2n = 4x = 36$ chromosomes), our results revealed that the plants from the Azores are diploid ($2n=2x=16$). These preliminary findings lend support to the recognition of Azorean plants as a distinct taxon, but further phylogenetic and morphological data are necessary to further investigate the distinctiveness of Azorean plants of this complex.

P.1418 DNA barcoding of an edible insect and its host plant in Southern Mexico

Sonia Trujillo-Argueta[1], Rafael F. del Castillo[1], Zaira Cortes-López[2], José Antonio Sánchez-García[1], Héctor Miguel Guzmán-Vásquez[1]

1 Instituto Politécnico Nacional CIIDIR, Sta. Cruz Xoxocotlán, México. 2 Universidad Autónoma Benito Juárez de Oaxaca, Oaxaca de Juárez, México.

In the world several insects are edible. In México, several cultural groups add insects to their diet. Although "grillos" (grasshoppers) and "chicatanas" (ants) are commonly eaten in Oaxaca State, there is an edible insect poorly known named by local people "tigrillos" found in a Fabaceae plant called "timbre". We used barcoding DNA technique to determine species name of this edible insect and its host plant. DNA was extracted from small sections of the leaves of the plants, and we used legs from the insects. In the case of the plants, we amplified DNA (PCR) using two chloroplast genes that are commonly used in DNA barcoding plants: *rbcL* and *matK* and we amplified gen *CO1* for the insects. In all cases universal primers were used. Percent amplification and sequencing success observed on both genes used in plants was 100%, while percent amplification and sequencing obtained in insects were 68.75% and 45.45% respectively. DNA sequences obtained were edited and aligned with CodonCode software. We used BLAST analysis to compare our DNA sequences to the base data of GenBank and BOLD. In the case of the host plant, we obtained 100% identity to *Acaciella angustissima* using both genes *rbcL* and *matk*. Nevertheless, in the insect DNA sequences we observed a maximum percentage identity of 84% to *Umbonia crassicornis*. An insect taxonomy specialist determined that our insect was *U. reclinate*, a membracid species that is not yet registered in the taxonomy base of GenBank, and therefore, it explains the low similarity found to *U. crassicormis*. Metadata obtained with the edible insect and its host plant were submitted to the base data of BOLD in the project registered as EDINO. This work contributed to generate a DNA library of sequences of an edible insect, *U. reclinate*, and its host plant *Acaciella angustissima*.

S.158. THE EVOLUTION AND BIOGEOGRAPHY OF APOMICTIC PLANTS.

P.1420 Invasive apomictic hybrid dandelions: DNA content changes in Western Japan indicate increased backcrossing

Toru Jogaki[1], Yuuki Osafune[2], Taishi Kodama[2], Tsukiya Kubo[1], Satoshi Nanami[1], Akira Itoh[1]

1 Osaka Metropolitan University, Osaka, Japan. 2 Osaka City University, Osaka, Japan.

Hybridization is important for invasive apomictic plants, which can rapidly expand by asexual seed production. Although apomixis enables rapid dispersal, it cannot counteract the reduced genetic diversity caused by the founder effect, which hinders adaptation to new environments. Therefore, hybridization with native species is essential for increasing genetic diversity and adaptation to new environments. The European common dandelion, *Taraxacum officinale*, primarily reproduces through apomixis but can hybridize with native Japanese dandelions. The resulting hybrids are more abundant than pure *T. officinale* in Japan because they acquire genes from Japanese species and may be better adapted to the Japanese environment. Backcrossing with native species can further acquire genes from native species and invade the environments where native dandelions are abundant. However, the occurrence and spread of backcrossing individuals in natural settings is not well understood. This study aims to investigate the proportion of backcross hybrids in Western Japan. To achieve this, the nuclear DNA content of hybrid seeds collected during the Dandelion Survey Western Japan 2005-2020 was measured by flow cytometry. The proportions of F1 and backcross hybrids were estimated using a Bayesian model based on the DNA content data obtained. The results showed that the proportion of backcross hybrids has been increasing annually. The increase of triploid backcross hybrids was particularly significant in areas where native species were abundant. The results suggest that backcross hybrids that acquire more genes from native species may become better adapted to native growth conditions. If backcrossing continues, it could lead to the emergence of hybrids that are well-adapted to the environments dominated by native species, potentially threatening the growth of native species. Further research is necessary to investigate the ecological characteristics of backcross hybrids and understand their potential impact on the growth of native species.

P.1421 Genotypic and phenotypic diversity of apomictic dandelion introduced about 120 years ago in Hokkaido, Japan

Shuhei Matsuyama[1], Tamaki Matsumoto[1], Takahiro Matsunaga[2], Yui Saito[1], Akira Itoh[2]

1 College of Agriculture, Food and Environmental Sciences, Rakuno Gakuen University, Ebetsu, Japan. 2 Graduate School of Science, Osaka Metropolitan University, Osaka, Japan.

Plants introduced to an island environment are thought to reproduce evolution and adaptation in a novel environment, so it gives us an opportunity to observe how the adaptation and evolution have proceeded or how much time has been taken to mutate. *Taraxacum officinale* is a facultative apomictic plant introduced in Hokkaido, Japan, about 120 years ago. The species shows high genotypic diversity in Japan, it may be caused by mutation, and crossing and backcrossing with native diploid Taraxacum species. As a step to understand the contribution of sexual production and apomixis in the genotypic diversity, the SSR genotypic diversity was evaluated for the species from 21 sites in Hokkaido, where there is no native diploid sexual *Taraxacum*. To examine whether the genotypes show different responses to environmental conditions, we evaluated and compared the difference among genotypes in the response to the light environmental change through a cultivation experiment. In Hokkaido, collected *T. officinale* was triploid, and two common genotypes and minor genotypes were detected. The genotypes were classified into three groups in the analysis considering errors in the PCR and electrophoresis. The response to the light environmental change was similar within a genotype group, whereas not among genotype groups. These suggest that introduced *T. officinale* itself includes at least some genotypes with different phenotypes in present, and it might have evolved through mutation and natural selection for 120 years, or some genotypes of *T. officinale* might have been introduced in Japan.

P.1422 Geographical distribution patterns of apomictic plants and their phylogenetic diversity

Robin Matzl, Diego H. Hojsgaard[2], Agostina Sassone[2], Laura Rose[1], Piyal Karunarathne[1]

*1 Institute of Population Genetics, Heinrich-Heine-University, Düsseldorf, Germany. 2 Leibniz Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany. *piyal.karunarathne@hhu.de.*

Apomixis is an asexual reproductive strategy in which plants are able to produce viable seeds from somatic cells or unfertilized megaspores. Studies on apomictic species suggest that apomixis is an ancestral trait to angiosperms which can re-emerge in angiosperm genera and enables the host species to take a pioneering role in new environments and broaden their niche. This has led to the hypothesis that apomixis may show a latitudinal gradient. Using an up-to-date dataset of apomictic plant species, we explored the geographical distribution of apomictic species, paying special attention to the latitudinal gradient. We obtained the distribution data from the World Flora Online database and visualized the species richness across the globe. Our results show that higher percentages of native vascular plant species are apomictic in higher latitudes compared to their tropical counter parts. While Asteraceae, Poaceae and Rosaceae showed the highest number of apomictic species, their distribution in different continents varied significantly. Further, we explored the geographical distribution of phylogenetic diversity in apomictic species to visualize macroecological patterns. This can grant us insight into the evolutionary history of apomixis and the role it plays in speciation events. Our initial results show that the distribution of the phylogenetic diversity in apomictic species does not follow the same latitudinal pattern as species richness and varies substantially across different regions.

P.1423 Tracking of the early stages of apomixis formation in nature: insights from the genus Hieracium s.str. (Asteraceae)

Patrik Mráz[1], Begoña Quirós-de-la-Peña[1,2], Pavel Zdvořák[1], Eliška Záveská[1,2] Yann J. K. Bertrand2, Jiřina Josefiová[2], Shook Ling[2], Barbora Tomešová[2], Daniel Papež[3], Alexander Belyayev[2], Jindřich Chrtek[1,2]

1 Department of Botany, Charles University, Prague, Czechia. 2 Institute of Botany of the Czech Academy of Sciences, Průhonice, Czechia 3 University of West Bohemia, Plzeň, Czechia.

Hieracium s.str. is one of the apomictic genera with the highest incidence of gametophytic apomixis (clonal embryos derived from unreduced embryo sacs without fertilization). All polyploid accessions analysed to date have been found to be obligate or near-obligate apomicts. Large-scale flow cytometric seed screening revealed that residual sexuality was present in only about 1% of plants and about 0.4% of seed progeny. Furthermore, in facultative apomictics, sexually formed progeny are a minority, whereas apomictic progeny clearly predominate. These quantitative patterns suggest strong selection for full penetrance of apomixis, which is also reflected in high seed set in stabilised apomictic polyploids. As apomixis is a derived state and 'only' modifies a normal sexual pathway, we can logically expect more reproductive perturbations in young apomictic polyploids. These should be more sterile, have a higher rate of sexuality and a lower rate of apomixis compared to stabilised polyploids. In 2014, we found a population of reproductively unstable, triploid species of the *H. nigrescens* group (morphologically between *H. alpinum* and *H. murorum*) that could represent such a young polyploid lineage. It is morphologically very similar to one of its putative parents, *H. alpinum*, which occurs at the site with two other, but morphologically more distinct and presumably stabilised tetraploid species of *H. nigrescens*. This situation suggests a recent origin of the unstable triploid, which could arise from hybridisation between diploid sexual *H. alpinum* and tetraploid apomictic *H. nigrescens*. To gain a deeper insight into this evolutionarily compelling system, we assessed seed sets of all co-occurring taxa, determined the mode of reproduction by flow cytometric seed screening, and assessed their relatedness using genomic RADseq, cpDNA and a cytogenetic approach. These data are confronted with those obtained from experimental hybridization between *H. alpinum* and *H. nigrescens* s.str.

S.159. THE FUNCTIONAL ROLE OF NONCHARISMATIC BIODIVERSITY IN THE FACE OF A CHANGING WORLD

P.1424 Strategies to design and develop substantial air quality gardens for urban air pollution abatement to remove particulate matter

Moumita Basu[1]

1 Department of Botany, Kalna College, West Bengal, India.

Air pollution is now regarded as an increasingly threatening major environmental risk for human health and the leading cause of death worldwide. According to WHO reports, 7 million deaths per year are attributed to air pollution each year involving almost 99% of the global population that breathe polluted air. The one of the most harmful, hazardous and dangerous forms of pollution is caused by the Particulate Matters (0.10 - 0.25 nm) consisting of solid and liquid particles suspended in the air which causes respiratory and cardiovascular diseases. In the 21st century, an exponential growth of urbanization is observed in the metropolitan cities of India causing continuous and alarming increase of urban air pollution for the last few decades. Several urban plants like (*Ficus bengamina, Swietenia hondura, Araucaria heterophylla, Couroupita guainensis, Kigellia, Tamarindus indica, Eucalyptus gunnii,* *Manilkara zapota*) can directly reduce particulates by absorbing them in to the leaves and filters atmospheric pollutants (SO$_2$, NO$_2$) through leaves acting as "the lungs of the Ecosystem ". Planting only tree species is not as much beneficial sometimes if they are not so well PM absorbers or there is not enough space of planting tree species. With the help of Horticopia Database, i-Tree Species Software and Phyto- Sensor Toolkit it is concluded that herbs like *Aster spp.*, *Salvia nemorosa*, *Convolvulus cneorum*, *Alchemilla mollis*, *Euphorbia characias*, *Hedera helix* etc. can take over that landscapes with their high PM absorbing capacity. Green walls, green screens also enhance the biodiversity in polluted urban areas. In this scenario, it is important to design quality gardens in the modern Indian urban landscapes in which the herbs, shrubs and trees together can combat the Particulate Matter levels of a particular geographical area.

P.1425 Macrofungi and lichenised fungi as biological indicators: the case of Pyrenean oak and chestnut forests in Castilla y León (Spain)

Sonia Perfecto Arribas[1], David Rodríguez de la Cruz[1], Luis Delgado Sánchez[1]

1 Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain.

In recent decades, fungi have started to be used as bio-indicators to assess the biodiversity and conservation status of different habitats. Their usefulness as bio-indicators is due to their high adaptability and sensitivity, allowing them to reflect changes in ecosystem quality. In this study, in order to compare fungal diversity among the Pyrenean oak (*Quercus pyrenaica* Willd.) and chestnut (*Castanea sativa* Mill.) forests of Central Spain, we compiled records of macrofungi and lichenised fungi from the GBIF database using ArcGIS 10.8., and then analysed the possible implications of their presence for the conservation of these forest habitats. 560 species of macrofungi and 526 species of lichens were obtained in the Pyrenean oak forests and 127 species of macrofungi and 85 species of lichens in chestnut groves. In terms of macrofungal life mode, in Pyrenean oak forests there were 71.8% saprophytic species, 27.7% mycorrhizal and 0.5% parasitic, while in the chestnut groves there were 55.1% saprophytic, 44.1% mycorrhizal and 0.8% parasitic. Furthermore, analysing lichen sensitivity to contamination, 55.3% of the species showed high sensitivity in oak woods, while 56.5% showed medium sensitivity in chestnut forests. Assessment of fungal diversity provides a holistic view of the health of forest ecosystems and could help identify areas requiring specific conservation measures. A better understanding of the relationship between fungal diversity and habitat quality would also contribute to the development of more effective management strategies for better habitat management. However, it would be advisable to carry out specific studies on a smaller scale to obtain more accurate results.

P.1426 Dynamics of grassland plant diversity and productivity after the cessation of long-term nutrient additions

Miao He[1], Yann Hautier2, Kathryn. E. Barry[2], Forest Isbell[1]

1 University of Minnesota, Twin Cities, Saint Paul, the United States. 2 Utrecht University, Utrecht, the Netherlands.

Many grassland ecosystems are experiencing nutrient enrichment, which generally increases grassland biomass production but causes diversity decline, shifting species interactions and composition. These impacts may exacerbate as nutrient inputs and effects accumulate over many years and decades. However, it remains unclear whether and to what extent the impacts of nutrient addition are readily reversible after the cessation of nutrient addition. In a 40-year grassland experiment, we monitored the dynamics of plant species diversity, composition, and aboveground biomass production in plots that had either: (1) no nutrient addition (control plots), (2) 40 years of continuous nutrient addition at one of eight rates of annual nitrogen (N) input ranging from 0 to 270 kg/ha, or (3) 10 years of nutrient addition followed by a 30-year opportunity for recovery after cessation of nitrogen addition. Earlier studies of this experiment considered the first three decades of the study and reported that: (1) plant diversity gradually recovered after cessation of lower rates (0-95 kg N / ha / year) of nutrient inputs, whereas (2) plant diversity failed to recover after cessation of higher rates (95-270 kg N / ha / year) of nutrient inputs. Here we found that plant diversity has started to recover in the third decade after cessation of high rates of nutrient inputs. We also found a gradually diminishing effect of former fertilization on community biomass within 30 years after cessation of nutrient inputs. Change of species composition contributes to the different return rates towards control levels of species richness and community biomass. Most of the recovered species are native species and non-legume forb, while few C3 grasses species remain dominant. These results could help elucidate the long-lasting impacts of agricultural management on plant communities and the pace of unassisted recovery in plant diversity and productivity following the cessation of nutrient enrichment.

P.1427 Lichen recolonization of volcanic quarries in a Mediterranean climate

Esteve Llop[1]

1 Department of Evolutive Biology, Ecology and Environmental Sciences, University of Barcelona, Barcelona, Spain.

The most recent and largest volcanic area on the Iberian Peninsula is located in the north-eastern part, in the county of La Garrotxa. The volcanic remains include volcanos, lava flows and rootless volcanic cones. These materials have been altered by human activity for centuries, mainly exploited as quarries for the construction of houses, bridges and other buildings. The end of exploitation of quarries has allowed the renaturalization of the affected areas, and also the colonization of exposed volcanic cone walls and hillocks by vascular plants, mosses and lichens. The study of lichen diversity on three quarries has included epiphytic, saxicolous and terricolous and muscicolous communities, and a list of 83 species has been produced. The list does not include menaced taxa, according to the current catalogue of threaten flora. Unfortunately, the knowledge on the current situation of the lichen biota is still poor. The sites share a 42% of the lichen species, however the saxicolous communities only have a 22% of similarity in their species composition. On the other hand, epiphyte communities show a 58% of similarity between species composition. The response to ecological factors seems to be more similar between sites, with an 88% of similarity, being a bit lower in saxicolous communities (73%) compared to epiphytic ones (81%). The main differences in saxicolous communities are related with orientation, as areas facing south hold higher abundances of species tolerating high levels of eutrophization or aridity. Epiphytic communities do not show a significant pattern on the response to ecological factors, however sites located in more natural areas tend to hold higher diversity and lower abundances of species tolerating high levels of eutrophization or aridity.

P.1428 The study of Acarosporaceae in Central Europe

Tereza Pušová[1], Kerry K. Knudsen[1], Jana Kocourková[1]

1 Department of Ecology, Faculty of Environmental Sciences, Czech University of Life Sciences, Prague, Czech Republic.

Acarosporaceae is a global family of crustose lichens on rocks and soil with seven genera, *Acarospora*, *Lithoglypha*, *Myriospora*, *Pleopsidium*, *Sarcogyne*, *Timdalia*, and *Trimmatothelopsis*. Acarosporaceae are especially adapted to arid, hot and sunny locations. The diversity of the family in Europe is over 200 described taxa, but many are poorly known, and many are in need of modern revisions. Molecular analysis is also discovering greater diversity of Acarosporaceae in Europe. In the beginning of our study of the genus *Acarospora* in central Europe, *A. discreta* is revised. It has long been considered problematic. Our new study provides a detailed analysis of its morphology and genetic characteristics, allowing precise identification. We are also studying *A. crozalsii, A. nitrophila,* and *A. praeruptorum*.

P.1419 H3 serine 10 phosphorylation patterns during meiosis in sexual and asexual Limonium species

Catarina Gomes-Domingues[1,*], Nelly Silva[1], David Cortiço[1], Ana D. Caperta[1]

*1 LEAF—Linking Landscape, Environment, Agriculture and Food Research Center, Associate Laboratory TERRA, Instituto Superior de Agronomia, Universidade de Lisboa, Tapada da Ajuda, Lisboa, Portugal. *catarinaagomes01@gmail.com*

In plants, cell cycle dependent H3 phosphorylation at serine 10 (H3Ser10ph) is required for sister chromatid cohesion during metaphase I and for sister chromatid pericentromeres in metaphase II (Houben et al. 2007). *Limonium* species (sea lavenders, Plumbaginaceae) are an interesting case study for male sporogenesis since diploid species present regular meiosis whereas polyploid species show several chromosome paring and segregation irregularities (Rois et al. 2012). In this preliminary study, we hypothesised different H3Ser10ph patterns in diploid *L. ovalifolium*, triploid *L. algarvense* and tetraploid *L. multiflorum* during meiosis. Through cytogenetic approaches diploid species showed no signs of unpaired chromosomes while in polyploids both chromosome paired and unpaired regions were detected. H3Ser10ph immunodetection revealed a variable number of nucleoli with H3Ser10ph signals at pre-meiotic interphase cells in all species. At prophase I in diplotene and diakinesis, and during metaphase and anaphase I the H3Ser10ph labelling was mostly visualized in chromosome pericentromeric regions in all species. Polyploid species had univalent chromosomes and micronuclei without any H3Ser10ph marks. In these species, nonreduced nuclei via meiotic restitution presented H3Ser10ph signals in nucleoli as found in pre-meiotic interphase cells. Our preliminary findings highlight the presence of different H3Ser10ph patterns during meiosis I in *Limonium* species with different ploidies.

References: Houben, **et al.** (2007), Phosphorylation of histone H3 in plants—a dynamic affair, **BBA-Gene Structure and Expression**,1769: 5-6; Róis **et al.**, (2012), Male fertility versus sterility, cytotype, and DNA quantitative variation in seed production in diploid and tetraploid sea lavenders (*Limonium* sp., Plumbaginaceae) reveal diversity in reproduction modes, **Sexual Plant Reproduction**, 25:305-318.

P.1429 Preliminary analysis of macrofungi in forest ecosystems of the central-western Iberian Peninsula: considerations on fungal diversity

Abel Fernández Ruiz[1], Prudencio García Jiménez[1], David Marcos Vidal[1], José Sánchez Sánchez[1], David Rodríguez de la Cruz[1]

1 Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain.

A knowledge of the diversity of organisms and their functioning in Mediterranean forest environments could play a relevant role in understanding the effects of climate change and, possibly, some factors that could mitigate it. In this case, the study of macrofungi and their temporal fructification over several years is proposed, in order to increase the knowledge of their ecosystemic roles. This study was carried out in two very fragmented forest plots in central-western Spain, 19 kilometres apart. The first is located in Monte de La Orbada (41°08'03.9 "N 5°28'58.8 "W), it has 7.5 hectares and is dominated by holm oak (*Quercus ilex* subsp. *ballota*) accompanied by a diverse undergrowth with more helophilous species (*Cistus* spp., *Thymus* spp.) and others of shadier environments and deeper soils (*Rosa canina* L., *Crataegus monogyna* Jacq.). The second, which occupies the entire Monte de Villoria (40°59'50.9 "N 5°20'32.0 "W), has 23.59 hectares with 3 subplots dominated respectively by holm oak, Pyrenean oak (*Quercus pyrenaica* Willd.) and cork oak (*Quercus suber* L.), and a shrubland of brown-eyed rockrose (*Cistus ladanifer* L.). Sampling was carried out between October 2020 and September 2023, with line transects and a biweekly frequency. Sporocarps were identified through macro and microscopic characters. Alpha diversity was higher in the second plot (216/172 species), and beta diversity (Sørensen's index) between the two was 0.45. Fruiting was recorded in most of the weeks sampled, including summer weeks, with the appearance of taxa exclusive to this season, such as *Boletus (=Imperator) rhodopurpureus* Smotl. and *Suillellus luridus* (Schaeff.) Murrill. This underlines how important it is to conduct fruiting studies throughout the year and not only at times of peak sporocarp production

P.1430 Contributions to the macrofungal diversity of Benavides de Órbigo (León, NW Iberian Peninsula)

David Marcos Vidal[1], Abel Fernández Ruiz[1], David Rodríguez de la Cruz[1]

1 Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain.

The study of mycocoenosis emerges as a necessary line of research to address the traditional absence of fungi in Conservation Biology, both in applied and academic contexts. Among possible approaches, the search for macrofungi fruiting bodies provides insights not only into species presence, but also into fruiting dynamics and the relationship of fungal taxa with ecosystem vegetation This communication presents a preliminary catalog of macromycetes in the locality of Benavides de Órbigo (León), along with information regarding their fruiting throughout the year. Three distinct Mediterranean forest zones were selected based on vegetation: 1) Spanish oak forest (**Quercus pyrenaica** Willd.), 2) wooded pasture with spanish oak and holm oak (**Quercus ilex** subsp. **ballota**), as well as abundant shrubs (**Cytisus** spp.), and 3) holm oak forest with abundant rockrose (**Cistus laurifolius** L.). Specimen sampling was conducted via biweekly linear transects, considering the presence of viable fruiting bodies. Classic mycology techniques (observation of fresh specimens and in situ photography, microscopy, and the use of mycological reagents) were employed for taxon determination. The highest fungal species diversity was observed in zone 1 (spanish oak forest). Conversely, Beta diversity analysis reveals greater similarity between zones 2 and 3, both containing holm oaks. A preliminary assessment of zone disturbance status was conducted by taking into account the proportions of the three main macrofungi trophic groups: mycorrhizal, saprobic and parasitic. Zone 2 exhibits a higher percentage of saprobic species compared to other zones, likely corresponding to greater organic residue abundance resulting from livestock activity.

P.1431 Bleaching as a stress response to experimental warming in Arctic lichens

Jiri Subrt[1], Claudia Colesie[1], Kevin Newsham[2], Mariana García-Criado[1]

1 University of Edinburgh, Edinburgh, UK. 2 British Antarctic Survey, Cambridge, UK.

Lichens in the Arctic are recognized as extremophiles. However, they also serve as sensitive climatic indicators. Studies have indicated a decline in Arctic lichen abundance due to climate warming and an increase in other plant functional groups. However, most observational studies lack a mechanistic understanding of lichen decline. Moreover, despite their prominent roles in Arctic ecosystems, the extent to which lichens can acclimatise to changing climates over the long term remains poorly understood. Our research focused on investigating the physiological and morphological responses of lichens subjected to one decade of experimental warming using the open-top chamber experiment in Ny-Ålesund, Svalbard. This investigation aims to enhance our understanding of the carbon balance of polar lichens under warming conditions and ascertain whether these lichens and their symbionts possess adaptive capabilities or experience physiological degradation. Such deterioration may manifest as bleaching, disrupting lichen symbiosis similar to corals, potentially leading to widespread ecosystem collapse. The results indicate that lichens subjected to warming physiologically and morphologically deteriorated and did not acclimatise after experiencing warmer conditions. These findings hold significance within the context of the imminent threat posed by climate warming in the Arctic, as well as the potential impact on the biodiversity and ecosystem services provided by lichens.

P.1432 Chemical profile and bioactivities of extracts from Antarctic lichens of the genus Cladonia (Cladoniaceae, Ascomycota)

Alfredo Torres-Benítez[1,2,*], José Erick Ortega-Valencia[3], Jaqueline S. Ley-Martínez[3], Marta Sanchez[4], María Pilar Goméz-Serranillos[4], Mario J. Simirgiotis[1]

*1 Universidad Austral de Chile, Valdivia, Chile,*aljotobe19@hotmail.com. 2 Universidad del Tolima, Ibagué, Colombia. 3 Instituto Tecnológico de Tlalnepantla, Estado de México, México. 4 Universidad Complutense de Madrid, Madrid, Spain*

Lichens constitute a mutualistic symbiosis between a mycobiont and photobiont associated with a microbiome and present a high chemical richness with pharmacological interest. They are distributed throughout the world and in the Antarctic continent there is a great diversity of species among which those belonging to the genus *Cladonia* stand out. This work aims to determine the chemical composition of the ethanolic extract of *Cladonia chlorophaea* and *C. gracilis* species, their digestive enzyme inhibition activity (α-glucosidase and pancreatic lipase), and cytoprotection against oxidative stress induced by H_2O_2. Nineteen metabolites were identified in each of the *Cladonia* species by liquid chromatography coupled with quadrupole-time-of-flight mass spectrometry (UHPLC-ESI-QTOF-MS), and citric acid, cryptostic acid derivate, constictictic acid/siphulellic acid and usnic acid were highlighted as major compounds. In the α-glucosidase assay, the extracts of *C. gracilis* and *C. chlorophaea* obtained an IC_{50} of 91.323 ± P.10 and 108.590 ± P.06 μg/mL, respectively, and in the pancreatic lipase assay, the extract of *C. gracilis* showed an IC_{50} of 345.1355 ± P.0 μg/mL and that of *C. chlorophaea* an IC_{50} 125.310 ± P.49 μg/mL. Both extracts showed high viability in the SH-SY5Y cell line; subsequently, the protective effect against H_2O_2 with *C. gracilis* was 98.7%, 104.7% and 90.2% at concentrations of 5.0, 10 and 25 μg/mL, respectively, and for *C. chlorophaea* it was 100% and 88% at concentrations of 0.5 and 0.7 μg/mL, respectively; likewise, treatments with the extracts significantly reduced the production of reactive oxygen species versus cell treatment with H_2O_2.This study contributes to the knowledge of compounds present in Antarctic lichen species and the opportunity to continue with the validation of biological activities related to treatment mechanisms in metabolic syndrome and neurodegenerative diseases.

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S.160. THE IMPACT GENOME SIZE AND CHROMOSOME EVOLUTION ON THE ARCHITECTURE OF THE GENOME

P.1433 Deciphering the evolutionary trajectory of the ancestral fagales karyotype and syntenic regions

Yu Cao[1,2,3], Heng-Chi Chen[2,3], Da-Yong Zhang[1*], Zhen Li[2,3], Yves Van de Peer[2,3,4,5]

1 State Key Laboratory of Earth Surface Process and Resource Ecology and Ministry of Education Key Laboratory for Biodiversity Science and Ecological Engineering, College of Life Sciences, Beijing Normal University, Beijing, China. 2 Department of Plant Biotechnology and Bioinformatics, Ghent University, Ghent, Belgium. 3 VIB – Center for Plant Systems Biology, Ghent, Belgium. 4 Center for Microbial Ecology and Genomics, Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, South Africa. 5 College of Horticulture, Nanjing Agricultural University, Nanjing, China.

Fagales, a diverse and ecologically dominant plant group primarily inhabiting temperate areas of the Northern Hemisphere, exhibit a mosaic of genome dynamics characterized by fractionation after whole-genome duplication, gene family expansion and contraction, and chromosomal rearrangements. While the overarching genome architecture within the Fagales order remains conserved, our understanding is evolving to recognize the variability in rearrangement rates among different families. Through the computational reconstruction of ancestral karyotypes and syntenic relationships across 32 nodes spanning the Fagales phylogeny, we unveil a landscape of macro-synteny marked by conservation, with Betulaceae exhibiting pronounced chromosomal rearrangements. Our analysis suggests an ancestral Fagales karyotype consisting of seven chromosomes, boasting 98% BUSCO completeness. Furthermore, we identify 91 rearrangement breakpoints distributed over 62 branches, indicative of an average rate of 0.95 breakpoints per million years. Additionally, our investigation explores the interplay between genomic features, such as transposable elements and gene density, and gene functions within regions prone to chromosomal rearrangement, as well as the regions exhibiting the most conserved syntenic adjacency. Our findings offer a comprehensive ancestral genome blueprint for the Fagales order, addressing the nuances of genome assembly and annotation quality essential for robust comparative genomic analyses. This resource enhances our understanding of Fagales genome evolution and provides insights into broader questions of plant genomic architecture and its implications for speciation and adaptation.

P.1434 Genome-wide expansion and reorganization during grass evolution: from 30 Mb chromosomes in rice and Brachypodium to 550 Mb in Aven

Qing Liu[1], Trude Schwarzacher[1,2], Pat Heslop-Harrison[1,2]

1 South China Botanical Garden, Guangzhou, China. 2 University of Leicester, Leicester, United Kingdom.

Diploid genome sizes in the BOP (Bambusoideae, Oryzoideae, and Pooideae) clade of grasses (Poaceae) range from rice, *Oryza sativa* (2n=24; genome size 389 Mb) and *Brachypodium*, *Brachypodium distachyon* (2n=10; 271 Mb) to Triticeae and Aveneae species (2x=14) of about 4,000 Mbp. Focusing on comparisons between rice or *Brachypodium*, with ancestral-like karyotypes, and new *Avena* chromosome-scale genome sequence assemblies, we show the nature of genomic expansion, structural variation, and chromosomal rearrangements. Most of the *Avena* chromosome arms show relatively uniform expansion over the 10-fold to 15-fold genome-size increase. Apart from non-coding sequence diversification and accumulation around the centromeres, blocks of genes are not interspersed with blocks of repeats, even in subterminal regions. In both Aveneae and Triticeae tribes, blocks of conserved synteny are seen between the analyzed species with chromosome fusion, fission, and nesting (insertion) events showing deep evolutionary conservation of chromosome structure during genomic expansion. In Aveneae, contrasting with Triticeae, terminal gene-rich chromosomal segments (representing typically 50 Mb of the 400 Mb chromosomes) show translocations between chromosomes during speciation, with homogenization of genome-specific repetitive elements. Newly formed intergenomic translocations of similar extent are found in the hexaploid *A. sativa*. The study provides insight into evolutionary mechanisms and speciation in the BOP clade, which is valuable for measurement of biodiversity, development of a clade-wide pangenome, and exploitation of genomic diversity through breeding programs in Poaceae. Further information and references are given at www.molcyt.com .

P.1435 Whole-mount fluorescence in situ hybridization for organ-level 3D analysis of chromosome dynamics in plants

Suzuka Kikuchi[1], Takuya Sakamoto[2,3], Sachihiro Matsunaga[4], Munetaka Sugiyama[5], Takumi Higaki[1], Akitoshi Iwamoto[2]

1 Faculty of Advanced Science and Technology, Kumamoto University, Kumamoto, Japan. 2 Faculty of Science, Kanagawa University, Yokohama, Japan. 3 Faculty of Science and Technology, Tokyo University of Science, Noda, Japan. 4 Graduate School of Frontier Sciences, University of Tokyo, Kashiwa, Japan. 5 Graduate School of Science, University of Tokyo, Bunkyo, Japan.

Whole-mount fluorescence in situ hybridization (WM-FISH) is a valuable tool for examining chromosome behavior in tissues or organs. It is difficult, however, to obtain a precise spatial profile of fluorescent signals in roots using conventional WM-FISH, because damages occur in cells during processing. To address this issue, we developed a WM-FISH analysis for intact *Arabidopsis thaliana* roots and successfully obtained the precise spatial depiction of nuclear size and centromere signals. We then assessed the degree of chromosome polytenization in the root cortical cells of the *Arabidopsis* autopolyploid series (diploid, tetraploid, hexaploid, and octoploid) using our novel WM-FISH method. The WM-FISH analysis revealed that the degree of chromosome polytenization was similar in all autopolyploid strains in the cell proliferation zone. In contrast, chromosomes in high-polyploids (hexaploid and octoploid) exhibited more polytenization than those in the diploid and tetraploid in the volume growth zone. Combined with the results of kinematic analysis for root growth, this study suggests that severe chromosome polytenization in the cell volume growth zone is associated with significant suppression of the increase in cell volume in high-polyploids. Our WM-FISH analysis provided valuable insights into the chromosome behavior in intact roots of autopolyploids. We will also apply this WM-FISH analysis to the spatial profiles of the chromosome behavior in the leaf cells of *Arabidopsis thaliana*, which includes two different type cells, pavement and palisade mesophyll cells. The analysis will elucidate the variation of the chromosome dynamics in *Arabidopsis* leaves related to endoreduplication.

P.1436 Genome downsizing in fern genus Sceptridium (Ophioglossaceae)

Li-Yaung Kuo[1], Susan Fawcett[2], Atsushi Ebihara[3], Sosuke Ishii[4]

1 Institute of Molecular & Cellular Biology, National Tsing Hua University, Hsinchu, Taiwan. 2 University and Jepson Herbaria, University of California, Berkeley, Berkeley, USA. 3 Department of Botany, National Museum of Nature and Science, Tsukuba, Japan. 4 Department of Biology, Graduate School of Science and Engineering, Chiba University, Japan.

Flowering plants are characterized by rapid genome downsizing after polyploidization. By contrast, ferns, the most polyploidy-prone plant lineage, predominantly show no obvious downsizing in polyploid genomes, which maintain a highly conserved chromosome structure. *Sceptridium* in Ophioglossaceae is exceptional among ferns. Using flow cytometry, we conducted a comprehensive genome size survey in this fern genus, and successfully acquired C-value data from 19 of the 25 species. Compared to the diploids, polyploids have significantly lower monoploid genome sizes (*i.e.* 1Cx-value), which are only 75-83% the size of diploids. Using a phylogenetic framework, we further demonstrated evolutionary trends of average DNA content per chromosome across the diploid and polyploid taxa. With this unique fern case, we also highlight *Sceptridium* ferns as an excellent exemplar to study whether similar evolutionary mechanisms are involved behind independent genome downsizing in other plant lineages.

P.1437 Plastid DNA is a major source of nuclear genome complexity and of RNA genes in the orphan crop moringa

Juan Pablo Marczuk-Rojas[1,2], Antonio Salmerón[3], Alfredo Alcayde[4], Viktor Isanbaev[4], Lorenzo Carretero-Paulet[1,2]

1 Department of Biology and Geology, University of Almería, Almería, Spain. 2 "Pabellón de Historia Natural-Centro de Investigación de Colecciones Científicas de la Universidad de Almería", University of Almería, Almería, Spain. 3 Department of Mathematics and Center for the Development and Transfer of Mathematical Research to Industry, University of Almería, Almería, Spain. 4 Department of Engineering, University of Almería, Almería, Spain.

Unlike Transposable Elements (TEs) and gene/genome duplication, the role of the so-called nuclear plastid DNA sequences (NUPTs) in shaping the evolution of genome architecture and function remains poorly studied. We investigate here the functional and evolutionary fate of NUPTs in the genome of the orphan crop *Moringa oleifera* (moringa) (Chang et al. 2022), featured by the highest fraction of plastid DNA found so far in any plant genome (Ojeda-López et al. 2020, Marczuk-Rojas et al. 2024), focusing on i) any potential biases in their distribution in relation to specific nuclear genomic features, ii) their contribution to the emergence of new genes and gene regions, and iii) their impact on the expression of target nuclear genes. In agreement with their potential mutagenic effect, NUPTs are underrepresented among structural genes, although their overall transcription levels and broadness were only lower when involved exonic regions; the occurrence of plastid DNA generally did not result in a broader expression, except among those affected in introns by older NUPTs. In contrast, we found a strong enrichment of NUPTs among specific superfamilies of retrotransposons and several classes of RNA genes, including those participating in the protein biosynthetic machinery (*i.e.*, rRNA and tRNA genes) and a specific class of regulatory RNAs. A significant fraction of NUPT RNA genes was found to be functionally expressed, thus potentially contributing to the nuclear pool. Our results complete our view of the molecular factors driving the evolution of nuclear genome architecture and function, and support plastid DNA in moringa as a major source of i) genome complexity and ii) the nuclear pool of RNA genes. References: Chang, J...Carretero-Paulet, L. Plant Genome 15 (2022); Ojeda-López, J... Carretero-Paulet, L. Sci Rep 10 (2020); Marczuk-Rojas, JP... Carretero-Paulet, L. BMC Genomics 25, 60 (2024).

P.1438 Kinematic analysis of the effects of haploidization on root growth in Arabidopsis thaliana

Takafumi Miyashita[1], Ruka Nakajima[1], Suzuka Kikuchi[2], Akitoshi Iwamoto[1]

1 Kanagawa University, Kanagawa, Japan. 2 Kumamoto University, Kumamoto, Japan.

Genome polyploidization affects the plant growth in various aspects. We have analyzed the root growth of the autopolyploid series of *Arabidopsis thaliana* (diploid, tetraploid, hexaploid, and octaploid). The kinematic analysis at the cellular level revealed that tetraploidization promotes cell volume growth but suppresses cell proliferation. On the other hand, polyploidization to high-polyploids (hexaploids and octoploids) suppresses not only cell proliferation but also cell volume growth. In the haploids of *Arabidopsis thaliana*, we confirmed that the root growth is suppressed compared with that in the diploids, but it is yet unclear how haploidization affects cell volume growth and cell proliferation in the root growth. In this study, we analyzed the root growth of the haploids and diploids of *Arabidopsis thaliana* using the kinematic method. At first, we measured the elongation rate of the haploids and found it was constant at 10 DAS. Then we performed the kinematic analysis on the root growth of the haploids at 10 DAS. The analysis revealed that the haploidization suppresses the volume growth rate in the whole root. The spatial profile of the relative elementary growth rate showed that the volume growth zone in the haploids was also smaller than that in the diploids. The haploidization promoted the cell proliferation to the contrary. The local cell production rate of the haploids exceeded that of the diploids in the cell proliferation zone. These results suggest that genome haploidization may decrease the gene expression related to cell volume but increase the efficiency of genome replication and in turn cell proliferation.

P.1439 On the introduction history and plant ecology of the alien Salpichroa origanifolia in Tuscany (Italy)

Viola Alessandrini[1], Iduna Arduini[1]

1 Department of Agriculture, Food and Environment, University of Pisa, Pisa, Italy.

Invasive alien species are a major threat to biodiversity worldwide. The invasion of *Salpichroa origanifolia* (Lam.) Baillon (Solanaceae), an herbaceous climber native to South America, is recently rising concern in several Mediterranean countries. In North America, Australia, Japan and New Zealand, where it has a longer history of introduction, it is already a threat to critical habitats and native species. We, therefore, recommend listing it as an invasive alien species of EU concern and include it in the EPPO list. In Tuscany (central Italy), *S. origanifolia* has successfully colonised a mesophile forest (San Rossore Regional Park), showing to be a strong competitor towards the resident understorey vegetation, which also led to the progressive depletion of the soil seed bank (Arduini & Alessandrini, 2024). Although its first record in the Regional Park is from 1996, it is only in recent years that this species has massively spread. Giving insight into the spatio-temporal stages of alien invasion (transport, colonization, establishment, and spread) is important for planning targeted and effective conservation measures. Furthermore, explaining the arrival and spread of *S. origanifolia* within the Regional Park provides information to reduce the risk of introducing potential IAS. First aim of this research was to trace the history of introduction of *S. origanifolia* in Tuscany, and the invasion routes within the Regional Park. Moreover, we studied which environmental factors, primarily illumination and soil moisture, may have favoured the establishment at the current invasion spots, and the ecology (reproductive biology, functional traits) of this species in the introduced area. The invader *S. origanifolia* proved to adapt well to different light conditions, due to its ability to allocate resources differently between leaves and rhizomes. References: 1. Arduini, I.; Alessandrini, V. The novel invader *Salpichroa origanifolia* modifies the soil seed bank of a Mediterranean mesophile forest. *Plants* **2024**, 13, 226.

S.161. BIOTIC INTERACTIONS AND BIOLOGICAL INVASIONS.

P.1440 Recent advances in the understanding of Paraphysoderma sedebokerense and the infection to their valuable microalgal hosts

David Alors[1,2], Karel Mena[2], Sammy Boussiba[1], Aliza Zarka[1]

1 Microalgal Biotechnology Laboratory, University of Negev, Midreshet Ben Gurion, Israel. 2 Department of Biology and Chemistry, Catholic University of Temuco, Temuco, Chile.

The blastocladialean fungus ***Paraphysoderma sedebokerense*** is a facultative parasite that can complete the infection cycle as fast as 16 hours; it can also grow as saprobe. From its initial isolation in 2008, the resistance cysts were reported and described, and we recently showed empirically the ability *of P. sedebokerense* to resist dehydration and recover both, viability and infectivity, after resting cyst germination. *P. sedebokerense* gained attention because of his ability to infect economically important microalgae causing fast culture collapse and economical losses. We described the high preference to infect *Haematococcus lacustris* even in the presence of other suitable hosts like *Chromochloris zofingiensis* or *Scenedesmus dimorphus*. Since *P. sedebokerense* can use inorganic nitrogen sources the glutamine synthetase (Glns) is a target for pest control to avoid the infection of *H. lacustris*. By modelling the 3-D structure of H. lacustris decameric Glns isoforms (Glns2a and Glns2b) and the structure of *P. sedebokerense* hexameric Glns (Glns3), we studied the docking of the herbicide glufosinate to better explain the experimental results previously obtained. We studied the interaction of the amino acids of the active site of the different isoforms of the Glns. Our findings provide a direction of the next experimental research and saving time with the aim of control the infection of *H. lacustris* by *P. sedebokerense*. **References:** Alors, D., Boussiba S. and Zarka A. *Paraphysoderma sedebokerense* Infection in Three Economically Valuable Microalgae: Host Preference Correlates with Parasite Fitness. *J. Fungi* 2021, *7*, 100; Alors, D.; et al. *Paraphysoderma sedebokerense* GlnS III Is Essential for the Infection of Its Host *Haematococcus lacustris*. *J. Fungi* 2022, *8*, 561; Alors, D., Boussiba S. and Zarka A. Drought Resistant Resting Cysts of *Paraphysoderma sedebokerense* Preserves the Species Viability and Its Virulence. *Plants* 2023, *12*, 3230.

P.1441 Septoria lycopersici leaf damages: is it a problem of xylem dysfunction or impairment of the outside-xylem water pathway?

Douaa Bekkai[1], MariaT. Chiofalo[1], Daniele Torre[1], Stefano Mileto[1], Giuseppa Genovese[1], Patrizia Trifilò[1]

1 Department of CHIBIOFARAM, University of Messina, Messina, Italy.

Septoria leaf spot (SLS), caused by *Septoria lycopersici* Speg, is one of the most common and devastating leaf diseases of tomato. SLS impacts photosynthesis, photorespiration and respiration, leading to affect defense responses, defoliation and severe tomato yield losses. To the best of our knowledge, to date, no study has been carried out to disentangle the impact of this fungal infection on the leaf hydraulics, despite the tight relationship between leaf water transport efficiency and plant productivity. The aim of the present work is to measure changes in leaf water transport efficiency (leaf hydraulic conductance, K_L) during the SLS spread. Specifically, we measured the xylem (K_x) and the extra-xylem (Kox) water pathway in leaves at different stage of infection with the aim of identifying the primary mechanism leading to leaf damages and dehydration. Data of K_L, K_x and K_{ox} were correlated with gas exchange, photosynthesis efficiency and several leaf indexes. SLS caused severe leaf xylem blockage and, thus, decreased K_x. The loss of about 50% of K_x led to an impairment of the light-driven K_L enhancement and a relevant stomatal closure, resulting in reduced carbon gain. Moreover, likely because of the low water supply caused by K_x dysfunction, severe damage occurred to the photosynthetic machinery. The role of dysfunction of leaf xylem and outside-xylem water pathway caused by SLS in driving leaf hydraulic impairment, dehydration and death is discussed.

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P.1442 Understanding multigenerational responses of native plants to the allelochemicals of aggressive invader, Alliaria petiolata

Megan A. Brown[1,2], Andrea L. Case[1,2]

1 Kent State University, Kent, USA. 2 Michigan State University, East Lansing, USA.

Decades of ecological research have identified a variety of mechanisms that may facilitate the recruitment, establishment, and success of invasive species. Allelopathy—the excretion of chemical compounds that affect the fitness and/or competitive ability of neighboring plants—is a process associated with some successful invaders. However, little is known about the effect of invasive allelopathic compounds across multiple generations of native plants. Because the parental environment can affect the phenotype of offspring, multigenerational and factorial experiments may provide insights into the temporal dynamics of interactions between native and invasive plant species. We are investigating the interactions between the annual plant *Erythranthe nasuta* (snout nosed monkeyflower; syn. *Mimulus nasutus*, Phrymaceae) and a North American allelopathic invasive species, *Alliaria petiolata* (garlic mustard, Brassicaceae). Fitness-related traits have been measured for two generations of monkeyflower plants grown in the presence or absence of garlic mustard allelochemicals (i.e., whole root exudates and isolated sinigrin). Replicates in the first generation of *Erythranthe* were exposed to water, garlic mustard root exudates, or sinigrin. The offspring of these plants were either exposed to the parental treatment or used as controls. We predict exposure to garlic mustard allelochemicals will negatively affect fitness in native plants, with exposed individuals having less flower production and reproductive biomass (i.e., combined fruit and seed weight) compared to controls. We also predict that successive *Erythranthe* generations exposed to garlic mustard allelochemicals will have increased fitness if their parent was exposed to garlic mustard (i.e., adaptive phenotypic plasticity), compared to offspring of control plants. Preliminary data analysis for the first generation of *Erythranthe* indicates that flower production was influenced by treatment; however, reproductive biomass varied by genotype. Further investigation utilizing more genotypes and generations of *Erythranthe* is ongoing and will help elucidate to what extent garlic mustard allelochemicals affect fitness-related traits within and between generations.

P.1443 Genomic evidence of the introduction source and expansion of a transformer weed, Passiflora foetida s.l., in Australia

Margaret Byrne[1], Tara Hopley[1], Bruce Webber[2], S. Raghu[3], Louise Morin[4]

1 Department of Biodiversity, Conservation and Attractions, Perth, Australia. 2 CSIRO Health and Biosecurity, Perth, Australia. 3 CSIRO Health and Biosecurity, Brisbane, Australia. 4 CSIRO Health and Biosecurity, Canberra, Australia.

Genomic analysis is a valuable tool for management of non-native invasive species, through determining source and number of introductions as well as levels of genetic diversity. *Passiflora foetida sensu lato* is native to central and south America with a current pan-tropical distribution. In northern Australia it is a transformer weed threatening tropical environments. We used whole chloroplast sequencing to investigate the introduction history of *P. foetida* in Australia and ddRAD to identify diversity in the introduced range. Phylogenetic analysis of chloroplast genome data identified three separate genetic lineages of *P. foetida* present in Australia, indicating multiple introductions. These introductions had affinities to samples from Ecuador, Brazil and the Caribbean that represent phylogenetically distinct lineages. These results provide a basis for a more targeted search of the native range of *P. foetida* for candidate biological control agents that have coevolved with this species and are thus better adapted to the lineages present in Australia. Results also indicated that *P. foetida* and other introduced *Passiflora* species cultivated in Australia are in a sperate clade to the *Passiflora* species native to Australia. Analysis of samples from across the introduced range in northern Australia show predominance of one introduced lineage and generally very low genetic diversity within populations, except for a few populations where there is evidence for some crossing between lineages. This knowledge is important for targeting management, including any future deployment of biological control agents.

P.1444 Areca triandra, an introduced palm is colonizing small forest fragments in the biodiverse rain forests of Sri Lanka

Dilini Wickramasinghe[1*], Thilakawansha Chandrathilake[1], Neela de Zoysa[2], Pradeep Rajatewa[3]

1 Department of Forestry and Environmental Science, University of Sri Jayewardenepura, Nugegoda, Sri Lanka. 2 Consultant Botanist, Massachusetts, USA. 3 Environmental Consultants, Education and Rehabilitation Organization, Gampaha, Sri Lanka.

Areca triandra Roxb. Ex Buch-Ham, an ornamental palm introduced to Sri Lanka in 1867, is now naturalized and spreading aggressively in the humid south western Sri Lanka. An island-wide survey showed that this palm is well-established in gardens, vacant areas and forest edges in this part of the country, which is a “biodiversity hotspot” with high endemicity and loss of habitat. A population and reproductive biology study of this palm was carried out in Meethirigala and Yagirala Forest Reserves, in disturbed areas of varying topographical conditions, with heavy colonization, using total of six 20 m × 20 m plots, where stems above 1 m in height were enumerated, and twenty-four 1 m × 1 m plots for sampling ground layer below 1 m in height. *A. triandra* accounted for 57% of mature individuals, 61 % of average crown cover and 69% of seedlings in the ground layer. Vegetative reproduction was high with 66% of individuals occurring in clumps with multiple stems. Sexual reproduction was exceptionally high with prolific production of fruits (140-250 per infructescence, average of 250 - 440 fruits per clump). The fruits with bright red fleshy pericarp attracted a variety of frugivores that aided seed dispersal. Vegetation analysis also indicated that *A. triandra* is displacing native understory species, and suppressing canopy species, some of which are on the National Red List.An evaluation through an Invasiveness assessment protocol concluded that *A. triandra* poses a moderate risk in the wet zone, where 80% of forest cover is in fragments smaller than 500 ha. This study highlights a typical trajectory of an introduced ornamental species that has become invasive over a period of a century due to land use changes and urbanization. It shows the importance of safeguarding biodiverse ecosystems from potentially invasive species through early detection.

P.1445 Floristic and phytosociological composition of weeds present in a wooded paddock of the Mesopotamian grasslands ecoregion Misiones

Maura Isabel Díaz Lezcano[1], Esteban Israel Moreira Rivas[1], Humberto Jorge Sarubbie Orué[1], Pedro Anibal Vera Ojeda[1], Fanni Petrona Ruiz Samudio[1]

1 Universidad Nacional de Asuncion, Facultad de Ciencias Agrarias, San Lorenzo, Paraguay.

To infer the impact of management systems on the dynamics of growth and occupation of communities infesting weeds in agroecosystems, the applicability of phytosociological indices is important. The general objective of the work was to evaluate the floristic and phytosociological composition of weed species and forest species existing in a pasture of the Mesopotamian grasslands ecoregion, in addition to determining the forest and herbaceous biomass of the grassland, characterizing the animal component of the pasture and finally assess the amount of total carbon sequestered in the entire paddock. The experiment was carried out in San Ignacio, Misiones, where different data were collected comparing two areas according to topography, high and low. The methodology to raise weeds was through isolated squares, for the grassland through a frame, for the soil through the cylinders and the forest component through the determination of the dasometric variables. The weeds identified with the greatest ecological weight were: *Chromolaena ivifolia*, *Bulbostylis* sp., *Solanum viarum* and *Sida rhombifolia*. The most important forest species were: *Acrocomia aculeata* and *Patagonula americana*. Through the correlation analysis between all the components, it was deduced that the spontaneous growth of forest species in the wooded pasture increases the potential of the pasture, affirming the existence of a positive correlation.

P.1446 Growth kinetics of an invasive wild cucumber (Echinocystis lobata) and their potential implications for ecosystem biodiversity

Alicja Dołkin-Lewko[1], Urszula Zajączkowska[1]

1 Department of Forest Botany, Institute of Forest Sciences, Warsaw University of Life Sciences, Warsaw, Poland.

In recent years, the surge in invasive alien species has substantially threatened native biodiversity, disrupting ecological processes and habitat structures. Notably, the wild cucumber (*Echinocystis lobata*) has an alarming increase in its occurrence across European countries. This study delves into the kinetics of the growth of wild cucumber, employing innovative methodologies to understand their ecological impact better. Utilizing the time-lapse movie method, we assessed growth parameters under varying support densities (5, 20, or 50 cm step size). Simultaneously, comprehensive analyses of the biometric features of the shoots were conducted. Our findings underscore the rapid growth of wild cucumbers, with growth rates contingent upon the density of available support. At the initial growth stage, nutation movements and stem elongation exhibited lower intensity than in mature plants, suggesting distinct growth phases. This research advances our understanding of invasive plant behavior and introduces innovative methodologies to plant science, offering nuanced insights into growth dynamics. The study's significance lies in its potential to inform targeted management strategies. Recommendations for further research include an in-depth exploration of the climbing mechanisms of wild cucumber and extending studies to examine their growth on natural supports, such as herbaceous plants and trees. These insights hold promise for developing holistic strategies to curb the expansion of invasive species, safeguarding native ecosystems.

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P.1447 Ecological risks of Humulus scandens invasion: a study on potential displacement of Humulus lupulus in Romania

Mioara Dumitraşcu[1], Alina Georgiana Cîşlariu[1], Anca Sârbu[1], Daniela Clara Mihai[1,2]

1 Department of Botany and Microbiology, University of Bucharest, Faculty of Biology, Bucharest, Romania. 2 Faculty of Horticulture, University of Agronomic Sciences and Veterinary Medicine of Bucharest, Bucharest, Romania.

Invasive plant species often possess competitive advantages over native counterparts, even within the same genus, leading to resource competition and displacement or replacement of native flora. Our research aims to investigate the potential of the alien invasive plant species *Humulus scandens* to outcompete the native species *H. lupulus*, in Romania. *Humulus scandens*, originating from East Asia, was introduced to Europe in 1886 as an ornamental plant and is currently listed as an invasive alien species of EU concern. The first mention of this species in Romania dates back to 1943. Both species are dioecious, herbaceous, climbing plants. While *H. lupulus* is a perennial species, *H. scandens* is annual. *H. scandens* thrives in shady and humid environments of riverside, exhibiting adaptability to diverse soil textures. Its competition abilities, such as deep root penetration, rapid growth, and dense stand formation, contribute to its invasiveness. *H. lupulus* prefers temperate regions with a moderate and humid climate, along rivers, streams, thickets, and roadsides. Our approach involves modeling the potential distribution of each species, assessing the extent of range overlap, and investigating their adaptive abilities through anatomical research of the vegetative body. We modeled the potential distribution of *Humulus scandens* and *H. lupulus* using R software with SSDM package. Environmental variables corresponding to the ecological preferences of each species, including climatic, pedological, anthropogenic factors, and water regime, were considered for modeling. Structural analyses on the vegetative body, utilizing cross-sections treated with differential stains, were conducted to study each species' adaptive traits. Results showed robust predictive ability for both models (AUC > 0.85). The overlap in potential distribution between the two species is approximately 21%, with *H. lupulus* exhibiting a broader distribution in Romania. At a structural level, both species exhibit characteristics that contribute to their competitive nature and resilience in varied environmental conditions.

P.1448 Rotenoids from Clitoria fairchildiana R.A.Howard in nanoparticle formulation for control of Aedes aegypti

Maria Aparecida Aride Bertonceli[1], Ivo José Curcino Vieira[1], Francisco José Alves Lemos[1], Letícia Oliveira da Rocha[1], Fábio Lopes Olivares[1], Antônia Elenir Amâncio Oliveira[1], Kátia Valevski Sales Fernandes[1]

1 Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes-RJ, Brazil.

Plant biodiversity harbors treasures that can provide technological advancements in several areas. Phytochemicals are among these riches and constitute 80% of the known 3P.00 natural compounds described so far. The Leguminosae family encompasses crucial species in the Brazilian flora, with significance in food supply, pharmacology, and a high potential for isolating insecticidal compounds. This family stands out as the most important among woody plants, particularly in Amazonian ecosystems. Therefore, the focal species of our study, *Clitoria fairchildiana*, commonly known as "sombreiro," is a legume native to the Amazon whose seeds are refractory to insect predation. A prior study by our group identified two rotenoids from *C. fairchildiana* seeds with larvicidal activity against *Aedes aegypti*, a vector for diseases such as dengue, Zika, and chikungunya. They caused the inhibition of V-ATPase, oxidative stress, and morphological alterations in the larvae. The literature already mentions nanosystems-based botanical insecticides, with the potential to generate lower environmental impacts and better maintenance of compound stability, compared to traditional formulations. In the present work, we encapsulated the rotenoids in nanoparticles and compared their efficacy as an *Aedes aegypti* insecticide with the free rotenoids. The use of chitosan as a coating material in the production of nanocomposites was successful, resulting in uniform nanoparticles. Bioassays indicated that the nanocomposites increased the efficacy of the rotenoids, dropping the LC_{50} from 120 to 90 PPM. Morphological analysis of the larvae suggests that the nanocomposites caused damage to the peritrophic matrix, triggering a cellular immune response, tissue melanization and pseudotumor formation. The results point to the potential of these encapsulated rotenoids from *C. fairchildiana* seeds as an efficient tool for *Aedes aegypti* control, representing a sustainable and effective approach in combating this vector insect.

P.1449 The emerging threat of Campylopus introflexus in Iberian Ecosystems: An analysis of its impact on native moss species

Gabriela Riestra[1], Nagore G. Medina[1,2], Claudia Ortega García[1], Belén Estébanez Pérez[1]

1 Departamento de Biología, Universidad Autónoma de Madrid, Madrid, Spain. 2 Centro de Investigación en Biodiversidad y Cambio Global (CIBC-UAM), Universidad Autónoma de Madrid, Madrid, Spain.

Invasive plants can drastically alter ecosystems, often leading to reduced biodiversity and disrupted ecological balance by outcompeting native species. While invasive mosses can significantly impact ecosystems and diversity there are comparatively few recognized invasive moss species, and their specific ecological impacts remain largely unexplored. In Spain, no bryophyte species is officially recognized as invasive. However, the moss *Campylopus introflexus* (Hedw.) Brid., a moss identified as invasive in several European countries, is not only present in the Iberian Peninsula but also showing an increasing prevalence. In this study, we evaluate experimentally the impact of *Campylopus introflexus* on the growth of three common, native moss species in the Iberian Peninsula: *Syntrichia ruralis (Hedw.)* F. Weber & D. Mohr., *Hypmnum cupressiforme* Hedw. and *Ptychostomum capillare* (Hedw.) Holyoak& N.Pedersen. The experiments were done 1) in vitro, where we analyzed the interaction between shoot tips of *C. introflexus* with spores of the three native species, and 2) in mixed communities growing on seedbeds in a culture chamber, where we tested interactions between adult shoots. We observed an inhibitory effect, both on the development *in vitro* of the protonemata of the three native species analyzed, and on the growth and health status of the adult shoots of *Syntrichia* and *Ptychostomum*. Our results confirm that *C. introflexus* has a significant detrimental effect to the development of these three moss species, affecting both juvenile and adult phases. We are extending this experiments to other native moss species, with diverse ecological affinities, in order to assess the threat level posed by *C. introflexus* to Mediterranean moss communities.

P.1450 Control of pepper plant pathogens, in vitro and in vivo, by a peptide bioinspired from Capsicum annuum defensins

Valdirene M. Gomes[1], Larissa M. Resende[1], Érica O. Mello[1], Anderson Y. S. Fukuji[1], Antônio A. S. Alencar[1], Cláudia P. Sudré[1], Gabriel B. Taveira[1], André O. Carvalho[1], Rosana Rodrigues[1]

1 Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes-RJ, Brazil.

Phytopathogens, notably bacteria and fungi, play a significant role in food production losses. For example, plants of the *Capsicum* genus can suffer up to 30% loss in production and postharvest due to phytopathogens. Given this scenario, research that seeks alternatives to mitigate such losses is essential for guaranteeing well-being and food security. Plant antimicrobial peptides (Plant AMPs) have emerged as molecules of interest, due to their antimicrobial activities. In this study, we investigated the inhibitory effects of the synthetic peptide CaDef2.1G27-K44, bioinspired from *C. annuum* plant natural defensin, against *Colletotrichum scovillei* and *Xanthomonas euvesicatoria* and explored its action mechanism. The minimum bactericidal concentration against *X. euvesicatoria* was 5 µM/mL, while minimum exposure time for the inoculum to lose viability was 3 h. CaDef2.1G27-K44 also caused plasma membrane permeabilization. For the fungus *C. scovillei*, a concentration of 200 μM/mL resulted in 63.9% inhibition growth within 24 h, accompanied by morphological changes in the hyphae. The minimum fungicidal concentration was established at 400 μM/mL, at which point the fungal spores completely died within 18 h. The mechanism of action involves permeabilization of plasma membranes, increase in reactive oxygen species, lipid peroxidation and impairment of mitochondrial functionality. We have also inoculated bacteria into *Capsicum annuum* leaves to evaluate the ability of CaDef2.1G27-K44 to control the development of *X. euvesicatoria in vivo*. This assay conducted under greenhouse conditions, used the bacterial inoculation method by infiltration. Symptoms were assessed through a visual assessment with rating scales, leaf reflectance index and the capture of thermal images of leaves inoculated for 8 days. The results revealed a visible reduction of symptoms in leaves treated with the synthetic peptide. These findings represent promising insights into the potential application of CaDef2.1G27-K44, a bioinspired peptide, in controlling plant pathogens in agriculture.

P.1451 Structural response of Schinus areira leaf to gall inducer insect Calophya schini (Hemiptera: Phylloidea)

Lidia González-Atabales [1], Paulette I. Naulin[1]

1 Laboratorio Biología de Plantas, Universidad de Chile, Santiago de Chile, Chile.

Plant organs are susceptible to external stimuli that result in alterations to the normal patterns of tissue growth and differentiation. Galls are specific plant structures induced by parasitic organisms. The leaves of *Schinus areira* are specific hosts of *Calophya schini* (Hemiptera: Phylloidea), whose main damage is the deformation of leaf tissues and, in the long term, premature defoliation of the tree. This research describes the morphoanatomical foliar response of *S. areira* to the induction by *C. schini*. Leaves and shoots from 12 individuals were collected over a 4-week period during the budding season. Observations were conducted through optical microphotography of fresh, permanent, and SEM samples. In the phenology of interaction, it is observed that *C. schini* eggs are deposited on tender shoots, and first-instar nymphs settle at the beginning of leaf deployment, developing their nymphal stages in parallel with leaf development. Conical galls are formed on both the adaxial and abaxial parts of the leaflets, where chlorosis conditions are observed in proximal areas and in the rachis, even showing deviation of the growth axis. Gall density per leaflet is 2.5 per cm2 and average ratio between the affected area of the proximal part of the gall and the leaf area is 9%. The leaf responds to the nymph by developing hyperplastic parenchymal tissue on the proximal surface and atrophy of tissue on the distal surface of the gall. There is also an increase in the accumulation of tannins. Young tissues are more sensitive to insect stimuli. The growth patterns of the leaf are disrupted from the early development stages. Functional differentiation of tissues is affected due to insufficient chlorophyll in the affected areas. Effective leaf area reduction could result in a decline in photosynthesis.

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P.1452 Invasive alien plant Ageratina adenophora rhizosphere dynamics in the oak and pine-dominated forests in Central Himalaya, India

Priya Hansda[1], Shailendra Kumar[1], Satish C. Garkoti[1]

1 Jawaharlal Nehru University, New Delhi, India.

Biological invasion has emerged as one of the most severe environmental and socio-economic problems and has increased drastically over the decades. This study focuses on understanding the rhizosphere dynamics of invasive shrub species *Ageratina adenophora* in the banj-oak (*Quercus leucotrichophora*) and chir-pine (*Pinus roxburghii*) forests in the Central Himalayan region of Almora district, Uttarakhand, India. The rhizosphere soil (RS) samples were collected from two shrub species, i.e., *Ageratina adenophora* (invasive alien shrub) and *Rubus ellipticus* (native medicinal shrub). Soil that strictly adhered to the roots was considered RS. Soil physical and bio-chemical properties namely, soil moisture (SM), soil organic carbon (SOC), soil available phosphorus (AP), soil total nitrogen (TN), and soil microbial biomass carbon (MBC) were analyzed.

One-way ANOVA was used to test the significant differences in soil properties between the two forests that were dominated by different vegetation and between the native and invasive shrub species. Our results indicated that the RS of *Ageratina adenophora* had significantly higher (*p* < P.5) SM, SOC, AP, TN, and MBC in the banj oak-dominated forest than RS of *Ageratina adenophora* in the chir pine-dominated forest. In the Banj oak forest, the RS of *Ageratina adenophora* had significantly (*p* < P.5) higher SOC, AP, TN, and MBC compared to the RS of native *Rubus ellipticus*. However, in the chir pine forest, SOC and TN did not vary significantly between the RS of the native and invasive shrubs. Our findings suggested that in comparison to the chir-pine forest, the banj oak forest's microclimatic conditions facilitate the successful invasion of *Ageratina adenophora.*

P.1453 Biological patterns in the global invasion of the pampas grass (Cortaderia selloana)

Ainhoa Hernández-García[1], Adrián Lázaro-Lobo[1], Clara Espinosa del Alba[1], Eduardo Fernández-Pascual[1], Víctor González-García[1], Borja Jiménez-Alfaro[1]

1 Biodiversity Research Institute IMIB (Univ.Oviedo-CSIC-Princ.Asturias), Mieres, Spain.

Humans have always dispersed plant species beyond their natural ranges but, in the last centuries, some of these species have adapted so well to novel environments that they have changed dramatically the composition and structure of natural ecosystems. We present a global collaborative project focused on the regenerative patterns of the pampas grass (*Cortaderia selloana*, Poaceae), one of the most ecologically impact ful invasive plants globally, causing strong effects on regional ecosystems and economies. In collaboration with 25 researchers from five continents, we sampled populations in the native (South America) and invaded (North America, Europe, South Africa, Australia, and New Zealand) regions to evaluate the environmental requirements necessary for germination and establishment of the species. The global samples will be used to evaluate the genetic differentiation among populations and to investigate ecological adaptations and past pathways of introduction. In addition, we investigated the impact of local natural enemies of the species, and the extent and potential of biological control agents in different continents. By combining ecological and genetic methods, our study provides comprehensive insights to understand the mechanisms underlying the biological invasion of *Cortaderia selloana* at the global scale, which will help managers to prevent further spread of this globally invasive plant. This study has been supported by the National Geographic Explorer grants to generate and disseminate biological information on the problem of global plant invasions.

P.1454 Ecological characterization of two dominant plant communities within Bidention tripartitae in the Ramsar sites of the SE Central Europe

Vera Stanković [1,*], Nevena Kuzmanović [2], Eva Kabaš [2], Snežana Vukojičić [2], Dmitar Lakušić[2], Slobodan Jovanović [2,†]

*1 Institute of Criminological and Sociological Research, Belgrade, Republic of Serbia. 2 University of Belgrade, Faculty of Biology, Institute of Botany and Botanical Garden "Jevremovac", Belgrade, Republic of Serbia. *vera.batanjski@gmail.com.*

Wetlands are very fragile and endangered worldwide, and they are particularly susceptible to biological invasions. Having this background, we carried out surveys in the Ramsar sites in SE Central Europe (Southeastern part of the Pannonian Plain) to assess the presence of herbaceous invasive species in specific habitat types. Phytocenological relevés were made in the period 2011-2015 on the vegetation of tall-growing, annual wetland herbs (all. *Bidention tripartitae* Nordhagen ex Klika et Hadač 1944). The matrix for analyzes consisted of 119 relevés and 261 plant taxa. The concept of dominant and diagnostic species was used to define groups and Borhidi's ecological indices for the ecological characterization of the studied stands. Two groups of releves were identified in the analyzed stands, informally named after the dominant species: *Alisma plantago-aquatica - Aster lanceolatus* and *Mentha aquatica - Bidens frondosa* community types. The dominance of neophytes in this alliance in the surveyed Ramsar sites is due to anthropogenic influences, with *Aster lanceolatus* Willd. and *Bidens frondosa* L. being among the most common invasive herbaceous plants recorded. *Mentha aquatic-Bidens frondosa* community was recorded in Zasavica and Obedska Bara. It is represented with 13 relevés, with the total cover 80-100%, and the presence of nine invasive species in these stands (15.24% of the total number of recorded species). *Alisma plantago-aquatica-Aster lanceolatus* community was recorded in Ludasko Lake, Koviljsko-Petrovaradinski Rit, Zasavica and Obedska bara. It is represented with 31 relevés, the total cover 98%, and the presence of seventeen invasive species in these stands (14.53% of the total number of recorded species). *Mentha aquatic-Bidens frondosa* comm. was positively correlated with the soil moisture, while *Alisma plantago-aquatica-Aster lanceolatus* comm. with nutrients.

P.1455 Invasion pathways in Colombian highlands

David E. Lara[1], Magda R. Escobar[1], Juan E. Carvajal[1], Juan D. González[1].

1 Grupo de Biodiversidad y Conservación, Universidad Pedagógica y Tecnológica de Colombia, Tunja, Colombia.

Biological invasions present a significant challenge to nature conservation. Invasive species jeopardise the stability of ecosystems in natural environments and are a major cause of the worldwide extinction of native species. They can also have a negative impact on social, cultural, and economic dimensions. Invasive species are primarily transported by human activities, whether intentional or accidental, for industrial, food, ornamental, or economic purposes. Although progress has been made in characterising invasion pathways, there are still gaps, particularly in tropical mountain regions. This study identifies the most common invasive plant species in high altitude ecosystems in Colombia, as well as their main routes of introduction, spread and distribution. A systematic search of specialised databases such as the "Catálogo de plantas y líquenes de Colombia", COL, JBB, UDBC, Jstor, SIB, GBIF and Tropicos.org was used to collect and compile information on pathways. Out of the fifty-five invasive species reported for Colombia, nineteen were found above 2,800 m a.s.l. 40% of these species are widely recognised as highly invasive and have a significant impact. The most frequent invasive pathways were ornamental, reforestation and unintentional. It is suggested that a combination of airborne dispersal and intentional cultivation for harvest provides the greatest potential for invasion, taking into account both actual distribution and pathways. The information on pathways can collectively improve environmental management policies to prevent the spread of invasive and alien plants in natural environments in Colombia.

P.1456 iCONNECT - integrative CONyza NEtwork for Contemporary Trait evolution

Rosche C. B.[1,2], Lucas M. S.[1,2], Nagy D. U.[2], Callaway R.[3], Lekberg Y.[3,4], Durka W.[5,1], van Dam N.[1,6], Barratt C. D.[1], Onstein R. E.[1,7], Shah M. A.[8], Uthe H.[1,6], Döll S.[1,6], Pöschl-Grau Y.[1,6], Weinhold A.[1,6], Hensen I.[1,2]

1 German Centre for Integrative Biodiversity Research, Halle-Jena-Leipzig, Germany. 2 Martin Luther University Halle-Wittenberg, Germany. 3 University of Montana Missoula, USA. 4 MPG Ranch Missoula, USA. 5 Helmholtz Center for Environmental Research – UFZ, Germany. 6 Friedrich Schiller University Jena, Germany. 7 University of Leipzig, Germany. 8 University of Kashmir, India.

Rapid evolution is a common occurrence in plant invasions. However, our understanding of rapid evolution is limited because most studies underestimate among-population variation (APV) within native and non-native ranges and/or do not disentangle how population histories drive APV. Furthermore, integrative frameworks of APV-focused research are lacking but could help identifying molecular mechanisms of rapid evolution. We here present the integrative network iCONNECT. iCONNECT is an open collaboration of researchers who contribute to the sampling of *Conyza canadensis* populations across the Northern hemisphere and researchers who investigate APV in their particular research field using these sampled populations. The first study within the iCONNECT framework will be a greenhouse experiment in which 120 native and 150 non-native *C. canadensis* populations will face a competition × drought treatment combination. For the study populations, we collected field data as proxies for population history in terms of plant competitive regime, drought regime and fungal interactions in the rhizosphere. The samples will be analyzed in a coherent manner for 1) phenotypic APV (competitive ability under dry vs. mesic conditions), 2) eco-metabolomic APV (mass spectrometry analyses of root exudates), 3) APV in root-fungal interactions (amplicon sequencing), and 4) population genomics (ddRADseq). Our experiments will shed light on the principles of rapid evolution by investigating how population history dictates biotic interactions across large spatio-environmental scales. Moreover, studying correlations between the investigated APVs may unravel how belowground mechanisms determine competitive ability and may identify metabolites and genomic regions that are associated with competitive ability and root-fungi interactions.

P.1457 Test of specificity in signalling between potato plants in response to infection by Fusarium solani and Phytophthora infestans

Lucía Martín-Cacheda[1], Gregory Röder[2], Luis Abdala-Roberts[3], Xoaquín Moreira[1]

1 Misión Biológica de Galicia (CSIC), Pontevedra, Galicia, Spain. 2 Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland. 3 Universidad Autónoma de Yucatán, Mérida, Yucatán, México.

Plant-plant signalling via volatile organic compounds (VOCs) has been widely studied in response to herbivore attack, but effects of pathogen infection and its specificity based on pathogen identity and how these shapes the outcome of VOC-mediated pathogen interactions has received little attention. To address this gap, we carried out a greenhouse experiment with two fungal pathogens (*Fusarium solani* and *Phytophthora infestans*) to test for specificity in VOC induction and signalling between potato plants (*Solanum tuberosum*) determining plant-mediated pathogen interactions. For this, we paired potato plants in plastic cages, one acting as VOC emitter and the other as a receiver, and subjected emitters to one of the following treatments: no infection (control), infected by *F. solani*, or infected by *P. infestans*. We measured total emission and composition of VOCs released by emitter plants to test for pathogen-specificity in VOC induction, and then conducted a bioassay of pathogen infection (i.e., percentage of damaged leaf area) on receivers by subjecting half of the plants of each emitter treatment to *F. solani* infection and the other half to *P. infestans* infection. In doing so, we aimed to test for pathogen specificity in plant VOC signalling effects and its consequences for plant-mediated pathogen interactions. We found no evidence of quantitative (total production) or qualitative (compound composition) changes in volatile organic compound emissions due to infection by *F. solani* or *P. infestans.* Likewise, infection treatment on emitters had no significant effect on pathogen infection levels on receiver plants, suggesting a lack of signalling or pathogen-based specificity in such effects. Overall, this study builds towards a better understanding of the ecological consequences of pathogen specificity in VOC-mediated plant-plant signalling shaping the outcome of plant-pathogen multi-species interactions.

P.1458 Effects of herbivore density and damage pattern on volatile emissions and their consequences for plant signalling in wild cotton

Lucía Martín-Cacheda[1], Yeyson Briones-May[2], Carlos Bustos-Segura[3], Ted C. J. Turlings[3], Víctor Hugo Ramírez-Delgado[2], and Luis Abdala-Roberts[2]

1 Misión Biológica de Galicia (CSIC), Pontevedra, Galicia, Spain. 2 Universidad Autónoma de Yucatán, Mérida, Yucatán, México. 3 Fundamental and Applied Research in Chemical Ecology, Institute of Biology, University of Neuchâtel, Neuchâtel, Switzerland.

Plant-plant signalling via volatile organic compounds (VOCs) has been extensively studied, but its contingency on herbivory amount and its within-plant distribution remains poorly or no studied. We tested whether signalling between cotton (*Gossypium hirsutum*) plants in response to herbivory by the specialist caterpillar *Alabama argillacea* was affected by different levels of herbivore density and within-plant damage distribution. We placed three plants in mesh cages, where one plant acted as a VOC emitter and the other two as receivers. We subjected emitters to one of the following treatments: control (no larvae), low density (one larva on one leaf), high concentrated density (four larvae, two on each of two leaves), and high dispersed density (four larvae, one on each of four leaves). Two days later, we collected emitter VOCs to test for treatment effects on VOC emissions and placed *A. argillacea* larvae on receivers to test for signalling effects on leaf consumption (i.e., induced resistance). High density significantly increased total VOC emissions and changed VOC composition, whereas low density did not result in a significant effect on total emissions. However, there was no difference in total VOCs emissions between high dispersed vs. concentrated damage treatments. In turn, receivers exposed to damaged emitters showed greater resistance to herbivory relative to those exposed to control emitters, but this signalling effect was no contingent on either the amount or distribution of herbivory. Overall, these results suggest no evidence that the distribution of herbivore damage affects VOC induction and provide a better understanding of the effects of herbivory variability on plant-plant signalling.

P.1459 Invasive ability and ecosystems susceptible to the spread of Asclepias syriaca in Romania

Daniela Clara Mihai[1,2], Alina Georgiana Cîşlariu[2], Mioara Dumitraşcu[2], Mihaela Ioana Georgescu[1], Florin Toma[1]

1 Faculty of Horticulture, University of Agronomic Sciences and Veterinary Medicine of Bucharest, Bucharest, Romania. 2 Department of Botany and Microbiology, Faculty of Biology, University of Bucharest, Bucharest, Romania.

Numerous ornamental plant species introduced to Europe have become invasive. *Asclepias syriaca* L. is a notable example and the focal point of our research. Originating from North America, it was introduced to Europe in 1629 and is currently listed as an invasive alien species of concern under EU Regulation 1143/2014. In Romania, the species was first reported in 1836. *Asclepias syriaca* displays a high capacity to adapt to different climatic and edaphic conditions. Soil type and physical properties emerge as the key pedological factors influencing its occurrence. In Europe, it mostly inhabits abandoned agricultural lands, wet and dry meadows, road edges, and tree plantations, negatively impacting agriculture. The species exhibits competitive traits such as height, shaded tolerance, vegetative propagation, drought resistance, and allelopathic potential. Modeling the potential distribution of invasive species provides advantages, including early detection and better understanding of ecological requirements. Our study aims to model the potential distribution of *Asclepias syriaca* in Romania, identifying the ecosystems susceptible to its spread, and the anatomical traits ensuring the species' resilience in various environmental conditions. We studied the species' adaptive ability through structural analyses on vegetative organs, using cross-sections treated with differential stains. The potential distribution of *Asclepias syriaca* was modeled using the R software (SSDM package) and environmental variables (bioclimatic, topographic, pedologic factors, and anthropogenic impact) corresponding to the known ecological preferences of the species. The modeling results showed good predictive ability (AUC > 0.85), with the human impact index predominantly influencing *Asclepias syriaca*'s distribution in Romania. According to the SDM, the species overlaps 37% on arable land. The species' structural characteristics highlighted its adaptability to diverse environmental conditions. This study contributes to the understanding of the ecology and adaptive capacity of the species, with significant implications for the managing ecosystems affected by this invasive plant in Romania.

P.1460 Do plant conservation efforts scale up to their pollinators?

Cheyenne Davis[1], Nina Fogel[2,3], Colby Kapp[1], Emily Buerhle[1], Josh Felton[1], Jessica Clones[1], Nicole Miller-Struttmann[1]

1 Department of Natural Sciences and Mathematics, Webster University, St. Louis, USA. 2 Department of Biology, Saint Louis University, St. Louis, USA. 3 Department of Biology, Washington University, St. Louis, USA.

Maintaining biodiversity and ecosystem services in lieu of human-driven environmental change is one of the most pressing challenges of the century. As urbanized landscapes expand, wild organisms must rely on managed greenspaces. However, greenspaces are often not optimized to support biodiversity, resulting in hectares of biodiversity-poor habitats. "Backyard conservation" programs seek to improve biodiversity conservation by encouraging landowners and managers to plant more diverse plant communities, with the assumption that biodiversity of their partners will also increase. Regional factors, such as barriers to movement, may interfere with those efforts, leading to slower gains than expected. In collaboration with 200+ volunteers enrolled in the Shutterbee Citizen Science Program in St. Louis, MO, USA, we tested whether urbanization influences the relationship between plant and bee diversity in residential and community gardens. Shutterbee participants conducted biweekly photo-surveys in a greenspace of their choosing and uploaded their observations to iNaturalist. We used model comparison to select the best performing model including the following factors: urbanization, flower richness, flower density, and interactions among the factors. As predicted, rarified bee richness increased with plant richness. However, in more urban landscapes, bee richness was high regardless of flower richness; whereas in the suburbs and exurbs, bee richness increased with plant richness. Network properties (i.e., nestedness and modularity), on the other hand, were more strongly affected by flower richness. While urbanization had a significant moderating effect, it had very low explanatory power (R^2 = P.12 and R^2 = P.46, respectively). Our results suggest increasing plant diversity in residential gardens supports pollinator diversity and establishes more complex, stable communities. While the socio-environmental matrix surrounding a greenspace altered bee diversity, it did not affect community structure and dynamics, suggesting that local factors are more important than regional factors for supporting bee diversity in urban greenspaces.

P.1461 Nitrogen transfer between plant species in natural and agro-ecosystems

Alicia Montesinos Navarro[1], Diego Intringliolo[1]

1 Centro de Investigaciones sobre Desertificación, Moncada, Valencia, Spain.

Here we explore the often-overlooked phenomenon of nitrogen transfer within plant communities aiming to uncover the underlying patterns and driving forces that have the potential to influence both natural ecosystems and agro-ecosystems. While phenological segregation has traditionally been seen as a coexistence strategy, we propose an alternative mechanism: the transfer of nitrogen from low nitrogen-demand plants to high nitrogen-demand plants, resulting in reciprocal benefits over time instead of competition avoidance. This process can reduce water dependency and prevent nitrogen loss through leaching, influencing plant communities and ecosystem functioning. Concurrently, we use broad ecological knowledge of plant-plant interactions in natural semi-arid plant communities to address sustainability challenges in horticulture, designing optimal intercropping systems to reduce water and nitrogen-based fertilizer use in agro-ecosystems.

P.1462 Invasive neo-species and how to name them

Daniel Montesinos[1]

1 Australian Tropical Herbarium, Cairns, Queensland, Australia. 2 College of Science and Engineering, James Cook University, Cairns, Queensland, Australia. 3 Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal.

Range-expansion and speciation are not new to life on Earth, but they have been scarcely observed contemporarily and, likely, never over several continents simultaneously. Evidence of incipient reproductive isolation between native and non-native regions of some invasive alien species indicates that invasive speciation is closer than we expected. Some neo-allopatric populations are likely to qualify as distinguishable subspecies already. Given their trajectory, whether they will become new species is not an if, but a when. I present two decision tables to help to (1) assess the coining of new invasive species or subspecies with the current taxonomical approach or (2), introduce the term “neo” to name invasive neo-species resulting from synchronous allopatric speciation from a single, known, living ancestor. This latter case can be exemplified with the hypothetical names: “*Ginkgo biloba* neo *americana*”, “*G. biloba* neo *europea*”, etc.

P.1464 Allelopathic effect of Hakea sericea and Acacia dealbata on native Mediterranean scrub species

Laura Nogales Gómez[1], Ismael Montero Fernández[1], Juan Carlos Alías Gallego[1], José Blanco-Salas[1], Natividad Chaves Lobón[1]

1 Departament of Plant Biology, Ecology and Earth Sciences, Faculty of Science, Universidad de Extremadura, Badajoz, Spain.

Biological invasion plays fundamental role for ecosystem dysfunctions through loss of biodiversity across the world. Biochemical interactions among plants have revived interest in invasion ecology, including tests of the “novel weapons hypothesis” (NWH): some invasive species may gain disproportionate competitive advantages through the effects of novel secondary metabolites to which species natives have not had the opportunity to adapt. *Acacia dealbata* is a species classified as invasive in the Iberian Peninsula and *Hakea sericea* is a species classified as invasive in Portugal. In this work, the allelopathic effect of these species on species native to Mediterranean ecosystems and that share habitat with these species has been quantified. The selected target species have been *Lavandula stoechas* and *Cistus salviifolius*. Tests have been carried out with aqueous extracts (100 g L^{-1}, 50 g L^{-1} and 25 g L^{-1}) and they have been maintained in a culture chamber (20ºC 16h-light/8h dark) for 20 days. Both the aqueous extracts from *A. dealbata* and *H. sericea* strongly inhibit the germination of both species at all concentrations tested, with *A. dealbata* being the one that exerts the greatest negative effect. These results show that *H. sericea* and *A. dealbata* can very negatively affect the ecosystems they invade, and the allelopathy exerted by these species may be the interaction that causes the displacement of native species from these ecosystems.

P.1465 Seasonal allelopathic potential of Hakea sericea, Acacia dealbata and Parkinsonia aculeata

Laura Nogales Gómez[1], Ismael Montero Fernández[1], Juan Carlos Alías Gallego[1], José Blanco-Salas[1], Natividad Chaves Lobón[1]

1 Departament of Plant Biology, Ecology and Earth Sciences, Faculty of Science, Universidad de Extremadura, Badajoz, Spain.

Invasive exotic plant species are considered dangerous to both global biodiversity and ecosystem dynamics and livelihoods. Among the invasive plants in the Iberian Peninsula is *Hakea sericea*, whose genus comes from Australia and is made up of 250 species, *Acacia dealbata*, which is typical of tropical and subtropical regions such as Australia, Tasmania, Asia, Africa and America and *Parkinsonia aculeata*, native to the semi-desert regions of America and Africa and introduced as an ornamental. One of the mechanisms attributed to the invasion capacity is allelopathy, an interaction mediated by compounds from the secondary metabolism of these species. In turn, the allelopathic activity of a species depends on the concentration of compounds present in its tissues and is therefore dependent on the season, which implies the need to study the allelopathic activity of a species in different seasons. In this context we tested the allelopathic potentials of three non-natives plant species in different seasons. Samples of leaves of each species have been collected and aqueous solutions have been prepared (1/10 w/v). The tests were carried out in Petri dishes (25 seed of *L. sativa* seeds per plate, 4 plates per concentration: 1, 1/2 1/4, 1/6), which were maintained for 10 days in a germination chamber at 20ºC 16h-light/8h dark. Germination is quantified daily, and after 10 days, the size of the roots and cotyledons of the seedlings are measured. The results obtained show that the aqueous extracts of the three species studied present allelopathic activity, but this effect differs between the species and between the seasons studied. The order established for the species from highest to lowest allelopathic activity is *P. aculeata>A. dealbata>H. sericea* in the samples collected in spring, and *P. aculeata=A. dealbata>H. sericea* for the samples collected in summer.

P.1463 Highly hazardous pesticides: the impacts of their use in aquatic ecosystems

Debbie Muir[1]

1 Department of Forestry, Fisheries and the Environment, SA, Cape Town, South Africa.

Highly hazardous pesticides (HHP's) are used widely in South Africa. There has been a global move through SAICM and other organizations to ban, phase out and/or restrict the use of HHP's. The Global Harmonization System of Classification and Labelling of Chemicals (GHS) identifies the hazards and exposure risks of a number of pesticides and classifies them into 10 hazard criteria (HC), where the first HC is the Multilateral Environmental Conventions (MEA's), the 2nd HC is Acute Toxicity and the following 4 HC are chronic health toxicity criteria. HC 7 and 8 deal with environmental toxicity and HC 9 is dioxins and HC 10, heavy metals. The identification and classification of HHP's are done using 8 criteria developed by the JMPM of the FAO/WHO. The HC that will be concentrated on are HC 7 and HC 8 as the emphasis of this presentation is regarding environmental toxicity and exposure and their impacts on aquatic life and ecosystem services. HHP's currently being used that impact on aquatic life and wetlands will be discussed together with their impacts on the ecosystem functioning. Human health impacts and exposure risks of these HHP's will be touched on and these impacts can either be direct (operator exposure) or indirect (fishing, drinking water). This is just one example of how pesticides negatively impact on biodiversity and ecosystems and have the ability to alter ecosystems. Pesticides, biodiversity and climate are intrinsically linked. Lastly, recommendations will be discussed on phase-out options for these pesticides, and alternatives to these HHP's will be given using the Hierarch of Control and Precautionary Principles, and mitigation measures on how to ensure compliance to the Paris Agreement targets with regards to the potential increase in temperatures and HHP's.

P.1466 Deciphering the key to the success of invasive Asteraceae in mainland Spain

Beñat Orbea[1,2*], Jordi López-Pujol[1], Neus Nualart[1], Juan Antonio Campos[3]

1 Institut Botànic de Barcelona, CSIC-CMCNB, Barcelona, Spain. 2 Department of Animal Biology, Plant Biology and Ecology, Faculty of Biosciences, Universitat Autònoma de Barcelona UAB, Bellaterra, Spain. 3 Department of Plant Biology and Ecology, University of the Basque Country UPV/EHU, Bilbao, Spain.

Biological invasions are one of the main challenges facing biodiversity conservation, as they are one of the major causes of species extinctions. Spain is becoming one of the areas of the planet with the greatest rates of entry and expansion of invasive alien species (IAS), which is likely the result of the country's high rate of habitat destruction, its large diversity of climates and landscapes, and its key role as a global commercial/transportation hub and a leading touristic destination. The key to the success of alien species (AS) goes through one of Darwin's two hypotheses: the "pre-adaptation" hypothesis or the "naturalization" hypothesis; sometimes both coexisting or varying depending on the geographic scale and scope of study. On the one hand, the pre-adaptation hypothesis argues that AS closely related to native species would be more likely to become established because they might share adaptations to local environmental conditions. On the other hand, the naturalization hypothesis maintains that phylogenetically more distantly related AS could succeed by establishing in empty ecological niches. Both hypotheses assume a correlation between phylogenetic distance and ecological distance. This project aims to determine the ecological and evolutionary dynamics that led to the success (naturalization or invasion) of AS in peninsular Spain, thus being able to solve the "Darwin's naturalization enigma" at a regional scale. Moreover, the project will analyse the risk (e.g., through implementing IUCN's EICAT) but also the effect of the presence of AS on native biodiversity, particularly on the composition, diversity and structure of plant communities. The focus will be on the subfamily Asteroideae, the one with the highest number of AS within the Asteraceae family, and the most diverse in Spain. The results of this study may ultimately lead to improved knowledge and management of IAS.

P.1466 Genomic insights into invasion: a comparative transcriptomic study of Thunbergia (Acanthaceae) species

David Ruiz-Londoño[1], Pablo A Pérez-Mesa[2], Harold Suárez-Baron[1]

1 Pontificia Universidad Javeriana Cali, Cali, Colombia. 2 Universidad Nacional de Colombia, Bogotá, Colombia.

The rise in the dispersal rate of invasive species, propelled by globalization and climate change, has resulted in economic, environmental, and health impacts. Invasive species induce substantial changes in ecosystems, influencing the structure and composition of native species and setting off cascade effects. Furthermore, they can adversely affect agriculture and ecosystem services. Despite the consideration of physiological and ecological aspects, it is imperative to provide further attention to the genetic component of these species. *Thunbergia alata* is a climbing species native from Africa, which has been widely distributed mostly in tropical countries for its ornamental characteristics. However, this species is considered invasive, affecting native ecosystems, especially in Latin America. This project proposes a comparative transcriptomic study between *T. alata* and *Thunbergia grandiflora*, which, despite sharing similarities in morphology and habit, exhibit considerable ecological differences, such as niche requirements, adaptability, and invasive capacity. This makes them a suitable choice to identify and understand the genetic mechanisms underlying the invasive and adaptive traits of *T. alata* in the Valle del Cauca region of Colombia. To achieve this, RNA extracted from both vegetative and reproductive tissues for both species at two different developmental stages was sequenced using the Illumina NovaSeq PE150 system. The transcriptomes were assembled using Trinity, to identify differentially expressed genes associated with invasive traits. The candidate from *T. alata*, may explain their dispersal mechanisms, rapid growth, or accelerated flowering time when compared with *T. grandiflora*. Additionally, a targeted search for genes from the *expansin*, *HSP*, and *PR* families was performed, as they are reported in the literature as possible promoters of invasiveness. This approach would assist in understanding the genetic and molecular mechanisms underlying the traits of invasiveness, and it can help develop more effective strategies for controlling and managing this invasive species.

P.1468 Pteridum aquilinum invasion in cloud forest areas in Oaxaca and the possible rehabilitation by means of assisted planting

Miriam Ramírez Velasco[1], Rafael F. del Castillo[1], Raúl Rivera García[1]

1 Instituto Politécnico Nacional, Oaxaca, México.

The bracken fern, *Pteridium aquilinum* (L.) Kuhn (Dennstaedtiaceae) is the fifth-worst invasive species in the world. The invasion by this fern is evident in fallows previously cultivated by maize and other companion plants in cloud forest areas of southern Mexico. Because of such invasion, the fallows become disabled for further cultivation or natural regeneration of the original forest. The invasion by this fern is evident even in recently harvested lands, indicating the aggressiveness of this plant. We conducted a historical survey of this problem in the Agencia La Luz, Sierra Norte, in southern Mexico. We found that fern invasion is relatively recent (about 70 years) and has been increased. As a control method, the invaded lands are commonly burned and transformed into grasslands for cattle. This practice contributes to biodiversity losses and reduced ecosystem services, such as water capture and carbon sequestering. Very short fallow periods (3-7 years after harvesting) seem to favor the invasion by impeding tree species colonization, which canopy could inhibit the development of this fern. We find support for this hypothesis in a fallow land on which native N-fixing alder trees (*Alnus acuminata* Kunth, Betulaceae, Palo de Águila) were planted. After eight years, the bolt and height of the trees significantly increased. Furthermore, the alders inhibited the development of *Pteridium* and favored the establishment of other native species such as *Hedyosmum mexicanum* C. Cordem, Chloranthaceae; *Saurauia scabrida* Hemsl, Actinidaceae; *Liquidambar styraciflua* L, Altingiaceae, and *Clethra* sp, Clethraceae. The organic matter from tree debris has favored the development of saprobic fungi, and the soil displays a significant litter development. We conclude that the bracken fern invasion results from very short fallows and can be controlled with assisted native tree planting, such as alders.

P.1469 Pollination biology of Impatiens capensis Meerb. in non-native range

Agnieszka Rewicz[1], René Monzalvo[2], Monika Myśliwy[3], Grzegorz Tończyk[4], Andrea Desiderato[4], Saroj Ruchisansakun[5], Tomasz Rewicz[4]

1 Department of Geobotany and Plant Ecology, University of Lodz, Lodz, Poland. 2 Molecular Systematics Laboratory, Autonomous University of Hidalgo State, Hidalgo, Mexico. 3 University of Szczecin, Institute of Marine and Environmental Sciences, Szczecin, Poland. 4 Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Lodz, Poland. 5 Department of Plant Science, Mahidol University, Bangkok, Thailand.

Pollination biology in the widespread species *Impatiens capensis* Meerb. has only been studied in America, specifically in zones of the U.S.A and Canada. In this study, we investigated the pollination biology of *I. capensis* using an integrative approach identification using morphological and molecular tools from four populations of Northwest Poland. We also determined and compared the functional traits of pollinators from native and introduced study site species. Visitors were identified using standard morphological keys, including identifying and classifying insect mouthparts. Molecular identification was carried out using mitochondrial DNA's cytochrome oxidase subunit I (COI). We morphologically identified 20 species of visitors, principally pollinators and, with fewer records of nectar robbers. DNA barcoding of 59 individuals proved the identification of 18 species (also 18 BINs). The frequency of pollinator species was primarily represented by the representatives of Diptera (50%) and Hymenoptera (37.5%). The morphological traits, such as the chewing and sucking mouthparts, small and big body height, and robber and pollinator behavior explained mainly the native and introduced visitors' arrangements that allow pollination success. However, further investigation of other causalities in pollination success and understanding the diversity of pollinators in outer native ranges, are necessary to understand the process comprehensively.

P.1470 Analysis of buoyancy in Impatiens spp. seeds with varying levels of invasiveness: the influence of shape and structure of seed.

Agnieszka Rewicz[1], Monika Myśliwy[2], Justyna Polit[1]

1 University of Lodz, Lodz, Poland. 2 University of Szczecin, Szczecin, Poland.

One of the key factors determining the success of invasive species is their ability to disperse seeds, enabling them to colonize diverse habitats and effectively compete with native species. Understanding the mechanisms contributing to the colonization success of invasive species is crucial for predicting future expansion patterns and ranges. Additionally, it allows for the development of optimal strategies to prevent their introduction, as well as control and management of their populations and impacts on native species. Experimental investigations were conducted on seeds of three *Impatiens* species, differing in invasiveness levels: the American *Impatiens capensis*, the Asian *Impatiens parviflora*, and the European native *Impatiens noli-tangere*. It was hypothesized that differences in competitiveness stem from variations in the seeds' ability to float on water, a capability dependent on seed shape and structure. The question concerns the time for which the seeds of the studied species can float on water and, consequently, reach distant territories and colonize them. To assess the hydrochoric dispersal capacity of seeds, their buoyancy and time of floating on the water surface were examined. Additionally, the influence of seed shape, mass, and seed coat structure on seed buoyancy was analyzed. The results indicated that seeds of *I. capensis* remained buoyant on the water surface for the longest duration, strongly correlated with the shape and structure of the seed coat in this species. We suggest that the presence of ridges on the seed coat of I. capensis, serving as structures increasing buoyancy, is of significant importance. A shorter duration of floating was observed for seeds of *I. parviflora*, and the shortest for *I. noli-tangere*. This suggests that the native species - *I. noli-tangere* is least effective in colonizing and competing for diverse habitats, especially those distant from existing populations.

P.1471 Unravelling the importance of landscape effects for seed dispersal in restored ecosystems

Jairo Robla[1], Alejandro Rodríguez[1]

1 Estación Biológica de Doñana, Sevilla, Spain.

Anthropogenic activities have led to extensive habitat loss, resulting in fragmented and degraded ecosystems with remnants of natural habitat. This fragmentation, combined with human-induced disturbances, contributes to species loss and the decline of critical ecological functions. Seed dispersal, a fundamental ecological process, significantly shapes plant community dynamics by assisting seed escape from high-mortality areas and enabling colonization of vacant niches. Birds, as key contributors to seed dispersal, act as mobile connectors between diverse habitats. Traditional approaches to understanding seed dispersal focus on local and regional factors, including vegetation cover, fruit availability, and bird abundance. However, the role of landscape characteristics in conditioning seed rain, especially in restored areas, has been overlooked. To fill this gap, we conducted a two-year study, establishing 24 (or 8 in the second year) 50 m-radius plots along the 40 km Guadiamar Green Corridor—a protected and restored landscape within an agricultural matrix and semi-natural habitat gradient. Plots were categorized into low and high-density halves, each equipped with seed traps (20 in high-density, 10 in low-density) to assess seed rain under different woody plant canopies. A comprehensive characterization of plot surroundings and the landscape within a 5 km buffer was also undertaken and several landscape metrics were calculated. We have found that landscape factors significantly influenced seed rain, with plots in complex landscapes, offering diverse resources to birds, receiving higher seed rain than those in simpler areas. Such landscapes could promote bird distribution, mobility, and subsequent seed rain by providing varied food resources and shelter. Additionally, fruit coverage and abundance, alongside traditionally considered factors, played crucial roles in seed rain. This study's consideration of landscape effects underscores the importance of context in restoration projects targeting ecological functions like seed dispersal and open a new line to continue studying these factors in a restoration context.

P.1472 Taking action: promoting biodiversity and environmental sustainability at Marimurtra Botanical Garden

Anna Sans[1], Pere Fraga[1,2], Jordi Fàbregas[1], Bonaventura Torroella[1], Iván Soto[1], Yago Plata [1], Pablo Garcia [1], Íker Muñoz [1], Guillermo Caba [1], Javier Jiménez[1], Antonio Aguilar[1], Sílvia Garriga[1], Enric Barril[1], Gisela Hernández[1], Jaissa Obré[1]

1 Marimurtra Botanical Garden, Fundació Privada Carl Faust, Blanes, Spain. 2 Institut Menorquí d'Estudis, Maó, Spain.

Marimurtra, as a Botanical Garden, living museum and science center, its basic function is to protect and promote the study of Mediterranean biodiversity, especially plants, and with this aim, to conserve and improve Marimurtra, for the benefit of scientific research and dissemination. This review highlights the actions of the botanical garden aimed at improving biodiversity and environmental sustainability. These actions include the efficient use of resources and the reuse of plant residues within the garden itself. Additionally, the practice of composting is emphasized as a measure of organic waste management, along with its use as fertilizer for the same garden, and the abstention from the use of chemicals. Instead, the control of plant pathologies, which can affect the plants grown in the botanical garden, is done by means of natural extracts made from plant species with recognized pesticidal or fortifying properties. This is another way to preserve the health of the ecosystems, maintain the ecological balance and thus contribute to the sustainability of the entire garden. Furthermore, the installation of insect hotels, nest boxes, and bird feeders promotes biodiversity by creating habitats that attract beneficial auxiliary fauna, which can be effective in pest control. Furthermore, the installation of insect hotels, nest boxes, and bird feeders promotes biodiversity by creating habitats that attract beneficial auxiliary fauna, which can be effective in pest control. The botanical garden also commits to the conservation of critical plant collections. Emphasis is placed on the transmission of scientific knowledge through outreach activities, with the aim of raising public awareness about the importance of biodiversity conservation and fostering participation in environmental protection initiatives. This communication highlights the multiple strategies adopted by the botanical garden to promote biodiversity and environmental sustainability, addressing both practical and educational aspects in the context of environmental conservation.

P.1473 Comparative analysis of mitochondrial genomes of invasive weed Mikania micrantha and its indigenous congener Mikania cordata

Zhen Wang[1], Ruonan Wang[1], Yatong Sang[1], Ting Wang[2,3], Wenbo Liao[1], Yingjuan Su[1,3]

1 School of Life Sciences, Sun Yat-sen University, Guangzhou, China. 2 College of Life Sciences, South China Agricultural University, Guangzhou, China. 3 Research Institute of Sun Yat-sen University in Shenzhen, Shenzhen, China.

Mikania micrantha and *M. cordata* are two very specific species in China. The former is one of the top 100 worst invasive species in the world, whereas the latter is harmless to native plants or environment as an indigenous species in China. They form an excellent congener couple for comparative investigation to understand the invasion mechanisms of exotic weed. In this study, we assembled and annotated the two species mitogenome based on Illumina and PacBio data and compared their characteristic differences. The complete mitochondria genome of the *M. micrantha* is a double-stranded DNA with length of 336,566 bp, while the mitochondrial genome of *M. cordata* is branched and assembled into two small circular molecules and six linear molecules, with total length of 335,460 bp. Compared to *M. cordata*, *M. micrantha* has less mitochondrial protein coding genes (PCGs), SSRs, tandem repeats, and dispersed repeats. They showed the high similar feature in codon usage. *Mikania micrantha* and *M. cordata* contained the same number of RNA editing sites in *atp*4, *nad*3, *nad*4L, *nad*5 and *rps*4. The nucleotide diversity of the 22 PCGs was highly variable among selected eight species. Longer synteny sequences with high similarity were detected between *M. micrantha* and *M. cordata* than between *M. micrantha* or *M. cordata* and other seven plants. Phylogenetic inference showed that *M. micrantha* is sister to *M. cordata*. Transferred length between chloroplast and mitochondrion genome of *M. micrantha* and *M. cordata* is 13,339 bp and 12,355 bp, accounting for 3.96% and 3.68% of the total mitogenome, respectively. The study revealed the structure and function of the *M. micrantha* mitogenome and laid a solid foundation for investigating deeper into the invasion mechanism of *M. micrantha*.

P.1474 New insights into adaptive evolution and invasion dynamics of Mikania micrantha based on comparative genomics and resequencing

Ruonan Wang[1], Zhen Wang[1], Xiaoxian Ruan[1], Yang Peng[1], Yatong Sang[1], Wenbo Liao[1], Ting Wang[2,3], Yingjuan Su[1,2]

1 School of Life Sciences, Sun Yat-sen University, Guangzhou, China. 2 Research Institute of Sun Yat-sen University in Shenzhen, Shenzhen, China. 3 College of Life Sciences, South China Agricultural University, Guangzhou, China.

Mikania micrantha H.B.K. (Asteraceae), commonly known as the 'mile-a-minute' weed, is an aggressive climbing vine native to tropical America. It poses significant threats to ecosystem and causes severe agricultural-economic losses. In this study, comparative genomics and resequencing were conducted to unravel adaptive evolution and invasion dynamics of *M. micrantha*. In view of inaccurate number of chromosomes in previously reported *M. micrantha* genome, we first performed karyotype analysis of *M. micrantha* using fluorescence in situ hybridization (FISH) to guarantee accuracy of chromosome number (2n=2x=36) for high-throughput chromatin conformation capture (Hi-C). We further obtained high quality chromosome-scale genome of *M. micrantha* and conducted a comparative analysis with an indigenous congener *M. cordata*, genome size of which was 1.53 Gb and 1.68 Gb, respectively. The two sister species was diverged at approximately 3.72 million years ago (Mya). The expansion of gene families related to plant growth and defense responses plays a key role in the invasive success of *M. micrantha*. Similarly, transposable elements (TEs) exist huge impact on *M. micrantha* genome evolution and expression. Long terminal repeat retrotransposons (LTR-RTs), particularly *Copia* and *Gypsy*, promote genomic diversity and gene duplication. The paralogous genes, related to plant-pathogen interactions and stress responses, have significantly differential expression. Whole-genome resequencing of native and invasive *M. micrantha* populations reveals high genetic similarity in southern China including multiple introductions, introgression, and gene flow. Especially, we detected selected candidate genes associated with adventitious root development and seed dormancy. The balancing selection of spliceosome related genes was beneficial to development and response to abiotic stress of *M. micrantha*. This study provides new insights into invasion and evolution of *M. micrantha* and lays solid foundation for further management of *M. micrantha* and ecosystem preservation.

P.1475 Invasive Rosa rugosa Thunb. (Japanese Rose) as ecosystem engineer accelerating ecological succession of Baltic coastal dunes

Marcin W. Woch[1]*, Paweł Kapusta[2], Anna M. Stefanowicz[2], Irena M. Grześ[3] and Małgorzata Stanek[2]

1 Institute of Biology, Nicolaus Copernicus University in Toruń, Toruń, Poland. 2 W. Szafer Institute of Botany, Kraków, Poland. 3 Faculty of Biology and Biotechnology, University of Warmia and Mazury, Olsztyn, Poland.

This study addressed the impact of the invasion of *Rosa rugosa* on the soil and vegetation of Baltic coastal grey dunes. To determine the changes occurring during the invasion, the space-for-time substitution approach was used, in which observations were made in plots representing different stages of the process. The study was conducted on the Hel Peninsula

(Poland) and included 11 sites, each consisting of three adjacent plots covering: the area shortly before the invasion (N – native vegetation patch), the area just invaded (E – the edge of *R. rugosa* thickets), and the area invaded years ago (C – the center of *R. rugosa* thickets). The invasion almost did not affect the physicochemical properties of the mineral soil (for example, there were no differences in the content of nutrients between plots), but it changed the soil structure, causing the formation of a solid organic horizon. This horizon was several centimeters thick in C plots, while it was very thin in E plots and virtually absent in N plots. Regarding vegetation, the invasion caused a shift in its species composition, from that characteristic of open dune communities to that typical of maritime forests (e.g. *Polypodium vulgare*). Interestingly, this shift was pronounced between plots E and C, being invisible between plots N and E. It suggests that native vegetation responds to the invasion in its later stages. This may be related to the organic horizon formation and also the loosening of thickets resulting from the death of older invader individuals. Unlike vegetation, the soil microbiome responded to the invasion at its beginning; both *R. rugosa* plots, C and E, were characterized by higher microbial activity (respiration, activity of some enzymes) than N plots. *R. rugosa* irreversibly changes the soil structure and creates microhabitats that accelerate the entry of late-successional species.

S.162. THE KEY ROLE OF REFUGIA IN FACING THE GLOBAL BIODIVERSITY CRISIS

P.1476 Analysis of the vascular flora in the Cajas National Park (Central Andes, Ecuador)

Raffaella Ansaloni[1], Danilo Minga[1], Nubia Guzmán[1], Javier Amigo[2], Jesús Izco[2]

1 Azuay Herbarium (HA), University of Azuay. Cuenca, Ecuador. 2 Botany Departament, University of Santiago de Compostela, Spain.

The Cajas National Park (CNP) is located 30 km from the city of Cuenca (Ecuador), in the western Andean chain and occupies an area of almost 30,000 ha, between 3300–4450 m of altitude and includes various ecosystems: subpáramo, herbaceous paramo and super-páramo. The dominant vegetal community is grasslands, followed by wetlands, *Polylepis* sp.pl. and scrubs; above 4200 m asl, bush communities adapted to extreme edaphoclimatic conditions dominate. For the elaboration of the catalogue of the vascular flora of the CNP, we compiled, refined and analyzed the information available in the herbaria of the Universidad del Azuay (Cuenca, Ecuador) (HA), Missouri Botanical Garden (MO), Pontificia Universidad Católica de Ecuador (QCA) and Tropicos® database, with records of altitudes above 3300 m asl and our collections in the years 2012–2021. 666 species are documented, belonging to 264 genera and 89 botanical families; we describe their biological form (biotype), habitat, distribution -with special attention to endemic and non-native species- and degree of threat. Finally, the data for each of these criteria are jointly analyzed and compared with other Andean mountain ranges. *Dichondra macrocalyx* Meisn. and *Piptochaetium tovarii* Sánchez Vega are reported for the first time in Ecuador.

P.1477 A model-based biogeographic reconstruction of the Iberian vegetation landscapes for the past 22,000 years

Manuel Casas-Gallego[1,2,*], José María Postigo-Mijarra[3], Rut Sánchez-de Dios[3], Eduardo Barrón[4], Helios Sainz-Ollero[5]

*1 Department of Geodynamics, Stratigraphy and Paleontology, Complutense University of Madrid, Spain. 2 Department of Paleoanthropology, Senckenberg Research Institute, Frankfurt am Main, Germany. 3 Department of Biodiversity, Ecology and Evolution, Complutense University of Madrid, Spain. 4 Museo Geominero, Instituto Geológico y Minero de España, CSIC, Madrid, Spain. 5 Department of Biology, Autonomous University of Madrid, Spain. * mancasas@ucm.es.*

Understanding past potential vegetation distribution is key for understanding present-day distributions, which in turn is necessary for accurate vegetation management, conservation and restoration. In this study, we use ecological niche modelling fed with inputs from high-resolution present and past climatic data together with data on current potential landscapes to simulate the dynamics and distribution of the main vegetation types in the Iberian Peninsula since the Last Glacial Maximum (22,000 years BP). The simulations show significant changes in the extent of each vegetation type through time. Non-forested vegetation mainly consisting of steppes with grasslands, savin juniper, broom and heather groves with occasional presence of scattered mountain pines, covered an extensive area during the Late Glacial (22,000 – 12,000 years BP). At their maximum (17,000 years BP), such steppes occupied more than half of the Iberian territory, extending to central and southern areas. Starting with the Holocene, increased temperatures and precipitation enabled the expansion of broadleaved deciduous forests from refuge areas located mostly on Mediterranean coastal regions. The north-east of the Iberian Peninsula is shown to have been the most prominent refuge area for various vegetation types, including the sclerophyllous Mediterranean forest of *Quercus suber*, *Q. ilex* subsp. *ilex* and relict thermophilic elements. The modelled distributions suggest that refuge areas also existed in the Atlantic coast of northern Spain and Portugal. These were particularly effective for the spread of deciduous oak forests dominated by *Q. robur* and sub-Mediterranean (marcescent) oak forests of *Q. pyrenaica*. Mediterranean pinewoods must have benefited from the occurrence of large areas of climatic suitability throughout the studied time interval. The modelled reconstructions presented here provide new ideas of biogeographic pathways of certain vegetation types, confirm biogeographic patterns indicated by paleobotanical data and help to understand the present-day occurrence of some taxa that remained unexplained to date.

P.1478 Doline microrefugia promote unique plant functional characteristics

Kata Frei[1], Csaba Tölgyesi[1], Zoltán Bátori[1]

1 University of Szeged, Szeged, Hungary.

Climate-change microrefugia are small areas with local favourable environmental conditions, in which viable populations can survive during large-scale and long-term climate changes. Such microrefugia are known to occur in topographically complex environments (e.g., in topographic depressions). Because of their diverse microhabitat structure and unique eco-evolutionary histories, microrefugia are known to display distinct functional trait signatures. Although approaches to studying microrefugia are wide ranging, there is a shortage of information about the functional characteristics of plant assemblages in microrefugia compared to their surroundings. To fill this knowledge gap, we selected 30 topographic depressions (i.e. dolines) in two karst regions in Hungary. We chose nine plant functional traits (plant height, specific leaf area, leaf area, seed mass, start and duration of flowering, pollination type, dispersal distance class, and life form) to describe the functional structure of the studied plant assemblages. We calculated community-weighted means (CWMs) on the microhabitat level (plateau, south-facing slope, north-facing slope, and bottom) for each trait, performed a functional PCoA, computed mean pairwise dissimilarity (MPD) for each microhabitat by combining the nine traits, and measured the standardized effect size of MPD (SES.MPD). We found that plant assemblages in dolines and on the plateaus displayed unique functional characteristics (i.e. trait syndromes). North-facing slopes and bottoms had more diverse trait compositions and occupied the largest area in the ordination space. Functional diversity expressed by MPD was highest in doline bottoms among doline microhabitats. All microhabitats had negative mean SES.MPD values. These findings suggest that each microhabitat is characterized by unique trait syndromes and species in each microhabitat are functionally more similar than expected by chance. As karst areas cover about 15% of the Earth's land surface and dolines are the dominant landforms in these landscapes, studying the mechanisms that influence refugial capacity in dolines is crucial for conserving biodiversity.

P.1479 Biogeography of Pinus sylvestris native forests in the Iberian Peninsula

Víctor González-García[1], Gianmaria Bonari[2], José Valentín Roces-Díaz[1], Eduardo Fernández-Pascual[1], Borja Jiménez-Alfaro[1]

1 Biodiversity Research Institute-IMIB (CSIC-Univ. Oviedo-Princ. Asturias), Mieres, Spain. 2 University of Siena, Siena, Italy.

Pinus sylvestris is distributed across all Eurasia, from Western Europe to the Russian Far East, being the most widely distributed *Pinus* species. The species reaches its southwestern distribution limit in the Iberian Peninsula, where it is considered native to certain mountain systems. Although the species has been widely cultivated, there is little information about the diversity and distribution of natural stands. Here we focus on forest surveys made in *P. sylvestris* native populations of the Iberian Peninsula, using vegetation plots dominated by *P. sylvestris* (cover > 30%) and stored in vegetation databases and unpublished data. We classified all plots assumed to occur in native forests using the modified TWINSPAN algorithm, interpreting the resulting clusters as ecologically and biogeographically distinct forest types. The Iberian forests dominated by *P. sylvestris* were classified into four major forest types: acidophilous oromediterranean forests, thermophilous mixed forests, acidophilous temperate forests and basophilous forests. We calculated the characteristic species of each forest type, as well as the environmental space occupied by their plant communities. Soil pH, precipitation and elevation were the most significant drivers explaining the occurrence of each forest type in the Iberian Peninsula. We also fitted distribution models of the four forest types for the Last Glacial Maximum (21ky BP), mid-Holocene (6ky BP) and present climates. Our models support that *P. sylvestris* forests found refugia in the mountains of the Iberian Peninsula during the LGM. We also found that their present distribution is narrower than expected, suggesting that human activities could be responsible for their decline in the Iberian Peninsula, as supported by palynological studies that show a sharp decline concurrent with the start of human habitation. Our results indicate that the Iberian mountain systems act as a current refugia for these relict forests, buffering them from climatic oscillations and human impacts.

P.1480 Sharp decrease of snowbed specialists in their southern European distribution limit in 20 years

Estela Illa Bachs[1,2], Oriol Lluch Oms[1], Josep M. Ninot Sugrañes[1,2] Empar Carrillo Ortuño[1,2]

1 Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Universitat de Barcelona, Barcelona, Spain. 2 Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, Barcelona, Spain.

In temperate high mountains, snowbeds are those environments that remain covered by snow until mid-summer where only a set of specialised species, mostly of arctic-alpine distribution, are able to thrive. Climate change, with the rising temperatures and the reduction of winter snowfall, cause an earlier snowmelt that allows the colonisation of snowbed patches by the more competitive grassland species from the neighbouring grasslands. This process is specially worrying in the Pyrenees, one of the southernmost refugia for snowbed communities and for many specialists, where nowadays snowbed patches are of reduced dimensions and have a scattered distribution throughout the range. Between years 2003-2005 we set eight permanent transects in central Pyrenean siliceous snowbed patches, each covering the steep snowmelt gradient existing from alpine grasslands to snowbed communities, where we sampled species composition and coverage in different plots distributed at regular intervals. We resampled all the transects between 2013-2015, and half of them in 2023. We characterized the vegetation groups present at each transect by grouping the plots according to their floristic similarity through the fuzzy-c-means algorithm, and for each period we computed the frequency of snowbed specialists and that of the most competitive grassland species both at transect level and for each vegetation group. Preliminary results evidenced the rapid colonisation of snowbed patches by some competitive grassland species, and the contraction of the area occupied by snowbed specialists. We observed a differential behaviour of snowbed specialists depending on the vegetation group and the period, usually showing a frequency decrease between 2003-2013, but a stabilisation the last decade, when a subset of them even experienced a slight increase towards the snowiest end of the transect. Overall, these results suggest that in the future many Pyrenean areas may no longer represent a refugia for siliceous snowbed communities and some of their specialist species.

P.1481 Effects of canopy gaps and topographic complexity on the microclimate and vegetation of karst landscapes

Gábor Li[1], Bonita Ratkai[1], Kata Frei[1], Benedek Tóth[1], Csaba Tölgyesi[1], Zoltán Bátori[1]

1 University of Szeged, Szeged, Hungary.

Karst landscapes maintain topographically complex environments that provide a variety of microclimatic conditions suitable for a wide range of organisms. Based on previous studies, karst depressions (i.e. dolines) may serve as microrefugia for many species under global warming due to their ability to decouple microclimate from regional climatic trends. North-facing slopes and bottoms of dolines provide cooler and more humid, while south-facing slopes provide warmer and drier microclimates than the surrounding plateaus. These patterns are less pronounced in forested dolines due to the climate-buffering effect of the canopy. Here we studied how the presence of small canopy gaps may influence the microclimate, vegetation and refugial capacity in dolines. We measured microclimatic conditions and sampled the vegetation in four habitat types: 1) plateaus with closed canopy, 2) plateaus with small canopy gaps, 3) doline bottoms with closed canopy, and 4) doline bottoms with small canopy gaps. We classified all plant species into four groups based on their habitat preference and used multivariate methods and linear mixed-effects models for statistical analyses. Doline bottoms with small canopy gaps showed the lowest mean temperature and the highest soil moisture. Relative air humidity and soil moisture were significantly higher in dolines than on the plateaus. Doline bottoms with small canopy gaps maintained several beech forest species (i.e. climate change vulnerable species) that were absent or rare in the other habitats. Our results suggest that the presence of small canopy gaps in doline bottoms may significantly influence microclimatic patterns (e.g., air temperature, soil moisture) and the distribution of plant species, and may increase the capacity of dolines to be future microrefugia. It can be concluded that topographic complexity and the presence of small canopy gaps jointly shape the biodiversity of karst landscapes.

P.1482 Flora of special interest of the Manzanares River in the city of Madrid

Pedro Molina Holgado[1], Fernando Allende Álvarez[1], Nieves López Estébanez1, Fátima Franco Múgica[2]

1 Department of Geography, Universidad Autónoma de Madrid, Madrid, Spain. 2 Department of Ecology, Universidad Autónoma de Madrid, Madrid, Spain.

The Manzanares River in the city of Madrid acts as a refuge of biodiversity. It is of special floristic interest due to the high number of species it maintains and the presence of rare elements on a local and regional scale. The renaturalization of the river has allowed the partial recovery of its hydrogeomorphological functioning. The sediments deposited since then have been rapidly colonized by many of the species characteristic of fluvial environments. The riparian flora is currently composed of 591 taxa that occupy the 13.58 km of the urban river section (76 ha), of which 197 can be considered of special interest. Some of them are new species for the flora of the city and the region of Madrid or species not recorded in the city since the 19th century. In addition, the Manzanares River has become an area of great importance for the recovery of the river flora downstream of the city of Madrid, allowing the connection of the upper and lower river sectors. We review the main characteristics of the flora and provide data on the distribution and population size of the elements of greatest conservation interest.

P.1483 The decline of a translocated population of the endangered plant, Baptisia arachnifera (Fabaceae): an 18-year reintroduction study

John B. Pascarella[1]

1 Sam Houston State University, Huntsville, USA.

Long-term studies of experimental translocations are needed to verify success of this method for conservation of endangered plant populations. In 2004 and 2005, a translocated population of the federally endangered Georgia endemic *Baptisia arachnifera* (Fabaceae) was established in similar outer coastal plain habitat of South Georgia, USA. The 2004 cohort consisted of two-year seedlings while the 2005 cohort consisted of one-year old seedlings. The population was censused annually from 2004-2015, 2019 and 2022. The site was burned during winter months (Feb.-March) in 2006, 2010, 2019 and a growing season burn in May 2013. Using a composite size index, translocated plants showed positive vegetative growth from 2005 to 2010, a decline in plant size with a minimum in 2013, and then an increase but remaining below the 2010 peak. Percent of plants flowering also showed a similar pattern which lasted until 2011 for the 2004 cohort and 2012 for the 2005 cohort. Flowering then decreased, reached a minimum in 2013 and has since increased but remains below the 2010-2011 peak. While annual survival from 2004-2015 was above 90%, the 2012-2013 period had a much lower survival period of 30-60%, as this period had a late-season prescribed burn followed by summer drought. Cumulative survival declined during this 18-year period with ~20% survival for both cohorts by 2022. In addition to the transplants, only 8 out of 43 seeds that germinated during trials in 2008 survived to 2022 (18.6%) and only 1 had reproduced by age 14. This study cautions that even with similar habitats and initial success, translocations will need long-term study to determine population persistence. As the species occurs in a fire-maintained habitat, the negative impact of the late-season prescribed burn makes timing of prescribed fire a key management concern.

P.1484 Exotic vascular flora in sub-Antarctic Chile: biodiversity threats in the southernmost natural laboratory

Sánchez-Jardón L.[1,2], Zúñiga P.[3], Durán M.[3], Squeo F.[4], Cavines T.[5], Bustamante R.[2,3], Rozzi R.[1,2,6]

1 Universidad de Magallanes, Punta Arenas, Chile. 2 Cape Horn International Center. Puerto Williams, Chile. 3 Departamento de Ciencias Ecológicas, Universidad de Chile, Santiago, Chile. 4 Departamento de Biología, Universidad de La Serena and Instituto de Ecología y Biodiversidad, La Serena, Chile. 5 College of Environmental Science and Forestry, State University of New York, New York, USA. 6 University of North Texas, Denton, USA.

Deforestation for the expansion of anthropogenic productive systems and infrastructure entails the introduction of exotic flora and fauna all over the world. Tierra del Fuego and the Cape Horn archipelago in sub-Antarctic Chile are unique ecosystems where these anthropogenic disturbances occurred rather recently. Thus, this remote area may be considered a natural laboratory for biological invasions. They are located as core zones of the UNESCO Cape Horn Biosphere Reserve (CHBR) where the construction of infrastructures is restricted. However, this world's southernmost natural laboratory is subject today to increasing pressure of development that are proposing the construction of new infrastructures, such as roads, ports, hotels, ecolodges. Even though some of these are recommended for transitions zones, particularly for Puerto Williams, the capital city of the Antarctic Province of Chile, its construction could catalyze a rapid arrival of exotic flora and fauna. Here we compile the information available on vascular plant species diversity in CHRB as published in specialized journals, books and management plans, as well as the result of recent scientific expeditions conducted by Chilean and international researchers in expeditions organized by the current team at the Cape Horn International Center. As a result, three exotic species observed from 1980 to 2013, however recent studies show that there are at least 15 species currently occurring. The spatial association with human activities such as roads, farms or towns and protected areas is evaluated. Finally, we describe a long-term monitoring in the southern section of the Y-85 Vicuña-Yendegaia road in Yendegaia National Park, an initiative of CHIC in the framework of the LTSER network that seeks to expand the knowledge of vascular and cryptogamic diversity in terrestrial ecosystems of Magallanes as well as to evaluate the impacts of linear infrastructure on the biodiversity of sub-Antarctic forests.

P.1485 Ecological significance of Berberis microphylla shrubs: a comprehensive study on understory vegetation, Patagonia, Argentina

Gimena Bustamante[1,2], Rosina Soler[1,3], MiriamArena[4], Paula Rodriguez[1], Matthew Ruggirello[1], Guillermo Ortiz[1], Alyssa Roudebush[5], Paulina Agostini[2]

1 Centro Austral de Investigaciones Científicas, CONICET, Ushuaia, Argentina. 2 Universidad Nacional de Tierra del Fuego, Ushuaia, Argentina. 3 Institute of Science and Technology of Austria, Klosterneuburg, Austria. 4 Universidad de Morón, Buenos Aires, Argentina. 5 School of Forestry, Northern Arizona University, Flagstaff, USA.

Understory biomass and diversity on human-degraded sites are important aspects for understanding habitat productivity and vegetation dynamics of terrestrial ecosystems to take action with restoration measures. Shrubs became relevant as potential nurse plants for other plants under the context of climate change. This study evaluates the role of

Berberis microphylla shrubs on understory plant biomass and understory species frequency in the southernmost native forests (***Nothofagus antarctica***), of Argentina disturbed by fire and cattle. Plant biomass and species frequency were recorded under and outside *B. microphylla* shrubs (n=44) in three different forest sites. The plant biomass was collected with a 650 cm2 quadrat, dried in the lab, and separated into dead and alive (differentiating woody, ferns, forbs, and grasses), which were subsequently weighed. Understory species frequency was evaluated in situ on a 45cm-transect under and outside the shrub, using the point intercept method every 5 cm. The accumulation of dead biomass was similar inside and outside the canopy. The only groups that showed differences in alive biomass were forbs and ferns which were higher under the shrubs compared to the out-of-shrub condition ($p=P.01$ and $p=P.1$, respectively). There was a higher frequency of forbs under the shrubs than outside ($p=P.33$), and higher woody plants outside than inside ($p<P.01$). There were no differences in species richness ($p=0.853$). The most frequent species under the shrub canopy were *Osmorhiza chilensis* and *Cerastium arvense*, two forest specialist species. Outside shrubs, the native palatable grass *Bromus unioloides*, and the resprouting *B. microphylla* were more abundant ($p<P.5$). Our results highlight the importance of thorny shrubs growing naturally in degraded ecosystems. These shrubs act as nurse plants contributing to understory biomass accumulation under their canopies and play a crucial role in conserving habitat conditions for species sensitive to herbivory and extreme weather exposure (e.g., solar radiation).

P.1486 Linear habitats as plant ecological refuges in fragmented agricultural landscapes: a method for condition assessment

Simone Valeri[1], María F. Schmitz[2], Belén Acosta-Gallo[2], Duilio Iamonico[1], María Villodre[2], Cecilia Arnáiz-Schmitz[2], Giulia Capotorti[1]

1 Sapienza University of Rome, Rome, Italy. 2 Complutense University of Madrid, Madrid, Spain.

In Mediterranean Europe, both the intensification and abandonment of traditional cultural practices are major factors leading to the degradation and loss of natural and semi-natural elements in agricultural landscapes. These non-crop habitats can serve as ecological refuges, which integrate the goals of biodiversity conservation and sustainable food production in agroecosystems. Therefore, they need to be conserved or restored to enhance the resilience and resistance of agricultural systems against biodiversity loss and socio-ecological changes. Notably, linear landscape elements (LE) are high-biodiversity features that must be increased in fragmented agricultural lands to facilitate species movement and provide a variety of ecosystem services. However, in the context of environmental accounting procedures, there is still a need for a comprehensive methodology to evaluate the condition of LE and of the hosting agroecosystems. This research therefore aims to (i) propose a method for a thorough assessment of LE conditions, with a focus on their capacity to support biodiversity, (ii) investigate the potential influence of external factors on LE conditions, such as proximity to protected habitats and the governance framework, and (iii) identify useful parameters to guide ecological restoration actions for LE. Using various structural, compositional, and landscape indicators, the proposed assessment method was tested in eight administrative units across two Mediterranean European countries. In the study sites, favorable LE conditions were closely linked to contiguity to protected habitats, exhibiting marked structural continuity, a prevalence of trees, active dynamics, and high-quality surrounding landscape mosaics. The potential applications of these findings have been explored in the context of ecosystem accounting and ecological restoration processes.

S.163. THE NEW VALUE OF SCIENTIFIC PUBLICATIONS IN THE DIGITAL AGE

P.1487 How to contribute to liberate data from publications and make them widely available

Jonas Castro[1], Donat Agosti[2]

1 Plazi, Porto Alegre, Rio Grande do Sul, Brazil. 2 Plazi, Bern, Switzerland.

In the digital age, taxonomic data can be extracted from scientific publications and turned into FAIR data - findable, accessible, interoperable, and reusable information. Then, this data is deposited in several internet repositories focused on different aspects of biodiversity. TreatmentBank (TB) is a service provided by Plazi to liberate data related to taxonomic treatments from scholarly publications, and convert, enhance, link, store, and disseminate it as FAIR data. Information extracted and liberated by Plazi is a source to Biodiversity Literature Repository (BLR) — a biodiversity information community in Zenodo — which mints persistent identifiers to the data, as well as compose datasets of articles and geographic distribution occurrences to Global Biodiversity Information Facility (GBIF). Collaborators and all the scientific community can be part of Plazi's mission of supporting and promoting the development of persistent and openly accessible digital taxonomic literature by using the searching tools provided and reusing the information that is available in various formats. Through Plazi's database, users may find several information regarding taxonomic treatments, that is, any taxonomic name associated with specific information such as descriptions, distributions, materials citations, synonymic lists, images, tables, and bibliographic references. Plazi has also a text-based, certificate granting online learning material for individual extractions. Data extraction consists in (1) searching for a specific information inside a document; (2) highlighting and analyzing it; and (3) making it available in other repositories or formats. Users can employ Plazi data to assess their own contribution to biodiversity knowledge, or create dashboards about any researcher, journal, institution, or taxonomic group that had information extracted by Plazi members and collaborators. Furthermore, Plazi hosts a community repository on Github that is the go-to open hub for external contributions, where users can post comments or requests that are addressed by the Plazi team as soon as possible.

S.164. THE ORIGIN AND EVOLUTION OF MODERN PLANT DIVERSITY: INSIGHTS FROM MULTIPLE DISCIPLINES

P.1488 Deciphering the genomes of the allopolyploid species Phalaris minor L. (2n=28)

Faiz Ahmad[1], Nirupan Vipulnanthan[2]

1 Biology Department, Brandon University, Brandon, Canada. 2 College of Health Sciences, University of Alberta, Edmonton, Canada.

It has been suggested that *Phalaris minor* (2n=28), an annual species related to canary seedgrass *P. canariensis*, is an allopolyploid hybrid of two other *Phalaris* species. Previous cytogenetic analyses in interspecific hybrids have shown that *P. coerulescens* was one of the parents present in *P. minor*. In the present genetic analysis, RAPD markers, genomic *in situ* hybridization (GISH), and somatic chromosome cytology were used to determine the other parental species (of putative species *P. paradoxa*, *P. brachystachys*, *P. truncata* and *P. caneriensis*) present in *P. minor*, while confirming *P. coerulescens* as one of the parents. RAPD markers based genetic similarities between *P. minor* and other species were higher for *P. paradoxa* and *P. coerulescens*, (0.36 and 0.33, respectively), while relatively lower for *P. brachystachys*, *P. truncata* and *P. canariensis* (0.11, 0.14, and 0.10, respectively). GISH analysis (along with reverse GISH) showed strong signals of *P. paradoxa* genome hybridizing to a subset of *P. minor* chromosomes. Additionally, somatic karyotype of *P. minor* clearly showed the presence of large and small chromosomes characteristic of *P. coerulescens* and *P. paradoxa*, respectively. The results of these studies, thus, clearly identify *P. coerulescens* and *P. paradoxa* as the genome donors to *P. minor*.

P.1489 Dissecting the impact of mating systems and genetic diversity in Euphrasia: insights into modern plant evolution

Yanqian Ding[1,2], Pete Hollingsworth[2], Alex Twyford[1,2]

1 Institute of Ecology and Evolution, University of Edinburgh, Edinburgh, UK. 2 Royal Botanical Garden, Edinburgh, UK.

The evolution of modern plant diversity is intricately linked to the dynamics of mating systems and genetic diversity. This study investigates the genus *Euphrasia*, known for its rapid speciation and diverse mating strategies, to understand these factors' roles in shaping plant diversification. We focus on a comparative analysis of *Euphrasia micrantha*, a predominantly selfing species, and *E. arctica*, a mixed-mating species, exploring their genetic structures, diversity, and runs of homozygosity. Our results indicate that *E. micrantha*, despite its high inbreeding levels, maintains nucleotide diversity comparable to the genetically more diverse *E. arctica*. This suggests that occasional outcrossing events may play a crucial role in preserving genetic diversity within selfing species. Additionally, the pronounced genetic structure observed in *E. micrantha* is consistent with expectations for selfing species. The runs of homozygosity analysis in both species reveal a full spectrum of demographic history related to inbreeding, indicating complex evolutionary strategies for sustaining diversity. This study enhances our understanding of the evolutionary mechanisms that drive plant diversity, especially in lineages undergoing rapid diversification. By integrating molecular phylogenetics with population genomics, our research sheds light on the intricate interplay between mating systems, genetic drift, and hybridisation in the evolution of modern plant diversity.

P.1490 How does selfing affect the pace and process of speciation?

Lucas Marie-Orleach[1,2], Sylvain Glémin[2,3], Marie K Brandrud[1], Anne K Brysting[4], Abel Gizaw[1], A Lovisa S Gustafsson[1], Loren H Rieseberg[5], Christian Brochmann[1], Siri Birkeland[1,6]

1 Natural History Museum, University of Oslo, Oslo, Norway. 2 CNRS, Université de Rennes, Rennes, France. 3 Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Uppsala, Sweden. 4 Centre for Ecological and Evolutionary Synthesis, Department of Biosciences, University of Oslo, Oslo, Norway. 5 Department of Botany and Biodiversity Research Centre, University of British Columbia, Vancouver, Canada. 6 Department of Chemistry, Biotechnology and Food Science, Norwegian University of Life Sciences, Ås, Norway.

Surprisingly little attention has been given to the impact of selfing on speciation, even though selfing reduces gene flow between populations and affects other key population genetics parameters. We reviewed recent theoretical work and compiled empirical data from crossing experiments and genomic and phylogenetic studies to assess the effect of mating systems on the speciation process. In accordance with theoretical predictions, we found that accumulation of hybrid incompatibilities seems to be accelerated in selfers, but there is so far limited empirical support for a predicted bias towards underdominant loci. Phylogenetic evidence is scarce and contradictory, including studies suggesting that selfing either promotes or hampers speciation rate. Further studies are therefore required, which in addition to measures of reproductive barrier strength and selfing rate should routinely include estimates of demographic history and genetic divergence as a proxy for divergence time.

P.1491 A novel environmental dataset compilation pipeline to identify potential environmental drivers of insular woodiness

L.S. Jansen[1], R.F.A. Brewer[1,2], F.P. Lens[1,3], L.M. Valente[1,2]

1 Naturalis Biodiversity Center, Leiden, the Netherlands. 2 Rijksuniversiteit Groningen, Groningen, the Netherlands. 3 Leiden Universiteit, Leiden, the Netherlands.

Island systems have fascinated evolutionary biologists ever since the voyages of Darwin and Wallace, and are widely recognized for their scientific value. Given their isolation from the eco-evolutionary processes shaping continental communities, islands have given rise to the evolution of many distinct morphological patterns, also referred to as 'island syndromes'. Among angiosperm lineages on islands, a striking difference can be observed in stem woodiness in comparison to their continental relatives. This phenomenon is termed 'insular woodiness' (the evolution of woodiness in a herbaceous lineage following island colonisation). Several hypotheses have been proposed to explain the development of woodiness in an insular context, including: (1) competition for capturing sunlight between herbaceous colonizing lineages, (2) a favourable, aseasonal climate and, more recently, (3) the increased protection of woody stems against drought-related stress. Using 835 angiosperm species native to the Canary Islands (~60% of the total flora), the archipelago with the highest insular woody species richness globally, we address the environmental drivers of insular woodiness. Here, a novel bioinformatics pipeline is introduced to construct a dataset of environmental variables for hundreds of plant species. The pipeline consists of: (1) automatic extraction of locality data from the GBIF repository, (2) subsequent cleaning of locality data to filter out spatially erroneous occurrences, (3) the extraction of environmental variables for occurrences based on heterogeneous data sources and (4) aggregation of values from an occurrence-level to a species-level.Furthermore, we use multivariate statistical modelling on the resulting environmental dataset to investigate which environmental variables are linked to insular woodiness. The results show that topographic complexity, geographic range size, and annual precipitation are most strongly correlated with insular woodiness. These findings support the hypothesis of increased drought protection and provide valuable insights into the drivers of this enigmatic island syndrome.

P.1492 Did European larch (Larix decidua) survive the Holocene in Central Europe? Combining paleoecology and phylogeography

Martin Prach[1], Tomáš Fér[1], Pavel Bednář[2], Petr Pokorný[3], Kristýna Hošková[1]

1 Department of Botany, Faculty of Science, Charles University, Prague, Czech Republic. 2 Research Station of Silviculture in Opočno, Forestry and Game Management Research Institute, Opočno, Czech Republic. 3 Centre for Theoretical Study, Charles University and the Czech Academy of Sciences, Prague, Czech Republic.

European larch (*Larix decidua*) is a common conifer tree species of high biological and economical value. Over the Holocene, its distribution range was gradually shrinking until it got artificially expanded by common forestry plantations in the last about 300 years. Its genetic structure, post-glacial range dynamics, and consequently also the nativity status are therefore difficult to understand. The native range of larch as recently assumed includes its core in the Alps as well as scattered populations in the Carpathians (Slovakia, Poland, Ukraine, Romania), the eastern Sudetes (Czech Republic) and Polish lowlands. Particularly these marginal populations, which can be considered Holocene refugia, are the most affected by artificial genetic mixing and considerably understudied. Paleoecological research brought up the possibility that larch might have survived in Czechia also outside of the small region where it is traditionally considered to be native. This hypothesis was supported by findings of pollen grains spanning the majority of the Holocene at several sites in northern Bohemia. Additionally, we analysed Czech populations of larch using nuclear microsatellite markers in order to describe their genetic structure and origin. We also aim to detect the potentially refugial populations. Our findings may cause the current native range of the European larch to be re-evaluated and have already an effect on forestry practices and nature conservation in the Czech Republic.

P.1493 Karyotype diversification and evolution in Iberian representatives of Silene (Caryophyllaceae) with sex chromosomes

Rubén Ramírez-Rodríguez[1], João Rocha[2,3], Antonio L. Crespí[2,4], Francisco Amich[1]

1 Evolution, Taxonomy and Conservation Group, Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain. 2 Herbarium, Department of Biology and Environment, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal. 3 Chemistry Center-Vila Real, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal. 4 Centre for the Research and Technology of Agro-Environmental and Biological Sciences, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal. rubenrr2608@gmail.com

Dioecism is a rare phenomenon among angiosperms although dioecy evolved several times through independent events. There are few examples of plant families with the presence of heteromorphic sex chromosomes. Caryophyllaceae presents dioecious species with heteromorphic sex chromosomes within the genus *Silene*. Here, we reported karyological data on the four closely related species of *Silene* section *Elisanthe* represented in the Iberian Peninsula, being the first time for *S. marizii*. We conducted several scatter plots between numeric variable pairs, a principal component analysis (PCA) and an UPGMA cluster analysis. The different karyotypes could be arranged in a series from the moderately asymmetrical to less asymmetrical. Based on their karyotypes, the species of the section *Elisanthe* could be classified into three groups: 1A, 2A, and 2B. The karyotypes were simply insufficiently different to distinguish between species as showed the scatter plots, PCA and UPGMA dendrogram. Minimum differences in karyotype formula and asymmetry indices among the study species were observed and no significant differences were also obtained for sex chromosomes. Our results supported the recent origin and the earliest stages of differentiation of the *Silene* sex chromosomes.

,**P.1494** Revolutionizing biodiversity conservation in the mountainous regions: Harnessing the power of artificial intelligence and big data

Saddam Saqib1, Fazal Ullah[1], You-Cai Xiong[1]

1State Key Laboratory of Herbage Improvement and Grassland Agro-ecosystems, College of Ecology, Lanzhou University, Lanzhou, China.

Biodiversity conservation is a complex and pressing global challenge that requires effective management of vast amount of data. The emergence of big data and advancements in artificial intelligence (AI) offer unprecedented opportunities to revolutionize biodiversity conservation efforts. This study aims to explore the potential applications of AI in managing and analyzing big data for biodiversity conservation. We discuss the potential of AI and big data techniques in identifying threatened species, protection areas, habitat monitoring, species identification and distribution models to address conservation challenges and enhance decision-making processes. Our findings show that AI techniques can help in arranging and analyzing the species occurrence records, elevation data, and environmental factors by automatically extracting relevant information and generating standardize databases. AI techniques can help in species identification and classification through image recognition and machine learning, predictive modeling and habitat suitability mapping through machine learning algorithms, and data driven decision making by analyzing complex relationships within plant distribution data. Furthermore, AI techniques can guide detection of invasive species by analyzing remote sensing data, such as satellite imagery or unmanned aerial vehicle (UAV) data, shifts in plant distribution patterns such as habitat loss and threats to plant species. This study also highlighted future directions and opportunities of big data and AI, suggesting the need of data integration from different sources such as, real-time monitoring, designing predictive models and identifying genetic markers to suggest breeding programs for endangered species. This study suggests that harnessing AI techniques and big data can accurately explore biodiversity of the global hotspots of the world.

P.1495 Tracing origins of a flora and drivers of speciation in a center of overlooked complexity in a North American biodiversity hotspot

Elizabeth White[1], Pamela Soltis[2], Douglas Soltis[1]

1 Department of Biology, University of Florida, Gainesville, USA. 2 Florida Museum of Natural History, Gainesville, USA.

The Gulf Coastal Plain is a unique region within the North American Coastal Plain (NACP), which is the 36th recognized biodiversity hotspot in the world. This region exemplifies the unique nature of the Southeastern United States as a biogeographic model– lacking stark elevational changes or clear barriers to gene flow but high in floristic diversity and endemism. In lieu of the lack of elevational change, the complexity of the processes having led to the modern assembly of floristic communities in the Florida Panhandle have been overlooked. This study catalogs what is known about this region's high plant diversity and endemism by presenting a review of biogeographic affinities as inferred from existing molecular data at the phylogenetic and phylogeographic levels. We trace the affinities of the modern flora of the Gulf Coastal Plain to multiple biogeographic locations including South America, Eastern Asia, and Western North America, and additionally highlight the understudied role of recent diversification events in contributing to the region's high diversity. These findings showcase the diverse composition and history of the region. It represents a crucial geographic location that is a site of climatic refugia, as well as an area housing a number of recent radiations across widely-spanning angiosperm groups. We parse the origins and drivers of this "mixed endemism" in the Florida Panhandle in a novel suite of analyses which integrate existing molecular data, spatial models of elevational heterogeneity, and ecological processes such as fire disturbance. This work provides a path forward for conservation of this region generally, while also moving towards a better understanding of how ecosystem-level management can best take place in an area that is so richly mosaiced with multiple distinct plant communities with varying evolutionary histories, separated by small changes in microclimate and/or topology.

P.1496 Trait space assembly and evolution in the flora of the Canary Islands

Wolf H. Wildpret Martín[1], Sarah-Sophie-Weil[1], Patrick Weigelt[1], Holger Kreft[1]

1 Georg-August-Universität Göttingen, Göttingen, Germany.

After the first characterization of the trait space of an oceanic island flora (Tenerife, Canary Islands, Spain) the next frontier lies at extending the analysis to the whole of the Canary Islands. With this project we therefore aim to create a complete trait database for the flora of the whole archipelago covering eight fundamental plant traits (leaf area, leaf dry matter content, lead dry mass, leaf thickness, leaf nitrogen content, stem specific density, seed mass and maximum plant height). This will allow to test important theories of island biogeography at the archipelago level, thus advancing functional island biogeography. Using this database, we expect to be able to reconstruct the assembly of the trait space and functional diversity over evolutionary time scales by conducting ancestral trait reconstruction on selected lineages, taking advantage of the extensive phylogenetic work done on the flora of the Canary Islands. By including three additional root traits to the trait database of Tenerife we will evaluate drivers of trait space assembly in belowground traits and interactions with aboveground traits. Finally, we aim at characterizing the same eight functional traits for the invasive flora of Tenerife to better understand the trait space dynamics which unfold during biological invasions. Through this ongoing project, we hope to advance our understanding of functional island biogeography in the Canary Islands and in oceanic archipelagos in general. We expect to contribute to the knowledge on the processes shaping ecosystem functioning and assembly processes at large spatial and temporal scales and to aid in the development of new research in this field.

S.165. THE PAST, PRESENT, AND FUTURE OF PALMS (ARECACEAE)

P.1497 Analyze the leaf production rate in cultivated wild palms

Angel Castillo[1], Rodrigo Bernal[2]

1 Universidad del Quindío. Facultad de Ciencias Básicas y Tecnológicas, Armenia, Colombia. 2 Jardín Botánico del Quindío, Calarcá, Colombia.

Palms play a crucial role in Colombia's tropical rural communities. As a family, their economic importance is only surpassed by grasses and possibly matched by legumes. However, beyond their economic value, palms generate significant scientific interest in various fields, such as understanding their growth, which is essential for their effective management and conservation. Hence, this study was focused on estimating the leaf production rate in 200 species of Colombian wild palms at different stages of development. The study was conducted in two research sites: the Quindío Botanical Garden and the Guadualito Natural Reserve in the Quindío department. Through four semiannual readings, variables such as palm development stage (seedling, juvenile, or adult), total size, number of expanded leaves, number of rings, and segments were recorded. Results revealed significant variations in leaf production rate according to palm development stage. Seedlings showed a constant increase in leaf number, while the leaf production rate stabilized during the juvenile-adult transition. In the adult stage, a decrease in growth rate and stabilization in leaf production were observed, with energy redirected towards reproduction. These findings underscore the importance of understanding palm growth dynamics for their proper management and conservation, providing valuable information for tools such as dendrochronology, allowing for the estimation of species age and future in situ comparisons. Moreover, there is a need for further research to better understand the complexities of growth and its impact on tropical ecosystems.

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P.1498 Bactris (Arecaceae) in the Atlantic Forest: challenges and perspectives

Mariana M. Lira[1], Larry R. Noblick[2], Reyjane P. Oliveira[1]

1 Universidade Estadual de Feira de Santana, Feira de Santana, Brazil. 2 Montgomery Botanical Center, Miami, USA.

Bactris is a monophyletic palm genus with Neotropical distribution and *ca.* 79 species are present in humid forests in South and Central America, as well as in some higher regions in the Andes. There are about 43 species of this genus in Brazil, of which 12 are present in the Atlantic Forest. This group has many specific delimitation problems with "over-description" of species in some cases. The last taxonomic treatment of the group was part of the Neotropical Flora and included 73 species with an estimate of other new taxa. Currently, much of what is known about *Bactris* involves studies in the Amazon, but species that occur in other Brazilian areas still have knowledge gaps, as is the case in the Atlantic Forest. In addition to the scarcity of studies, the difficulty in collecting specimens means that the group is undersampled, with few representatives in herbaria, several of them erroneously or incompletely collected. Furthermore, collections are concentrated in the same regions with many unsampled forest areas. The objective of this work was to carry out integrative studies in *Bactris* to update its taxonomy and geographical distribution in the Atlantic Forest. At least 350 specimens from physical herbaria were analyzed, and 23 specimens were collected in three collection expeditions. As a result, we confirmed the occurrence of 14 species in the Atlantic Forest, including *B. hirta* and *B. glaucescens*, which were limited in distribution to the Amazon Forest and Cerrado, respectively, according to the Flora of Brazil. Thus, the richness of *Bactris* in the Atlantic Forest can be considered potentially greater than previously known. Therefore, more collection effort is fundamental for better understanding the species boundaries and distributions, as well as for the establishment of conservation strategies.

P.1499 Unravelling ecological speciation: the role of plant-mycorrhizal associations in Howea palms of Lord Howe Island

Kyle Macleod[1], Martin Bidartondo[1,2], Colin Turnbull[1], Roger Butlin[3], Ian Sanders[4], Ian Hutton[5], Vincent Savolainen[1]

1 Imperial College London, London, UK. 2 Royal Botanic Gardens, Kew Richmond, UK. 3 University of Sheffield, Sheffield, UK. 4 University of Lausanne, Lausanne, Switzerland. 5 Lord Howe Island Museum, Australia.

This study proposes a novel mechanism for ecological speciation, focusing on the role of plant-mycorrhizal associations in driving local adaptation and plant species divergence, using Howea palms as a model system. By integrating field ecology, molecular systematics, and genomics, the research aims to elucidate the dynamics of sympatric speciation in Howea palms, with a particular emphasis on the coevolutionary interactions between plants and their mycorrhizal fungal partners. The study aims to reveal the significance of mycorrhizal symbioses in shaping plant evolution and speciation processes. By examining the Howea palms, which are endemic to the isolated Lord Howe Island and exhibit sympatric speciation across different soil types, the research seeks to uncover the mechanisms underlying adaptive responses to environmental conditions mediated by mycorrhizal associations. Specifically, the study investigates how coevolutionary interactions between plants and arbuscular mycorrhizal fungi (AMF) contribute to the amplification of habitat differences, leading to strong local adaptation and reproductive isolation. Through comprehensive analyses of mycorrhizal diversity, differential gene expression, and genotype-environment interactions in Howea palms and AMF, the research aims to provide insights into the processes driving ecological speciation. By using a PacBio approach to characterize the distinct communities of AMF associated with each Howea species and elucidating the co-orchestration of genes involved in local adaptation between plants and their fungal partners, the study aims to uncover the mechanisms underlying species divergence. Furthermore, by conducting common garden experiments to assess the fitness of hybrid palms and examining their ability to establish AMF associations, the research seeks to evaluate the role of mycorrhizal interactions in hybrid fitness and speciation outcomes. Overall, this study contributes to a deeper understanding of the ecological and evolutionary mechanisms driving speciation in plant-mycorrhizal associations, with potential implications for applied ecology, agriculture, and our broader understanding of ecosystem functioning and biodiversity maintenance.

P.1500 A revision on the fruit circularity distinction between two palm species from South America

Renan R. Ribeiro[1], Miklos M. Bajay[1], Eduardo M. Trajano[2], Enéas R. Konzen[2], Kaliana Ferreira[2]

1 Universidade do Estado de Santa Catarina, Centro de Educação Superior da Região Sul, Laguna, Brazil. 2 Universidade Federal do Rio Grande do Sul, Centro de Estudos Costeiros, Limnológicos e Marinhos, Imbé, Brazil.

Butia catarinensis and *B. odorata* are two threatened palm species of South America. *B. catarinensis*is classified as endangered in Santa Catarina (SC), critically endangered in Rio Grande do Sul (RS), and it is endemic of these two states of southern Brazil. Otherwise, *B. odorata* is distributed from Uruguay to RS, but is endangered in the latter. The fruits of these species have differences in many characters, including circularity. While the fruits of *B. catarinensis* are described as ovoid, those from *B. odorata* are usually characterized as globose, rarely globose/ovoid. This research is toward revising these descriptions. *Butia* fruits were collected in the summer of 2022. In total, we harvested fruits of 29 reproductive individuals randomly selected and georeferenced: 10 of *B. odorata,* from Palmares do Sul (RS), and 19 of *B. catarinensis,*10 from Osório (RS) and 9 from Laguna (SC). From each accession, 100 fruits were collected. The fruits were then photographed with a smartphone separately for each individual, using software SmartGrain to determine measurements based on the scale provided for circularity. To summarize the data, violin+boxplot graphs were created in R using ggplot2 package. The highest values of circularity were found in fruits of *B. catarinensis*. Furthermore, the highest mean was found in the Osório's population and some of the lowest circularities were from *B. odorata*. It indicates that there are globose fruits of *B. catarinensis* and that fruits of *B. odoratac*an be ovoid, even more than its kin. Moreover, the standard deviation of the circularity is higher in Laguna's population (0,033). Our results suggest that a change in the present descriptions of fruit circularity should be considered for these species, and draw our attention to further genetic diversity investigation in population of Laguna.

S.166. THE ROLE OF AGMATOPLOIDY AND SYMPLOIDY FOR DIVERSIFICATION OF FLOWERING PLANTS WITH HOLOCENTRIC CHROMOSOMES

P.1501 Haplotype-specific chromosome painting allows precise crossover detection in the holocentric plant Rhynchospora breviuscula (Cyperaceae)

Thiago Nascimento[1], André Marques[1]

1 Department of Chromosome Biology, Max Planck Institute for Plant Breeding Research, Cologne, Germany.

Rhynchospora Vahl genus (beaksedges) comprise ~381 accepted species with a worldwide distribution. Hitherto, all the species with their karyotype analyzed are composed of holocentric chromosomes, with centromere activity being diffused along the entire length of the chromosomes. Recently, our group reported the first insights about the dynamics of meiotic recombination in a plant species with repeat-based holocentromeres. Here, we developed haplotype-specific oligo-FISH probes for chr1, chr2 and chr3 based on the available haplotype-phased genome assembly of the beaksedge *R. breviuscula* (*n* = 5), aiming to better understand the patterns of meiotic recombination using homologous-specific chromosome painting. Each set of probes was labeled with different fluorophores and then *in situ* hybridized in reference plants and in 10 different individuals from a F1 generation of self-crossed reference plants. Our results allowed us the correct identification of both haplotypes from chr1, chr2 and chr3 in the reference plant and the meiotic crossover points that happened among the recombined F1 plants. Our results corroborate previous results from single cell recombination map and further allows to understand how these regions change among the crossed individuals. The approach used here to investigate the recombination in *R. breviuscula* is very efficient for analyzing the distribution of the meiotic crossovers in different generations. Furthermore, these sets of haplotype-specific probes will be a powerful tool to investigate the process of inverted meiosis, the mechanism pointed as the major responsible for the allowing correct chromosome segregation during meiosis in holocentric plants.

S.167. THE ROLE OF RESEARCH INFRASTRUCTURE TO ADVANCE BOTANICAL KNOWLEDGE AND RESEARCH

P.1502 Best practices for biodiversity data management

Andrés Aguilar[1], Paulette I. Naulin[1]

1 Universidad de Chile, Santiago, Chile.

Biodiversity data contained in repositories are scattered and in different formats. The solution to this problem lies in the integration of data into open science platforms such as the Global Biodiversity Information Facility (GBIF), which is currently the most important international biodiversity data infrastructure. The Darwin Core (DwC) standard is a common language that enables the automation of machine and human reading and analysis. The quality of primary data can be improved through standardization and data collection. This study proposes a guideline for data management to ensure maximum quality, from data collection in the field to processing in the office. A set of 2,372 primary flora data was standardized to DwC format. These were subjected to the necessary processes for publication in GBIF, identifying the main gaps. 26 basic fields were selected for field data collection to maximize data quality. Five processes for data quality management were identified: structuring, direct mapping, validation, indirect mapping and cleaning. In addition, commonly used tools and programs for data processing were described. The use of controlled vocabulary or the use of the DwC standard in field data collection reduces subsequent data manipulation, avoids errors and therefore reduces the investment of time and resources. Ensuring minimum information such as the datum with which the coordinates were taken, is necessary to add quality in georeferencing processes such as the calculation of uncertainty. The proposal of good practices for field collection and data processing allows maximizing the quality of data reported to GBIF.

P.1503 Unlocking botanical insights: specimens' digital twins and collaborative curation in DiSSCo research infrastructure

Wouter Addink[1], Quentin Groom[2], Dimitris Koureas[1]

1 Naturalis Biodiversity Center, Leiden, Netherlands. 2 Meise Botanic Garden, Nieuwelaan Meise, Belgium.

DiSSCo is a world-class European Research Infrastructure comprising 175 natural science collection institutions across 23 countries. It has embarked on a journey to revolutionise botanical research through innovative approaches to digitization, mobilisation, and accessibility of European natural science collections. Central to DiSSCo's mission is the acceleration of knowledge production in the realm of global biodiversity. By employing a distributed infrastructure model, DiSSCo will make both physical specimens and their digital counterparts accessible to scientists and researchers worldwide. This ambitious objective aligns seamlessly with Target 21 of the Global Biodiversity Framework. One of the cornerstones of DiSSCo's strategic and innovation program is the concept of "specimens' digital twins." These digital twins serve as digital surrogates of their physical counterparts, bridging the gap between the traditional and digital realms of botanical research. Furthermore, this digital twinning approach fosters a collaborative community curation model that transcends institutional, national and language boundaries. It facilitates the pooling of expert resources from diverse locations, thereby transforming the conventional practice of institutionally restricted curation into a shared and inclusive community-driven model. In this talk we will delve into the multifaceted impact of DiSSCo's research infrastructure on advancing botanical knowledge. We will explore how the integration of digital twins and community curation models are reshaping research, offering new possibilities for collaboration, knowledge dissemination, and biodiversity conservation.

P.1504 Non-glandular trichomes of sunflower are important in the absorption and translocation of foliar-applied Zn

Cui Li[1], Jingtao Wu[2], F. Pax C. Blamey[2], Linlin Wang[1], Lina Zhou[1], David J. Paterson[3], Antony van der Ent[2], Victoria Fernández[4], Enzo Lombi[5], Yuheng Wang[1], Peter M. Kopittke[2]

1 Northwestern Polytechnical University, School of Ecology and Environment, Xi'an, China. 2 The University of Queensland, School of Agriculture and Food Sciences, St Lucia, Queensland, Australia. 3 Australian Synchrotron, Clayton, Victoria, Australia. 4 School of Forest Engineering, Forest Genetics and Ecophysiology Research Group, Technical University of Madrid, Madrid, Spain. 5 University of South Australia, Future Industries Institute, Mawson Lakes, South Australia, Australia.

Trichomes are potentially important for absorption of foliar fertilizers. A study has shown that the non-glandular trichomes (NGTs) of sunflower (*Helianthus annuus*) accumulated high concentrations of foliar-applied zinc (Zn); however, the mechanisms of Zn accumulation in the NGTs and the fate of this Zn are unclear. Here we investigated how foliar-applied Zn accumulates in the NGTs and the subsequent translocation of this Zn. Time-resolved synchrotron-based X-ray fluorescence microscopy and transcriptional analyses were used to probe the movement of Zn in the NGTs, with the cuticle composition of the NGTs examined using confocal Raman microscopy. The accumulation of Zn in the NGTs is both an initial preferential absorption process and a subsequent translocation process. This preferred absorption is likely because the NGT base has a higher hydrophilicity, whilst the subsequent translocation is due to the presence of plasmodesmata, Zn-chelating ligands, and Zn transporters in the NGTs. Furthermore, the Zn sequestered in the NGTs was eventually translocated out of the trichome once the leaf Zn concentration had decreased, suggesting that the NGTs are also important in maintaining leaf Zn homeostasis. This study demonstrates for the first time that trichomes have a key structural and functional role in the absorption and translocation of foliar-applied Zn.

P.1505 Diagnosis of the quality of primary biodiversity data published in GBIF Chile

Marcelo Oyaneder[1], Paulette I. Naulin[1]

1 Universidad de Chile, Santiago, Chile.

Ensuring the availability of data in public repositories is essential to facilitate further research and decision-making processes. Adhering to the FAIR principles (Findability, Accessibility, Interoperability, and Reusability) can enhance the fitness for use of data, commonly referred to as data quality. However, the importance of proper data management is often underestimated during the curation process, leading to a decline in data quality. A total of 63 different datasets sourced from Chilean institutions in GBIF were analyzed, resulting in 435,439 data occurrence points. To assess data quality, information was categorized based on common issues identified in GBIF's "Issues & Flags" categories. The geospatial category exhibited the highest concentration of issues, accounting for 84% of all tags. This was followed by date-related issues (7.5%), issues related to the GBIF Scientific Collections Registry (GRSciColl) (5%), uncategorized issues (3.3%), taxonomic issues (0.64%), and vocabulary-related issues (P.3%). An analysis focusing on the spatial component of the data underscored the valuable contributions made by public and research institutions to biodiversity knowledge. Efforts were made to address issues that hinder the usability of geospatial, date, and taxonomic data, while recognizing the significant contribution of these institutions to advancing biodiversity knowledge. In conclusion, the findings highlighted notable cases for enhancing data usability, particularly concerning geospatial issues such as the absence of datum, which impacts the accuracy of reported data. Additionally, insights were gained into challenges associated with date reporting formats and taxonomic information, including gaps in data on highly endemic species in global databases and underreporting of species' biogeographic origins by publishers.

P.1506 Advanced plant retrieval with machine learning and textual traits: application to flora of Taiwan and flora of China data

De-Kai. Kao[1], Chih-Kai Yang[2], Chien-Hsing. Chen[3]

1 Department of Forestry, National Pingtung University of Science and Technology, Pingtung, Taiwan. 2 Department of Forestry, National Pingtung University of Science and Technology, Pingtung, Taiwan. 3 Department of Biomechatronics Engineering, National Pingtung University of Science and Technology, Pingtung, Taiwan.

In the field of botanical research, the precise identification of plant species was crucial. Traditional methods, although effective, often necessitate extensive field expertise and can be time-consuming. To tackle these challenges, we propose a novel approach that utilizes textual descriptions to speed up the identification of plant species. This methodology not only streamlines the process but also makes it more accessible to a wider range of users. Our research capitalizes on the rich biogeographical history between Taiwan and China, where a land bridge during the glacial period facilitated high species similarity. We organized 2,675 species textual traits of species from both the Flora of Taiwan and the Flora of China, creating a comprehensive dataset suitable for text classification applications. Utilizing the BERT multilingual base pretrained model, we transformed the complex botanical text into a format that can be easily interpreted by computers. The fine-tuning training data consisted of a diverse and randomly sampled collection from datasets in Taiwan and China, ensuring a wide and representative range of textual features. The model's performance was evaluated using separate datasets from Taiwan and China, with a focus on F1-score to assess its effectiveness. In our evaluations, the model achieved an F1-score of 89.76% for the Taiwan dataset and 96.64% for the China dataset. According to the results, they provide a solid foundation for developing a system that can quickly and accurately identify plant species by analyzing their textual traits. This approach not only enhances the use of botanical literature but also serves as an invaluable tool for researchers, conservationists, and enthusiasts to identify and explore the vast world of plant species. More importantly, it fosters a deeper understanding of the diversity and biogeographical connections of plants, with the hope of making contributions to the field of botanical science.

S.168. THE SPECIAL AND ENDURING VALUE OF MODEL CLADES IN EVOLUTION AND ECOLOGY

P.1507 Extrafloral nectary evolution is associated with leaf traits and water availability

Luana S. Prochazka[1,2], Suzana Alcantara[3], Juliana Gastaldello Rando[4], Anselmo Nogueira[2]

1 Instituto de Pesquisas Ambientais, São Paulo, Brasil. 2 Universidade Federal do ABC, São Bernardo do Campo, Brasil. 3 Universidade Federal de Santa Catarina, Florianópolis, Brasil. 4 Universidade Federal do Oeste da Bahia, Barreiras, Brasil.

Herbivory is a widespread phenomenon, and some plants have evolved biotic defense, like extrafloral nectaries (EFNs), to attract predators, most ants, against herbivores. In addition to the herbivores' presence, other factors, such as water availability and leaf structure, could modify the evolution of EFNs. In this study, we utilized phylogenetic comparative methods to investigate whether the EFNs evolution in a *Chamaecrista* (Fabaceae) lineage occurring in xeric environments is integrated with the evolution of leaf structure and whether the water availability modifies this integration. We predicted the evolution of larger EFNs would be associated with the evolution of leaves with a higher investment of leaf mass per unit of area (LMA). Also, we predicted that plants with larger EFNs would evolve under higher water availability. Our results revealed that EFNs and leaf structure vary greatly among species, with plant species with the largest EFNs up to 63 times larger than the smallest EFNs and some leaves up to 9 times more LMA than others. As expected, a positive evolutionary correlation exists between EFN size and LMA, indicating that the evolution of EFNs occurs in coordination with leaf traits and, consequently, leaves with higher LMA evolved a more increased investment in biotic defense. Also, the positive correlation between EFN size and water availability evidenced that the arid environment is probably prohibitive to ant-EFN interactions. In contrast, large and small EFNs can evolve under more water. Thus, our results indicate that the evolution of ant-plant protection mutualism is influenced by environmental resource limitations. These findings corroborate that arid environments increase EFN costs and decrease their value as a plant defensive strategy. However, other evolutionary forces may drive the EFNs' evolution when the resource availability barrier is overcome.

S.169. TOWARDS A MORE ETHICAL SCIENCE: DECOLONIZING BOTANICAL RESEARCH

P.1508 Strategies to design and develop substantial air quality gardens for urban air pollution abatement to remove particulate matter

Moumita Basu[1]

1 Department of Botany, Kalna College, West Bengal, India.

Air pollution is now regarded as an increasingly threatening major environmental risk for human health and the leading cause of death worldwide. According to WHO reports, 7 million deaths per year are attributed to air pollution each year involving almost 99% of the global population that breathe polluted air. The one of the most harmful, hazardous and dangerous forms of pollution is caused by the Particulate Matters (0.10 - 0.25 nm) consisting of solid and liquid particles suspended in the air which causes respiratory and cardiovascular diseases. In the 21st century, an exponential growth of urbanization is observed in the metropolitan cities of India causing continuous and alarming increase of urban air pollution for the last few decades. Several urban plants like (*Ficus bengamina, Swietenia hondura, Araucaria heterophylla, Couroupita guainensis, Kigellia, Tamarindus indica, Eucalyptus gunnii, Manilkara zapota*) can directly reduce particulates by absorbing them into the leaves and filters atmospheric pollutants (SO_2, NO_2) through leaves acting as "the lungs of the Ecosystem ". Planting only tree species is not as much beneficial sometimes if they are not so well PM absorbers or there is not enough space of planting tree species. With the help of Horticopia Database, i-Tree Species Software and Phyto- Sensor Toolkit it is concluded that herbs like *Aster* spp., *Salvia nemorosa*, *Convolvulus cneorum*, *Alchemilla mollis*, *Euphorbia characias*, *Hedera helix* etc. can take over those landscapes with their high PM absorbing capacity. Green walls, green screens also enhance the biodiversity in polluted urban areas. In this scenario, it is important to design quality gardens in the modern Indian urban landscapes in which the herbs, shrubs and trees together can combat the Particulate Matter levels of a particular geographical area.

P.1509 Addressing offensive plant common names at the U.S. Botanic Garden

Devin Dotson[1], Amy Highland[1], Dr. Susan K. Pell[1]

1 United States Botanic Garden, Washington, USA.

The words we use to communicate can ensure a successful transmission of our intentions or result in our audience disengaging or being offended. Many scientific communities are reevaluating the words we use to talk about discovery and species diversity. Plant names and stories are sometimes linked to racism, antisemitism, colonialism, or other offensive or difficult topics. Botanic gardens, which operate at the intersection of plant science, horticulture, and public engagement, are well-suited to address offensive plant common names. We interact with the public about plant nomenclature daily, whether actively with programming or passively with plant labels and interpretive signs. The public garden community and our visitors would also benefit from the changing of offensive scientific names. Replacing and/or interpreting offensive names creates a more welcoming environment for all visitors. At the U.S. Botanic Garden, we have taken a multi-pronged approach to addressing offensive plant names and welcoming people to appreciate plants. Our Horticulture team reviewed plant names in our living collection database with a focus on replacing offensive common names to help ensure public labels do not offend employees or visitors or make them feel unwelcome. As part of our ongoing process to ensure people feel welcome at the Garden, all employees are invited to flag plant common names they find problematic or offensive. We share transparent stories of our institutional history, addressing past practices we would not support today, and on some garden tours, we highlight the importance of replacing offensive plant names. Institutions have an opportunity to reach a wider audience by making relatively small changes to remove offensive plant common names. This work is a journey, not a single task, and involves conversations with garden audiences, local community members, and subject matter experts to lead to more people feeling welcome in public gardens and the plant sciences.

P.1510 Out with offensive English language plant names

Jaime E. Frye[1]

1 Newfields, Indianapolis, USA.

Botany is deeply intertwined with the history of colonialism, racism, and imperialism that bleed into both its everyday and botanical naming. Common names often travel through time with little consideration as to where they come from or why we continue to use them. That is due to change. In 2020, the Plant Nomenclature & Taxonomy Community of the American Public Gardens Association in conjunction with the Council on Botanical and Horticultural Libraries set forth to create a resource providing context for words within existing, currently used English language common names that hold the potential to be problematic. Over 30 data contributing North American institutions and 49 individual volunteers donated time and energy into the development of the initial attempt at this Potentially Problematic Common Name Project. This body of work can be used as a resource or spark a discussion for English speaking professionals that use, write with, or publish plant names (botanical or common). This includes herbaria employees, librarians, plant recorders, curators, interpretation specialists, educators, volunteers, and docents – anyone that interacts with guests, colleagues, or other professionals using language that has potential for positivity or harm. Thinking more about the words used within the botanical profession and its history can create a more rich, inclusive environment for anyone interacting with public horticulture. A single project barely scratches the surface, but it can create a jumping off point to begin holding the inclusiveness of the language we employ to a higher esteem, to begin the evaluation of the content held in the bowels of existing databases, to acknowledge the unjust practices of the past, and to have meaningful conversations around language use. Hear the story of this project about words and their power.

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P.1511 Cultural practices and taboos of the Gond community in central India and their role in sustaining wild plants

Nishanth Gurav[1], Zbynek Polesny[1], Mohamed Abdul Kareem[2]

1 Faculty of Tropical AgriSciences, Czech University of Life Sciences Prague, Praha – Suchdol, Czech Republic. 2 The University of Trans-Disciplinary Health Sciences and Technology, Bangalore, India.

In recent years, urbanization is threatening the population of wild plants in central India. To address these threats, local stakeholders such as the Forest Department and NGOs are looking for potential solutions to manage wild plants sustainably. The Gond tribal community of central India is known to have many cultural practices and taboos associated with plants but their indigenous knowledge has been neglected by the stakeholders. These practices consist of harvesting rules for specific wild plants that could be analyzed to address the problem of particular species' population decline. This study aims to analyze cultural practices in the context of plant conservation and their possible application in regional policies associated with sustainable use and management of local flora. The study was carried out in Kondagaon district, Chhattisgarh, India. Five focus group discussions were conducted in each of the randomly sampled villages. Each focus group discussion included 10-12 randomly selected participants, which accounted for total participation of 54 people (29 men and 25 women) aged between 30 and 80 years. Participatory observation was used to document the harvest and traditional processing of food plant species. The Gond community organizes five significant festivals and yearly ceremonies that include use-based restrictions according to the phenology of particular wild plant species. These cultural activities strictly restrict the use of wild plants to protect them during fruiting and flowering of particular species. During the particular festivals, use restrictions apply to 30% of the 100 wild edible plant species documented. The protected species include shrubs, trees, climbers, and tubers. The study reveals that cultural restrictions presented positively affect the natural reproduction of wild useful plants, especially the local cultural keystone species. The analysis shows that indigenous knowledge of the community can be helpful in sustainable plant management and conservation of wild plants in the region.

P.1512 Protecting stable biological nomenclatural systems enables universal communication: a collective, international appeal

Pedro Jiménez-Mejías[1*], Saúl Manzano Rodríguez [2,3,4,**], Vinita Gowda[5], Frank-Thorsten Krell[6], Mei-Ying Lin[7], Santiago Martín Bravo[1], Laura Martín-Torrijos[8], Gonzalo Nieto Feliner[9], Sergei L. Mosyakin[10], Robert F. C. Naczi[11], Carmen Acedo[3], Inés Álvarez[5], Jorge V. Crisci[12], Modesto Luceño Garcés[1], John Manning[13], Juan Carlos Moreno Saiz[14], A. Muthama Muasya[15],Ricarda Riina[5], Andrea Sánchez Meseguer[5], Daniel Sánchez-Mata[16,17], and 1383 signatories from 108 countries.

*1 Área de Botánica, Departamento de Biología Molecular e Ingeniería Bioquímica, Universidad Pablo de Olavide, Seville, Spain. 2 Quaternary Palynology Lab, Instituto de Medio Ambiente, Recursos Naturales y Biodiversidad, Universidad de León, León, Spain. 3 Área de Botánica, Departamento de Biodiversidad y Gestión Ambiental, Campus de Vegazana s/n. Universidad de León, León, Spain. 4 African Centre for Coastal Palaeoscience, Nelson Mandela University, Gqeberha, South Africa. 5 Department of Biological Sciences, Indian Institute of Science Education and Research, Bhopal, India. 6 Department of Zoology, Denver Museum of Nature & Science, Denver, U.S.A. 7 Engineering Research Center for Forest and Grassland Disaster Prevention and Reduction, Mianyang Normal University, Sichuan, China 8 Department of Mycology, Real Jardín Botánico, CSIC, Madrid, Spain. 9 Department of Biodiversity and Conservation. Real Jardín Botánico, CSIC, Madrid, Spain. 10. M.G. Kholodny Institute of Botany, National Academy of Sciences of Ukraine, Kyiv (Kiev), Ukraine. 11 New York Botanical Garden, Bronx, New York, U.S.A. 12 Museo de La Plata, La Plata, Argentina. 13 Compton Herbarium. South African National Biodiversity Institute, Cape Town, South Africa. 14 Departamento de Biología, Universidad Autónoma de Madrid, Madrid, Spain. 15 Department of Biological Sciences, University of Cape Town, South Africa. 16 Botany Unit, School of Pharmacy, Complutense University of Madrid, Madrid, Spain. 17 Harvard University Herbaria, Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, U.S.A. *pjimmej@gmail.com, pjimmej@upo.es, **smanzr@unileon.es.*

The fundamental value of universal nomenclatural systems in biology, and the key to their success, is that they have enabled unambiguous scientific communication among and across different cultures. These systems are codified in sets of rules for zoology, botany, and other branches of biology. Nomenclatural codes have been collectively developed for many decades, providing scientists with rules resulting in a sound and stable biological nomenclature system. Nomenclature sustains all other natural sciences through its foundational support of taxonomy and systematics, enabling efficient global communication. We identify four core values of our present adaptative nomenclature systems: **universality, stability, neutrality, and transculturality**. These principles usually are unnoticed and are taken for granted by scientists and the general public. Their implicitness has allowed for misunderstandings that have fueled a recent, very vocal movement of activism that demand a fairer biological nomenclature through bulk revisions. We come to the conclusion that bulk revision will hamper scientific studies across different regions. Therefore, the scientific community should favour processes that ensure nomenclatural stability, despite good intentions of those proposing mass revisions. Yet, we readily and explicitly acknowledge that social justice should be a pillar of nomenclature proactively and suggest thoughtfulness in future construction and revision of scientific names. We have ensured that our initiative is inclusive and has undergone public discussion through an interactive process including the self-motivated participation of scientists from diverse regions, research backgrounds, and career stages in various languages to understand the impact of nomenclatural changes on their research and region. Between November 2023 and January 2024 our plea for nomenclatural stability has been supported by over 1400 signatories from >100 countries and has received more than 30,000 reads on ResearchGate.

P.1513 Biopiracy or knowledge transfer. The case of Ka'a he'ẽ (Stevia rebaudiana Bertoni)

María Vera Jiménez[1], Luz M. Muñoz Centeno[2], Luis Delgado Sánchez[2]

1 National University of Asunción, San Lorenzo, Paraguay. 2 Department of Botany and Plant Physiology, University of Salamanca, Salamanca, Spain.

Stevia rebaudiana Bertoni is an herb native to Paraguay and South America known as Ka'a he'ẽ (sweet herb) used as a sweetener by the Guarani Indians long before the colonization of America. The leaves are 30 times sweeter than sugar and the extract obtained is about 300 times more. The most important market for Stevia today is the food industry. The world's largest grower of Stevia is China. Seventy percent of the total production is used to extract crystals called Steviosides and Rebaudiosides. The objective of this study was to record the current use of Ka'a He'e in folk medicine and to analyze the inclusion of Paraguay in the Nagoya Protocol. For this purpose, 40 vendors were interviewed in the markets of the eastern region of the country, and in particular the use and form of commercialization of Ka'a he' ẽ was recorded. Ka'a he' ẽ is marketed in all the markets recorded and its dried leaves and flowering stems are used to treat diabetes, as a slimming, stomachic, diuretic, sweetener and in infusion or mate for hypertension. Steviosides and rebaudiosides are not extracted in Paraguay. According to the Ministry of Environment and Sustainable Development (MADES), the Nagoya Protocol was not signed or ratified until 2019, so work is being done to reactivate the process of adopting it through workshops. Ka'a he'e has had a designation of origin since 2018 and in order to achieve a fair and equitable sharing of the benefits arising from the use of genetic resources and traditional knowledge associated with these resources, it is necessary for Paraguay to become a party to the Protocol and thus contribute to the conservation and sustainable use of biodiversity and traditional knowledge.

P.1515 Ethnobotanical study on plants used by the Kanakanavu Tribe in Namasia District, Kaohsiung City, Taiwan

Chih-Kai Yang[1], Xuan-Ning Bai[2]

1 National Pingtung University of Science and Technology, Department of Forestry, Pingtung, Taiwan.

The construction, importance, and urgency of indigenous knowledge systems are undeniable. Cultural knowledge directly influences the sustainability of ethnic groups, but traditional wisdom faces challenges in contemporary practice. The relationship between plants and people is intimate, shaping the unique ethnic cultures through various aspects of life like food, clothing, shelter, and recreation, derived from the utilization of locally nurtured flora. Namasia District in Kaohsiung City is a primary traditional domain of the Kanakanavu tribe, with the smallest legally recognized indigenous population in Taiwan. Their unique traditional ecological knowledge, explored through ethnic plants, contributes to cultural advancement. This study first compiled literature on Kanakanavu ethnic plants and conducted plant surveys in neighboring areas. Data collection involved participant observation and focused interviews. From April 2023 to February 2024, the study documented 103 plant species belonging to 47 families and 94 genera. A total of 205 entries of plant utilization knowledge were recorded, categorized into 12 usage types. Among these, food plants comprised the largest category with 59 species, followed by 30 species for daily living. Poaceae had the highest representation with 17 species, followed by Asteraceae and Fabaceae, each with six species. *Arenga tremula* and *Boehmeria nivea* were the most versatile species, each utilized in eight different ways. Applying the Index of Cultural Significance (ICS) identified four key cultural species: *Arenga tremula*, *Miscanthus floridulus*, *Setaria italica*, and *Microglossa pyrifolia*. The Cultural Significance Index evaluates plant knowledge as a method of ethnic identity and enhances knowledge transmission and the connection between the ethnic group and plants, while also fostering diverse Kanakanavu cultural expressions.

S.170. TOWARDS INTEGRATIVE TAXONOMY. THEORY AND PRACTICE.

P.1516 Anatomy of leaflets of Brazilian taxa of Senna ser. Interglandulosae (Leguminosae) and its taxonomic implications

Flávio S. Souto[1], Maria de Fátima Agra[2,*]

*1 Department of Biosciences, Federal University of Pernambuco, Recife, Brazil. 2 Department of Biotechnology, Universidade Federal da Paraíba, João Pessoa, Brazil. *agramf@ltf.ufpb.br*

Senna ser. *Interglandulosae* (Benth.) H.S.Irwin & Barneby (Leguminosae) comprises 20 species with Neotropical distribution. They are recognized by having leaves with extrafloral nectaries on the leaf rachis, between the first pair of leaflets, or even across all pairs, flowers strongly asymmetrical, which has the adaxial petals reduced, and anthers of the three abaxial stamens contracted into tubular tip. Leaf anatomy has been considered an important tool for the taxonomies of several genera of Leguminosae. We therefore assessed anatomical characters of the leaflets of Brazilian taxa of *Senna* ser. *Interglandulosae*, to highlight characters that could contribute to its taxonomy. The anatomical characters of the leaflets of 60 specimens of twelve taxa of ***Senna*** ser. ***Interglandulosae*** were studied by standard plant anatomical techniques. Studied taxa showed anisocytic, anomocytic, anomotetracytic and paracytic stomata, dorsiventral mesophyll, and collateral vascular system. Five patterns of anticlinal cell walls (straight, curved, sinuous, straight to curved, and curved to sinuous), were observed. In cross-section, they are 1-2-seriate on both surfaces, being strongly papillose on the abaxial surface of *Senna multijuga* (Rich.) H.S.Irwin & Barneby. The hypostomatic type was recorded in ten taxa. Amphistomatic pattern was observed in leaflets of *S. aversiflora* (Herb.) H.S.Irwin & Barneby, and *S. polyphylla*. Brachyparacytic stomata were present only by *S. multijuga*. The leaflet edges had three different outlines (rounded, acute and obtuse). Obtuse pattern was observed only in S. rostrata (Mart.) H.S.Irwin & Barneby. The median portion of midrib, in cross section, is predominantly plane-convex, while the concave-convex is exclusive to *S. formosa* H.S.Irwin & Barneby. Leaflet anatomical characters, including their outlines of epidermis, stomata distribution, edge shape, and midrib contour, were found to be useful as a support of the taxonomy of the *Senna* ser. *Interglandulosae*.

P.1517 The combination of anatomy, spectroscopic techniques and chemometrics for grouping and discrimination of Solanum subg. Leptostemon

Anauara L. de Silva[1], Marcelo S. da Silva[1], Josean F. Tavares[1], Maria de F. Agra[1]

1 Federal University of Paraíba, João Pessoa, Paraíba, Brazil.

Solanum subg. *Leptostemonum* Dunal (Bitter) is the second largest group of *Solanum* L. with wide distribution and having Brazil as a center of diversity and endemism. This subgenus includes about 500 species, characterized by the presence of prickles, stellate trichomes and attenuated anthers. Works using only morphological characteristics has not been able to solve the taxonomic problems existing in the group. Anatomy and chemical profile of many species remains unknown however they can be used to assist in the grouping and differentiation of species. In this research, anatomy and metabolic profiling coupled to chemometric tools was used to characterize and distinguish similar species of subgenus (*S. echidnaeforme*, *S. hexandrum*, *S. kollastrum* and *S. stagnale*). For anatomy analyses of leaf were performed using light and scanning electron microscopy and for chemical analyses hydroalcoholic microextracts were analyzed by ^{1}H NMR. Characteristics of petiole, leaf edge and mainly the epidermis were able to differentiate the species. All species presented multicellular stipitate stellate trichomes except *S. kollastrum* which presented multiangular glandular trichomes. The ^{1}H NMR was possible to observe the visual similarity between them, where the signals predominated in the region of 2.50 to 4.5, indicative of hydrogens linked to oxygenated carbons, signals in the region between 4.5 and 5.5 characteristic of anomeric hydrogens of sugars, signals between 0.7 and 2.5, corresponding to signals of aliphatic hydrogens and some signals in the region of aromatic. Principal component analysis (PCA) allowed the discrimination of the species, observing a tendency to group the replicates of each species into four different groups. Epidermal micromorphology and the ^{1}H NMR profile can be efficient and provide support for the taxonomic distinction between the species, in addition to contributing to chemophenetic studies and to the control of quality of the species.

P.1518 Use of integrative taxonomy to elucidate diversity in desmids: the case of Pseudomicrasterias (Desmidiaceae, Zygnematophyceae)

Camila B. De Araújo[1], Pavel Škaloud[2], Jan Šťastný[2], Kateřina Trumhová[2], Thaís G. Da Silva[3], Carlos E. M. Bicudo[4], Ana T. Lombardi[1]

1 Departamento de Botânica, Universidade Federal de São Carlos, São Carlos, Brazil. 2 Department of Botany, Charles University, Prague, Czech Republic. 3 Aix-Marseille Université, France. 4 Instituto de Pesquisas Ambientais, São Paulo, Brazil.

Pseudomicrasterias is a green microalgal genus belonging to the family Desmidiaceae (Zygnematophyceae). The genus was described based on integrative taxonomy performed on strains previously assigned as *Micrasterias arcuata* Bailey. This is a highly problematic species due to its wide morphological variation and the presence of poorly circumscribed infraspecific taxa. In this study, we aimed to evaluate the phylogenetic position of strains traditionally assigned to *M. arcuata* and perform morphometric analyses on Brazilian clonal cultures. Three strains were investigated, and we analyze seven morphological attributes for linear morphometry, as well as 49 landmarks for geometric morphometric analysis. Multigene analyses were conducted using three molecular markers: SSU rDNA, *rbc*L, and *psa*A. The genetic analyses revealed that all investigated strains of *M. arcuata* formed distinct, well-supported lineages separate from all species within the core *Micrasterias* lineage. Morphometric analyses highlighted several important trends: the width of the polar lobe, the depth of the apical margin incision, and the curve formed by the basal lobe were critical features for differentiation and delimitation. Additionally, linear morphometric features such as MCL, BLD, IW, and HPL were found to be important for characterizing infraspecific taxa of *M. arcuata*. Based on our findings, we propose the recognition of *Pseudomicrasterias* as a new genus within the family Desmidiaceae, including one new combination and the recognition of two new species. Studies taking polyphasic approaches are crucial for better understanding of biodiversity and ensuring accurate biological delimitation, especially in cases involving taxonomic and nomenclatural inconsistencies. Our study also underscores the usefulness of molecular markers, phylogenetic analyses, and combined morphological measurements (in a standardized manner) using linear and geometric morphometric methods, that is especially relevant for Desmidiaceae that include many infraspecific taxa and/or ecomorphae in need of taxonomic clarification.

P.1518bis Use of linear morphometry to evaluate species and infraspecific taxa of Euastrum (Desmidiaceae, Zygnematophyceae)

Camila B. De Araújo[1], Matheus H.P. Siqueira[2], Thaís G. Da Silva[3], Klaus von Schwartzenberg[4], Carlos E. M. Bicudo[2]

1 Universidade Federal de São Carlos, São Carlos, Brazil. 2 Instituto de Pesquisas Ambientais, São Paulo, Brazil. 3 Aix-Marseille Université, France. 4 Universität Hamburg, Hamburg, Germany.

Euastrum Ehrenberg *ex* Ralfs is a freshwater genus belonging the family Desmidiaceae (Zygnematophyceae). The taxonomy of the genus is based on morphological characters and cell dimensions, with markedly wide morphological variation, even at the population level, that has been causing taxonomic confusion with the description of many infraspecific taxa. Nowadays, it has 323 species and 678 infraspecific taxa described causing necessity to reassess and improve classification methods based on linear measurements for the genus. This study aims to perform morphometric analysis on six strains of *Euastrum* genus, maintained under cultivation conditions. Four morphological attributes commonly used in the literature, and the other four ones proposed herein were used for linear measurements. The results shows that six morphological attributes investigated: MCL, ACL, MCW, ACW, AW and MS successful differentiated all the strains, proving to be useful to identify and to expand knowledge about morphological characterization of the genus. Two strains identified as *E. ansatum* and *E. oblongum* presented the lowest and highest values, respectively, and they were differentiated by seven attributes. The species *E. pinnatum* was different in six attributes analyzed. Three strains containing two different populations of *E. didelta* and one of *E. humerosum*, showed remarkably overlapping values in most morphological attributes investigated, but in four of them (ACL, ACW, AW and AI) were observed slightly differences that may be useful in their distinction. The results obtained constitute an important advance for characterization and delimitation of species and infraspecific taxa of *Euastrum*, regarding the use of linear measurements in a standardized way, showing the importance of new characters or morphological attributes for traditional morphometry. Also, our results will support other studies, especially taxonomic and nomenclatural ones, contributing to a better understanding of biodiversity and the accurate biological delimitation.

P.1519 Cactus of the genus Parodia Spegazzini. (Cactaceae) in the department of Cochabamba-Bolivia

Caballero Mauricio[1]

1 Department and Career of Biology, Faculty of Science and Technology, Universidad Mayor de San Simon, Cochabamba, Bolivia.

The family Cactaceae presents a great diversity of species, among which is the taxa of genus *Parodia*, originating in South America with 62 species recognized today. They are distributed throughout in Argentina, Bolivia, Brazil, Paraguay and Uruguay. In Bolivia, a total of 21 of these species can be found, 18 of which are endemic. Gender presents complications at specific level in the identification, as a consequence, the number of species can vary depending on the author (specialist) consulted; in addition, most of these species need in-depth in-situ studies and collections of herbariums, the objective of this study is to evaluate the morphological characteristics in the *Parodia* specimen found in the Department of Cochabamba, in order to find consistent diagnostic characteristics, to support correct taxonomic identification. Field trips have been carried out from 2021 and 2023 out into, different provinces of Cochabamba, focusing on the dry Andean valleys and the yungueños dry valleys, reviewing also the specimen available in the National Forest Herbarium "Martín Cárdenas" (BOLV). The morphological analysis defined four diagnostic characteristics to differentiate the respective species: shape, and diameter of the stem, type and number of ribs, shape and size of thorns (erect or curved), shape and size of their flowers. Through these parameters, it has been concluded that there are six species present and recognized in the department of Cochabamba: *Parodia ayopayana* Cárdenas, *P. columnaris* Cárdenas, *P. hausteiniana* Rasuch, *P. ocampoi* Cárdenas, *P. schwebsiana* (Werderm.) Backeb. and *P. taratensis* Cárdenas.

P.1520 Taxonomically important characters in Commelina L. (Commelinaceae, Commelinales)

Marco Octávio de Oliveira Pellegrini[1]

1 The Royal Botanic Gardens, Kew, UK.

Commelina is the largest of Commelinaceae and Commelinales, being also one of the few Pantropical genera in the family and order. It is easily recognised by its spathaceous basal bract, inflorescences reduced to (1–)2 fasciculate cincinni, strongly zygomorphic flowers (*i.e.*, zygomorphic sepals, petals, androecium, and gynoecium), paired petals clawed, unequal and mostly sky-blue (but sometimes white or lilac, rarely yellow, apricot, orange, or pink), three posterior staminodes with cruciform antherodes, and three anterior dimorphic stamens. The inflorescence of *Commelina* lacks a developed main axis and cincinni bracts, with bracteoles that are generally hyaline, and so minute that they are virtually invisible to the naked eye. Nonetheless, *Commelina* is the most taxonomically complex genus of the order, caused by its large number of species, Pantropical distribution, and ephemeral and morphologically complex flowers preserved very poorly in herbarium specimens. For those reasons, taxonomic efforts in the genus have been few, generally limited to describing new species or local floras. Too much emphasis has been placed by Neotropical taxonomists on plastic characters like leaf-sheath indumentum colour, leaf-blade shape and symmetry, flower colour, and staminode number. Alternatively, despite being indeed taxonomically important, the overreliance on seed morphology has made identifying African *Commelina* unnecessarily laborious or impossible in case the specimens lack mature seeds. Thus, the goal of this talk is to provide an overview of the taxonomically important characters in *Commelina*, with a particular focus on characters that haven't been previously used by previous taxonomists.

P.1521 Integrative taxonomy of white-flowered Eranthis (Ranunculaceae), revision of section Shibateranthis (Nakai) Tamura

Andrey Erst[1], Elizaveta Mitrenina[1,2], Denis A. Krivenko[1], Vera Kostikova[1], Tatyana Erst[1,2], Lian Lian[3], Kunli Xiang[3], WeiWang[3]

1 Central Siberian Botanical Garden, Siberian Branch of Russian Academy of Sciences, Novosibirsk, Russia. 2 National Research Tomsk State University, Tomsk, Russia. 3 Institute of Botany, Chinese Academy of Sciences, Beijing, China.

An integrative taxonomic approach, based on cytogenetical, molecular and biochemical analyses, along with morphological data, was used to delimit revise the white-flowered section ***Shibateranthis*** (Nakai) Tamura of the genus ***Eranthis*** (Ranunculaceae).

P.1522 What explains the non-monophyly of the Canary Island endemic Argyranthemum adauctum (Link) Humphries (1976)?

Mariana H. Santana[1]; Oliver W. White[2]; Mark Carine[2]

1 Royal Botanic Gardens Kew, Richmond, UK. 2 Natural History Museum, London, UK.

Oceanic islands are widely known as natural laboratories providing the model that allows the investigation of the complex processes and patterns of the natural world. The Canary Islands, one of the five archipelagos of the Macaronesia region, comprises a high number of endemic species being considered a hotspot of plant diversity. The extremely rich flora is considered threatened especially by anthropogenic activity, however, the exact number of species present on the islands remains unknown, which brings light to the existent taxonomical gap. *Argyranthemum* is the largest genus of flowering plants in the Macaronesian region comprising 24 species, where *A. adauctum* differs from the other species as it is a multiple island endemic species distributed on four of the Canarian islands. Recently the phylogenetic analysis has revealed ***A. adauctum*** as non-monophyletic within three clades. This study aims to identify whether the morphological characteristics observed in the species reflect the pattern observed in the findings from the previous study. The results from morphological and environmental analysis demonstrate that the subspecies of *A. adauctum* can be separated by at least one character, except for the subsp. *erythrocarpon* and subsp. *palmensis*. We proposed that the similarity could be related to convergent evolution, however, the environmental analysis was not able to associate the climate parameters to the pattern observed. In light of the morphological and environmental findings of this study and the previous results from the phylogenetic analysis, we proposed that all the subspecies of *A. adauctum* should be reclassified into seven distinct species. These results increase the knowledge of the oceanic island endemic species and have important ramifications for conservation priorities.

P.1523 Comparative palynology of Spigelia spp. (Loganiaceae) endemic to Brazil: new insights into its outstanding morphodiversity

Arthur Macedo[1], Francisco A.R. dos Santos[2], Maria T. Buril[3]

1 Botanic Garden of the University of Coimbra, Universidade de Coimbra, Coimbra, Portugal. 2 Department of Biological Sciences, Universidade Estadual de Feira de Santana, Bahia, Brazil. 3 De-

partment of Biological Sciences, Universidade Federal Rural de Pernambuco, Recife, Bazil.

Recent studies in Gentianales demonstrate that pollen morphology plays an important role in testing taxonomic hypotheses. Pollen diversity is noticed in types of dispersal units, polarity; shape, size, type and number of apertures; exine ornamentation, and presence of orbicules. *Spigelia* L. (Loganiaceae) is a Native American genus, attractive by its colourful tubular flowers. More than half of its diversity occurs in Brazil, with high endemism rates. Due to the lack of a recent systematic study, interspecific delimitation needs to be clarified for several sympatric species and requires further investigations. We aimed to explore and describe the pollen morphology of Brazilian species of *Spigelia*, including endemic and never palynologically studied ones, and its systematic importance. Ten species from four of eight sections in *Spigelia* were sampled, processed, and studied under light and Scanning Electron Microscopy (SEM). Twenty-five pollen grains were measured, for each species. Here we provide pollen grains descriptions for 10 species of *Spigelia* (one-fourth of all Brazilian species), of which nine are endemic to Brazil and were described for the first time. Our results bring novelties in the ectexine ornamentation (rugulate, microrugulate, verrucate, etc.), pollen size, and apertures. We recorded the presence of orbicules (Übisch bodies) for five species, previously reported in the genus only to *Spigelia anthelmia*. Pollen morphology supports the identity of *Spigelia alboura*, an endangered species recently described for Northeastern Brazil. Six pollen types were recognised in the genus: *S. anthelmia* (monads, 3-colpate, smooth), *Spigelia ayotzinapensis* (tetrads, 4-colpate, regulate, gemmate and verrucate), *Spigelia flemmingiana* (monads, 2-colpate, smooth), *Spigelia nicotianaeflora* (monads, 3-colpate, microverrucate), *Spigelia pulchella* (monads, 3-colpate, microrugulate), and *Spigelia sellowiana* (monads, 3-colpate, microverrucate). Only type *Spigelia nicotianaeflora* reflects infrageneric classification. A dichotomic key is provided for the identification of pollen types. Higher morphological variability was found compared with species from Argentina and Mexico.

P.1524 First global study of the palynological characters of the genus Parablechnum (Blechnaceae, Polypodiopsida)

Sonia Molino[1,2], Irene Lafuente[2], Guillermo Santos[2], Carmen Prada[2], Miguel Berdugo Vera[2], Mario Mairal[2], Rafael Medina[2]

1 Department of Biosciences, Faculty of Biomedical and Health Sciences, Universidad Europea de Madrid, Madrid, Spain. 2 Dept. Biodiversidad, Ecología y Evolución, Facultad de Ciencias Biológicas, Universidad Complutense de Madrid, Madrid, Spain.

Spores play a crucial role in pteridophyte systematics, especially in taxa with intricate taxonomy, as their traits are typically conserved. *Parablechnum*, the most species-rich genus in the fern family Blechnaceae, encompasses approximately 68 species across the Austropacific, America, and Africa, and whose taxonomy has been discussed throughout during the last century. However, only 45% of Parablechnum species have undergone thorough spore examination. This study aims to investigate the spores of as many *Parablechnum* species as possible to assess their taxonomic significance. We examined spores from 127 herbarium specimens, targeting two individuals per species whenever feasible. Spore measurements were taken using an optical microscope, and scanning electron microscopy provided detailed images of perispore ornamentation. Our analysis covered spores from approximately 80% of the genus's species, revealing greater ornamentation variability than previously observed. We categorized the ornamentation into three groups, one further divided into three subgroups. Several ornamentations were newly identified for the genus, enhancing our understanding of *Parablechnum* spore characteristics. Furthermore, we discovered at least 12 species of *Parablechnum* with paraphyses on the sori, a feature unprecedented in the Blechnaceae family. Some paraphyses belonged to the sporangiasters type, a rare fern structure whose function remains debated. The studied characters facilitated species delimitation in complex groups, emphasizing their utility as systematic markers. Additionally, our findings pose new questions, exploring potential connections between spore ornamentation or the presence of paraphyses on sori and dispersal ability within this widely distributed group. This research contributes valuable insights into *Parablechnum* taxonomy and prompts further exploration of fern reproductive structures and their ecological implications.

P.1525 Parasitic plants in Mexico: a catalog of genera

Leonardo F. Laguna[1], Sonia Rojas[1], Carlos Castillejos[1]

1 Universidad Nacional Autónoma de México, Ciudad de México, Mexico.

A parasitic plant is one that obtains either a part or the totality of its nutrition needs from another plant through a specialized organ known as haustorium, the former are known as hemiparasites and the latter as holoparasites. The global diversity of parasitic plants consists of about 12 orders, 25 families, 292 genera and 4750 species. They are known for their impact in the agricultural and forestall areas, therefore conform a clear group of interest. However, derived from a scarce number of studies about their diversity in Mexico, the current knowledge is limited. The objective of this work was to elaborate a catalog of parasitic plant genera which are native to the Mexican territory, through the revision of specialized literature. Firstly, they were acknowledged the genera native to Mexico, by comparison of the global diversity of parasitic plants and the national diversity of vascular plants, considering the APG IV system, as well as databases: Plants of the World Online and World Flora Online. Secondly, characteristics of interest like morphology, type of parasitism, taxonomy, list of species, statal distribution and Spanish common names, were searched for each genus in literature such as floral studies, papers, botanic databases, and websites. Finally, the catalog was constituted including said information, in addition of online photographs of living plants and herbarium specimens. A total of 9 orders, 14 families and 43 genera of parasitic plants native to Mexico are reported in the results. A high number of species are contained in three genera: *Castilleja* (76), *Phoradendron* (66) and *Cuscuta* (54). Also, most genera are described within states: Chiapas (30), Oaxaca (29) and Veracruz (28). This catalog represents a straightforward tool for acknowledgment of the parasitic plant genera native to Mexico, moreover offers information to encourage research and envision future applications in various areas of study.

P.1526 Use of linear morphometry as a tool to distinguish infraspecific taxa of Micrasterias thomasiana (Desmidiaceae, Zygnematophyceae)

Caroline De S. Bellissimo[1], Carlos E. M. Bicudo[1], Thaís G. Da Silva[2], Klaus von Schwartzenberg[3], Camila B. De Araújo[4]

1 Instituto de Pesquisas Ambientais, São Paulo, Brazil. 2 Aix-Marseille Université, France. 3 Universität Hamburg, Hamburg, Germany. 4 Universidade Federal de São Carlos, São Carlos, Brazil.

Micrasterias thomasiana Archer belongs to the family Desmidiaceae (Zygnemtophyceae), and currently includes 16 intraspecific described taxa among varieties and taxonomic formae. All taxonomic varieties and formae were proposed based on their morphology and linear measurements. The aim of this study is to perform a morphometric analysis based on linear measurements on populations of *M. thomasiana* under cultivation conditions, using morphological attributes commonly applied in the literature, and to propose new attributes for a better characterization of the species and its infraspecific categories. Nine morphological attributes were evaluated in five strains. Four attributes are commonly analyzed in the literature and five were presently proposed, such as: CM (average cell length), CLP (length of the polar lobe), CT (total cell length), LAPIC (cell apex width), LBPolar (width of the polar lobe), LLat 1 (width of lateral lobe 1), LLat 2 (width of lateral lobe 2), LT (cell width), and IW (isthmus width). Our findings revealed significant differences between the strains, especially considering the new attributes analyzed: CLP, LBPolar, LAPIC, as well in both lateral width (LLat1 and LLat2). The traditional and commonly used attributes, such as total cell length (CT), isthmus width (IW), and total width (LT) of the semicell showed little variation among the strains, exhibiting close values to each other. Our results highlighted important trends for morphological characterization and delimitation of *M. thomasiana* and its infraspecific taxa. Also, this study showed the importance of new characters for traditional morphometry and the use of linear measurements in a standardized manner, especially in cases involving taxonomic and nomenclatural inconsistencies, or species with wide morphological variation and the presence of poorly circumscribed infraspecific taxa.

P.1527 Cytotypes of Acorus (Acoraceae) are pseudocryptic species with contrasting biogeographic patterns, but shared pollination biology

Dmitry D. Sokoloff[1,2], Galina V. Degtjareva[1], Mikhail V. Skaptsov[3], Nikolay A. Vislobokov[1], Alexander G. Kirejtshuk[4], Alexander N. Sennikov[5], Elena E. Severova[1], Victor V. Chepinoga[6,7], Tahir H. Samigullin[8], Carmen M. Valiejo-Roman[8], Sergey V. Smirnov[3], Alexander I. Shmakov[3], Elena A. Marchuk[9], Margarita V. Remizowa[1]

1 Biological Faculty, M.V. Lomonosov Moscow State University, Moscow, Russia. 2 School of Plant Sciences and Food Security, Faculty of Life Sciences, Tel Aviv University, Tel Aviv, Israel. 3 South-Siberian Botanical Garden, Altai State University, Barnaul, Russia. 4 Zoological Institute of the Russian Academy of Sciences, St Petersburg, Russia. 5 Botanical Museum, Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland. 6 Institute of Geobotany, Leibniz University Hannover, Hannover, Germany. 7 Faculty of Biology and Soil Sciences, Irkutsk State University, Irkutsk, Russia. 8 A.N. Belozersky Institute of Physico-Chemical Biology, Lomonosov Moscow State University, Moscow, Russia. 9 Botanical Garden-Institute FEB RAS, Vladivostok, Russia.

The helophyte and rheophyte genus *Acorus* is one of the most isolated genera in the angiosperm phylogeny. The *Acorus calamus* group is widely distributed in the Holarctic regions of Eurasia and America. These aromatic and medicinal plants are highly important in terms of ethnobotany. Earlier studies interpreted native diploids and invasive triploids occurring in North America as two species that differed in morphology and distribution ranges. In contrast, diploids, triploids, and tetraploids occurring in Eurasia are commonly interpreted as one species because they reportedly cannot be distinguished in collections. We resolve the controversy over taxonomic concepts between Eurasia and America and provide the first detailed multidisciplinary account of *Acorus* in temperate Asia. We used plastid and nuclear markers, leaf anatomy, seed micromorphology, pollen stainability, flow cytometry, and direct chromosome counts. Diploids and tetraploids show stable molecular and micromorphological differences. Triploids are their sterile hybrids, with the plastid genome inherited from the diploid parent. Diploids of America and Asia tend to differ in leaf characters. Coadaptative coexistence with pollinating beetles *Platamartus jakowlewi* and *Sibirhelus corpulentus* (Kateretidae) is conserved between diploids and tetraploids and over a distance of 4,700 km between Japan and Western Siberia. Diploids are self-compatible and can set seeds in the absence of kateretid beetles. Tetraploids are self-incompatible and/or cannot set seeds in the absence of *Platamartus* and *Sibirhelus*. Diploids (*A. americanus*) and tetraploids (*A. verus*) are two biological species; the former has two subspecies. *Acorus calamus* should be restricted to triploids; it apparently first evolved in temperate Asia. Diploids mostly occur in much cooler climates than triploids and tetraploids. Accessions of *A. verus* and *A. calamus* from tropical Asia are apparently derived from ancient introductions. Our data provide a new framework for the pharmacological use of *Acorus.*

P.1528 Betula buggsii sp. nov. (sect. Costatae) and Betula mcallisteri sp. nov. (sect. Acuminatae) as revealed by an integrative approach

Junyi Ding[1], Norbert Holstein[2], Nian Wang[1]

1 College of Forestry, Shandong Agricultural University, Tai'an, China. 2 Department of Life Sciences, The Natural History Museum, London, United Kingdom.

Taxa are traditionally identified using morphological proxies for groups of evolutionarily isolated populations. These proxies are common characters deemed by taxonomists as significant. However, there is no general rule on which character or sets of characters are appropriate to circumscribe taxa, leading to discussions and uncertainty. Birch species are notoriously hard to identify due to strong morphological variability and factors such as hybridization and the existence of several ploidy levels. Here, we present evidence for two evolutionarily isolated lines of birches from China that are not distinguishable by traditionally assumed taxon recognition proxies, such as fruit or leaf characters. We use

restriction site-associated DNA sequencing and flow cytometry to study the evolutionary status of the two previously unidentified samples. Molecular analyses show the two unidentified *Betula* samples represent distinct lineages and were turned out to be diploid. Phylogenomic analysis shows that one identified lineage belongs to section *Costatae* and another one belongs to section *Acuminatae*. We therefore conclude that the samples represent two unrecognized species, which is here described as *Betula buggsii* and *Betula mcallisteri*. Interestingly, we have discovered that some cultivated in the Royal Botanic Gardens Edinburgh, formerly recognized as *Betula luminifera*, is actually *Betula mcallisteri*. *Betula mcallisteri* differ from *B. luminifera* by having a peeling bark and a lack of cambial fragrance.

P.1529 Cribraria cancellata (Myxomycetes): a single variable species or yet another species complex?

Daniel Rodrigues Nunes[1], Juan Carlos Zamora[1], Carlos Lado[2]

1 Conservatory and botanical garden of Geneva, Geneva, Switzerland. 2 Real Jardín Botánico-CSIC, Madrid, Spain.

Myxomycetes (*Amoebozoa*) are a group of microorganisms with a multinucleate, mobile, usually macroscopic vegetative stage (the plasmodium), producing static fungal-like fruiting bodies where meiosis and sporulation occurs. More than 1000 species are known, and molecular studies are revealing that formerly recognized, widespread and variable taxa are often complexes of closely related species. Here we focus on *Cribraria cancellata*, a common and widespread species, known since the XVIII century. It currently comprises two accepted varieties: *Cribraria cancellata* var. *cancellata* and *C. cancellata* var. *fusca*, distinguished by their peridial features (presence of a calyculus in var. *fusca,* absent in var. *cancellata*). However, over a dozen heterotypic names for different character combinations (pattern of the peridial net, colour, calyculus, length of the stalk, etc.) have been coined, suggesting a more intricate taxonomic scenario. Our aim is to assess whether the large morphological variation displayed by this taxon, together with the ecology and distribution, correlates with separately evolving lineages (estimated through DNA analyses) that could be recognized as independent species.

S.171. TRANSPOSON TAKEOVER: TRANSPOSABLE ELMENTS IN PLANT GENOME EVOLUTION, ADAPTATION AND REGULATION

P.1530 Using pangenomes to elucidate the impact of TEs in the domestication of tetraploid cotton

Campos Dominguez L[1], Castanera R[1], Grover CE[2], Hu G[3,4], Wendel JF[2], Casacuberta JM[1]

1 Centre for Research in Agricultural Genomics, Bellaterra, Barcelona, Spain. 2 Department of Ecology, Evolution and Organismal Biology, Iowa State University, Ames, Iowa, EEUU. 3 Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzen, China. 4 State Key Laboratory of Cotton Biology, Institute of Cotton Research, Chinese Academy of Agricultural Sciences, China.

The current availability of multiple high-quality reference genomes is enabling the use of reference pangenomes for genomic and evolutionary studies, which significantly improves the capture of the genetic diversity within a species in comparison to single reference genomes. Recently developed genomic approaches to find specific transposon insertion polymorphisms (TIPs) in different genotypes allow establishing associations between TE insertions and trait variation during adaptation, domestication and selection processes (TIP-GWAS). *Gossypium hirsutum* and *Gossypium barbadense* are two allopolyploid species of cotton that have undergone two parallel domestication processes. Recent research has provided good quality reference genomes of 6 and 4 different accessions of *G. hirsutum* and *G. barbadense*. We have built species-specific and across-species pangenomes and are studying the structural variation caused by TEs. Preliminary results show different levels of TE insertion variation across cotton cultivars, especially in *G. barbadense*. The developed datasets are allowing us to study the recent dynamics of TE families and their role in the domestication of these cotton species. Moreover, with the aim of elucidating the roles of TEs in the parallel domestication processes of these two species, we are applying the TIP-GWAS method to the cotton pangenomes. We plan to find and investigate TIPs across a population of 643 re-sequenced cotton accessions spanning the wild-to-domesticated continuum of tetraploid cotton. By looking into TIP variation across accessions, species and subgenomes, our study will allow us to describe and compare the TE dynamics of parallel domestication and polyploidisation, which are two crucial processes in plant evolution.

P.1531 High diversity and complex organization of repetitive sequences in the pericentromeric heterochromatin of Cuscuta partita Choisy (Convolvulaceae)

Amalia Ibiapino[1], Juan Urdampilleta[1], Andrea Pedrosa-Harand[2]

1 Instituto Multidisciplinario de Biología Vegetal, Córdoba, Argentina. 2 Laboratório de Citogenética e Evolução Vegetal, Departamento de Botânica - Centro de Biociências, UFPE, Recife, Brazil.

The parasite genus *Cuscuta* includes species with high cytogenetic diversity. Part of this diversity is related to the organization and composition of the heterochromatin in some species. In *Cuscuta partita* (2n = 30), the primary constrictions of chromosomes show no affinity for AT or GC-rich heterochromatin-specific stains, such as DAPI and CMA, respectively, forming heterochromatic bands only after C-banding. To evaluate the heterochromatin organization of its pericentromeric region, we used long-read sequencing (Oxford NanoPore) and bioinformatic tools to assemble the structure of repetitive sequences previously characterized for *C. partita*. FISH was also used to map sequences of interest on chromosomes. All mapped transposable elements (Ty1/copia Angela and SIRE and Ty3/gypsy Retand and CRM) showed localized signals in the pericentromeric regions. The CparSAT1-157 satellite signals flanked the primary constrictions of some chromosomes, or were colocalized with the other mapped sequences. These repetitive sequences appeared interspersed with each other in long reads. Complete transposable elements, mainly Ty1/copia Angela and SIRE, were interspersed by CparSAT1-157, tandem repeats, while other reads showed only complete and/or truncated transposable elements interspersed with each other. The longest arrangement of CpaSAT1-157 found was 19kbp. Both bioinformatics and FISH data corroborate that the sequences analyzed here are arranged in an intercalary manner, forming a complex structure in the (peri) centromeric regions of *C. partita* chromosomes. In contrast to other monocentric species, the results suggest the association of different types of repetitive sequences in the (peri)centromeric region of *Cuscuta* chromosomes.

P.1532 Characterizing transposable elements and repetitive DNA in the giant genomes of three Fritillaria species

Alexandria Kurowski[1], Aaron Liston[2]

1 Oregon State University, Corvallis, USA.

The *Fritillaria* (Liliaceae) genus is notable for large genomes (30 -127 Gbp) composed predominantly of repetitive DNA. *Fritillaria gentneri* (Gentner's fritillary) is an endangered lily restricted to southwestern Oregon and adjacent northern California. *Fritillaria gentneri* is a putative triploid hybrid of *F. recurva* and *F. affinis*, as evidenced by their shared geographic distribution, as well as genetic, morphological, and phenotypic traits. Furthermore, chloroplast genome sequences provide evidence for multiple origins of *F. gentneri*. To evaluate these evolutionary hypotheses, we will document the repeat landscape in twelve individuals across four populations of the three species, using low-coverage (0.15-0.2X) whole genome sequencing. Our research will characterize the most common repeat families, comparing their distribution and abundance across individuals, populations, and species. We will conduct phylogenetic analysis of selected LTR families and estimate the timing of TE bursts.

P.1533 Small RNAs as drivers of genetic and genomic plasticity

Sara Lopez-Gomollon[1]

1 University of Kent, Canterbury, UK.

Genomic shock is an umbrella term used to define a situation leading to genome-wide misregulation of the transcriptome and changes in the epigenome, disrupting gene regulation and inducing chromosomal rearrangements and the mobilization of TEs. This effect is usually associated to hybridisation. Genomic shock can be seen as a source of heritable variation, able to trigger extensive phenotypic effects. However, the molecular mechanisms associated are not well understood. Small (s)RNAs can mediate gene silencing at transcriptional or posttranscriptional level. In hybrids, sRNAs from one parent may find new targets in the genome of the other parent, modifying gene expression. We have observed changes to gene expression in interspecific *Solanum* hybrids associated with small RNAs derived from endogenous pararetroviruses, a type of transposable element. There were prominent changes to sRNA profiles in these hybrids involving 22nt species produced in the DCL2 biogenesis pathway and the hybridisation-induced changes to gene expression were like those in a *dcl2* mutant. These findings indicate that hybridisation leads to activation of EPRV, perturbation of small RNA profiles and, consequently, changes in gene expression. Grafting is another potential source of genomic shock as a genome is exposed to the presence of foreign nucleic acids. Using grafting of two tomato genotypes, we study the mobility of small RNAs and the changes induced at genetic and epigenetic level. Such hybridization -or graft- induced variation in gene expression could increase the natural phenotypic variation in natural evolution or in breeding, so a better understanding will benefit crop improvement strategies.

P.1534 Demographic history of populations and genomic imprinting have traced the transposon patterns in Arabidopsis lyrata

Nélida Padilla-García[1], Audrey Le Vève[1], Vojtech Cermak[1], Ömer Iltas[1], Robert Horvath[2], Clément Lafon Placette[1]

1 Charles University, Prague, Czech Republic. 2 University of Freiburg, Germany.

A common assumption is that purifying selection is shaping the pattern of transposable elements given that TE insertions are deleterious for the fitness of the host, especially when located around genes, and if they are targeted by epigenetic mechanisms. However, the case of TEs near imprinted genes might be different because positive selection could be acting on those TEs if the genomic imprinting provides an advantage to the host. In addition, the number and frequency of TE insertions in natural populations are also conditioned by demographic events such as bottlenecks. In this study, we aimed to test how the demography and selection forces may affect the accumulation of TEs around genes, depending on their epigenetic silencing and with a particular focus on imprinted genes. To this aim, we compared the frequency and distribution of TEs in *A. lyrata* from Europe and North America showing different degrees of mutation load, from genetically diverse outcrossers, to poorly diverse margin outcrosser populations and selfers. Generally, we found that TE insertions showed a significantly lower frequency when they were inserted into or near genes, specially those TES targeted by epigenetic silencing. These results agree with the expectation that purifying selection acts against TEs to prevent the fixation of those TEs with more deleterious effects on the host. We also found that many TEs were lost or got fixed in North American populations during the colonization and the postglacial range expansion from refugia of the species in North America, as well as during the transition to selfing. Despite the action of purifying selection and demographic events, silenced TEs invariably increased in frequency when inserted nearby imprinted genes, suggesting that positive selection acted on imprinted alleles, and resulted in their spread, sometimes fixation, in *A. lyrata* natural populations.

P.1535 Characterization of transposable elements in Polygala vulgaris L. (Polygalaceae) provide an insight into autopolyploid origin

Zübeyde Uğurlu Aydın[1], İlayda Gülmez[1], Yasin Kaya[1], Ali A. Dönmez[1]

1 Molecular Plant Systematic Laboratory (MOBIS), Department of Biology, Faculty of Science, Hacettepe University, Ankara, Turkey.

Transposable Elements (TEs) can be found in the genomes of all organisms and they are especially essential in genomic and phenotypic evolution. With the recent development of both sequencing technologies and bioinformatic tools, we can obtain a valuable perspective into the field of repeatome. The native range of *P. vulgaris* is from Europe to Central Turkey, and diploid and tetraploid cytotypes are found in different populations. The study aims to characterise TEs in selected diploid and tetraploid populations of *P. vulgaris* and to compare the abundance and proportions of TEs. Specifically, we tried to reach the impact of TEs on polyploidy using second-generation sequencing. To characterise the composition of repetitive sequences in all five individual genomes, a set of analyses was performed. The results of repetitive identification from short-read data revealed TEs are a major component of the genome, ranging from 45% to 51% in the diploid population and from 43% to 49% in the tetraploid population. In addition, the proportion of the genome containing repetitive elements was almost similar for the two cytotypes. Ty3/Gypsy-like Long Terminal Repeats (LTR) elements dominate the repetitive components of each ploidy level, with genomic proportions of 16,46% in 2x, 14,46% in 4x, followed by Ty1/Copia LTRs.Most of the TEs were classified asTy3/gypsyand Ty1/Copia superfamilies, supporting the dominance of LTR retrotransposons across land-plant genomes. In light of our results, the repetitive components of the analysed samples are highly similar and conserved within different ploidy levels based on nonsynonymous (*Ka*) and synonymous (*Ks*) substitution rates and cluster analysis of repeats. These data provide insights into an autopolyploid origin of tetraploid *P. vulgaris* and increase our understanding of LTR-RTs and their roles in polyploid genome.

S.172. TROPICAL PLANT EVOLUTION ACROSS SPATIAL AND TEMPORAL SCALES

P.1536 Exploring the phylogeny and flower symmetry evolution in Posoqueria (Rubiaceae)

Sebastián Giraldo[1,2,3], Claes Persson[3,4], Christine D. Bacon[3,4]

1 Royal Botanic Garden Edinburgh, Edinburgh, UK. 2 Group of Botanical Studies-HUA Herbarium, University of Antioquia, Medellín, Colombia. 3 Gothenburg Global Biodiversity Centre, Göteborg, Sweden. 4 University of Gothenburg, Göteborg, Sweden.

The genus *Posoqueria* is a Neotropical group of shrubs and trees in the coffee family Rubiaceae. *Posoqueria* is phylogenetically poorly understood and presents several internal taxonomical difficulties. Previous studies using limited molecular data and taxon sampling suggest the species in *Posoqueria* could be split into two monophyletic groups based on the presence or absence of a unique, specialized pollination system known as the Pollen Catapult Mechanism (PCM). This split implies the need for the resurrection of the genus *Stannia*, which groups the species lacking the PCM. Here, 15 species were sampled with target sequence capture and a phylogeny of *Posoqueria* was generated based on 177 genes and the multispecies coalescent model. The study provides evidence of the phylogenomic distinctiveness of species such as *P. mutisii, P. longiflora, P. maxima, P. grandiflora,* and *P. williamsii,* but questions the current circumscriptions of *P. chocoana* and *P. costaricensis.* Particularly, the phylogeny supports the re-circumscription of *P. latifolia*, suggesting that populations from Central America and Colombia belong to a yet undescribed species in the genus. Furthermore, this phylogenomic study indicates that the unique catapult mechanism linked to zygomorphic flowers in *Posoqueria* is the product of several evolutionary transitions and is, therefore, a non-homologous trait. The results challenge the hypothesis that this trait played a significant role in the diversification of the genus and reject the recognition of *Stannia* as a valid taxon. This novel view of the phylogenetic relationships in *Posoqueria* expands the horizons for future research in the group, especially from the alpha-taxonomy, developmental genetics, pollination biology, ecology, and biogeography points of view.

P.1537 Speciation history of redclaw plants (Escallonia) across three hotspots of biodiversity inferred from genome data

Lindsay Reedy[1], Felipe Zapata[1]

1 Department of Ecology and Evolutionary Biology, University of California, Los Angeles, USA.

Redclaws are an eco-phenotypically diverse group of shrubs and trees in the genus *Escallonia*. Previous studies have shown that most *Escallonia* species have diversified repeatedly and independently within three biodiversity hotspots in South America: the tropical Andes, the Chilean Winter Rainfall-Valdivian Forests, and the mountains of Southeastern Brazil. These diversifications have generated complex patterns of genetic and phenotypic variation, leading to issues with species limits and with some lineages showing ecophenotypic similarities across isolated geographic regions. To shed light on this repeated speciation history, we are using hundreds of homologous loci generated via target capture probes to examine concordant patterns of population divergence, ancestral population sizes, and differentiated loci. To satisfy the assumptions of multilocus analysis, we verified substitution rates and chose potential neutral sites (introns and third codon positions) to estimate gene trees and a species tree under a full multispecies coalescent model. This approach is beneficial for modeling recent speciation, as it accounts for incomplete lineage sorting. We have already observed marked gene tree heterogeneity, which will provide valuable information for estimating various parameters, including ancestral population sizes and divergences.

P.1538 Curculigo (Asparagales: Hypoxidaceae): a comprehensive morphological framework for neglected genus of tropical herbaceous plants

Alena Uvírová[1], Michal Hroneš[1], Martin Dančák[1], Jana Leong-Škorničková[2,3]

1 Palacký University, Olomouc, Czech Republic. 2 Singapore Botanic Gardens, Singapore. 3 National University Singapore, Singapore.

The monocotyledonous genus *Curculigo* (including *Molineria*, family Hypoxidaceae) comprises of perennial rhizomatous herbs with simple, prominently plicate leaf blades and star-shaped yellow flowers in basal inflorescences. It is widely distributed in tropics with the highest species diversity in S and SE Asia. Despite the slight increase in the number of new species described from the Old-World tropics in last decade, the species diversity of *Curculigo*, with currently accepted 28 species, remains grossly underestimated. Although common in various habitats, the species of *Curculigo* are often overlooked and under-collected due to unclear taxonomy resulting in an extremely wide species concept, a common situation in many groups of tropical herbaceous monocots. This is mainly caused by the lack of detailed descriptions and/or original material in early described species, and no consensus on the terminology and usefulness of morphological characters, especially those which could be applied in herbarium taxonomy. Here we propose a standard terminology and methodology for measurements and description of characters we deem important based on our ongoing study of living flowering plants in Western Malesia and herbarium studies. These, in particular, concern the shape and arrangement of the bracts, floral and fruit morphology and indumentum on different parts of the plant. Some of these characters seem to be promising even for the study of herbarium material.

S.173. UNDERSTANDING FLORAL EVOLUTION ALONG MULTIPLE DIMENSIONS: EMERGING PATTERNS OF MORPHOLOGICAL, SCENT, AND COLOR VARIATION.

P.1539 Molecular characterization of flower color and fragrance mutations in fragrant cyclamens induced by ion-beam irradiation.

Yusuke Akita[1,2], Akira Watanabe[1], Shou Kusano[2], Kana Suzuki[2], Riho Mikami[1]

1 Graduate School of Engineering, Saitama Institute of Technology, Saitama, Japan. 2 Faculty of Engineering, Saitama Institute of Technology, Saitama, Japan.

Flower coloration and floral fragrance are very important traits for plants. We previously generated some mutants from three cultivars (named KM, UR, and KO) of fragrant cyclamen (*Cyclamen persicum* x *C. purpurascens*) by ion-beam irradiation. Two mutants (named MY and KMDp) that had been made from KM, have changed the structure of anthocyanin, which is the main component of flower coloration. In MY, the component of anthocyanin had changed from malvidin 3,5-diglucoside (Mv3,5dG) to malvidin 3-glucoside, suggesting the mutation of 5-*O*-glucosyltransferase (5GT). KMDp had delphinidin 3,5-diglucoside, instead of Mv3,5dG, suggesting that anthocyanin *O*-methyltransferase (AOMT) would be mutated in KMDp. Other two mutants (named TN and KN), made from UR and KO, were changed the amounts of anthocyanin. In TN, the amounts of three kinds of anthocyanins in petals had been increased, while almost no anthocyanins were detected in the petals of KN. Further analysis showed that KN had lost the aromatic components, cinnamaldehyde and cinnamic alcohol. Therefore, we expected that the double mutation of anthocyanins- and aroma components- biosynthesis pathways would have occurred in KN. To identify these causal factors, we conducted differential expression analysis between these mutants and their original cultivars by RNA-seq analysis, and isolated several genes that related to flower coloration or aroma-biosynthesis. In this presentation, we introduce the results of these analysis and discuss the factors 'truly' involved in the biosynthesis of flower coloration and fragrance in cyclamen. Acknowledgments: This work was supported by Lotte Research Promotion Grant (LF000569).

P.1540 The relevance of the thermogenesis in the pollination by insects

Eduardo Barrón[1], David Peris[2], Enrique Peñalver[3], Jaume Pellicer Moscardó[2,4], Constanza Peña-Kairath[5,6], José Mª Postigo-Mijarra[7]

1 Centro Nacional Instituto Geológico y Minero de España, CSIC, Madrid, Spain. 2 Institut Botànic de Barcelona, CSIC, Barcelona, Spain. 3 Centro Nacional Instituto Geológico y Minero de España, CSIC, Valencia, Spain. 4 Royal Botanic Gardens, Kew, Richmond, United Kingdom. 5 Department de Dinàmica de la Terra i de l'Oceà, Facultat de Ciències de la Terra, Universitat de Barcelona, Barcelona, Spain. 6 Institut de Recerca de la Biodiversitat, Universitat de Barcelona, Barcelona, Spain. 7 Department of Biodiversity, Ecology and Evolution, Faculty of Biological Sciences, Complutense University of Madrid, Madrid, Spain.

Endothermy is the ability for an organism to maintain its body at a metabolically favorable and constant temperature, a phenomenon well known in birds and mammals. Although plants are ectotherms and rely on their external environment as a principal source of heat, some plant tissues have the ability to generate heat from metabolic processes. The raising of a plant's temperature above air temperature is mainly focused on reproductive structures and is a phenomenon conventionally referred to as thermogenesis. Although heat production in plant reproductive structures ensures their protection in cold environments by stabilizing tissue development and facilitating an optimum temperature for suitable pollen tube growth, the most important benefit for plants is the increase in their odds of being pollinated by insects. Thermogenesis enhances evaporation and subsequent dispersion of floral scent, providing competitive advantage for attracting insect pollinators, mainly beetles, flies and thrips. In this regard, multiple volatiles have been identified across thermogenic angiosperms, but also in cycads. These volatiles attract insects to a warm microenvironment offered by thermogenic reproductive structures, thus enabling the insects to reduce their metabolic energy cost for various aspects such as the development of eggs and their larvae if they occur in reproductive structures. Nowadays, thermogenesis is exhibited by early-diverging lineages of angiosperms (Nymphaeaceae, Schisandraceae, Magnoliaceae, Annonaceae and Aristolochiaceae), and a few monocots (Arecaceae, Cyclanthaceae) and eudicots (Nelumbonaceae, Rafflesiaceae, Santalaceae), being Cycadales (Cycadaceae and Zamiaceae) the only gymnosperm group that exhibits it. The presence of thermogenesis in extant descendants of early diverging angiosperms and cycads indicates its importance as an ancient character shared by predecessor plant lineages.

P.1541 You could be red, you could be yellow: flower colours and their perception by pollinators and nectar robbers

Antonella Costa[1], Marcela Moré[1], Mariana Pereyra[1], Adrián Giaquinta[1], Andrés Issaly[1], Valeria Paiaro[1]

1. Instituto Multidisciplinario de Biología Vegetal (CONICET-UNC), Córdoba, Argentina.

Floral colour is a primary signal in plant–animal interactions. The association between red flowers and bird pollination is well known, explained by both the 'bee avoidance' and 'bird attraction' hypotheses. Nevertheless, these two hypotheses have rarely been tested together at the population level in terms of colour perception *per se*. *Nicotiana glauca* is a hummingbird-pollinated plant whose tubular flowers are also visited by nectar robbing bees in its native range. Flowers are typically yellow for the human eye, while scattered populations in northwestern Argentina include from yellow-flowered plants to red-flowered plants. We quantified flower colour by measuring the spectral reflectance (300-700 nm) of tube, limb and calyx of five flowers from 60 plants in a colour polymorphic population. To estimate flower colour perception by pollinators and nectar robbers, we analysed the reflectance spectra using colour vision models for birds and bees. We recorded the visits of hummingbirds (legitimate) and bees (illegitimate) to different colour-flowered plants. PCA analyses of spectral reflectance showed continuous variation for limb and calix, and two separated groups for corolla tube, one with high reflectance at long wavelengths (red) and the other at medium wavelengths (yellow). Visual models revealed that such colour groups could be distinguished from each other by both hummingbirds and bees, while yellow flowers would be more easily distinguished from foliage than red flowers by bees. Hummingbirds would discriminate red and yellow tubes from other floral parts, but bees only could distinguish red tubes from limbs (yellow to the human eye). Legitimate and illegitimate visits did not differ between flower colour groups. Our results partially support the bee avoidance hypothesis for the red flowers of *N. glauca*. Further studies are needed in order to assess whether flower colour variation in this species could be shaped by mutualist- or antagonist- mediated selection.

P.1542 Genetic basis of pistil length variation between monkeyflower species with different pollination syndromes

Bianca T Ferreira[1], Yaowu Yuan[1]

1 Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, USA.

The evolution of floral traits associated with specialized plant-pollinator interactions (pollination syndrome) enables divergence in reproductive strategies and is key for the diversification of flowering plants. Pollination syndromes are widely observed in flowering plants with a prime example in the *Mimulus* genus where hummingbird-pollinated *M. cardinalis* flowers are larger, red in color, with exserted stamens and pistils whereas self-pollinated *M. parishii* have small, inconspicuous, pale pink flowers with minimal anther-stigma separation. Although the variation of some pollination syndrome traits such as flower color has been relatively well understood from a genetic perspective, very little is known about the genetic mechanisms underlying the variation of more polygenic traits such as flower size, stamen length, and pistil length. Here we report the identification of a quantitative trait locus (QTL) controlling pistil length variation between the hummingbird-pollinated *M. cardinalis* and self-pollinated *M. parishii*. Introgression of this QTL from *M. cardinalis* to *M. parishii* resulted in a near-isogenic line with increased pistil length (3 mm longer than the wild-type *M. parishii*). Fine-scale recombination mapping using the near-isogenic line narrowed the causal gene down to a small genomic region. Transcriptomic data indicated several potential candidate genes controlling the pistil length variation observed. Functional characterization of candidate genes in this interval is underway. These results suggest that even polygenic, dimensional traits such as pistil length can be genetically dissected through the construction of near-isogenic lines, recombination mapping, and subsequent transgenic characterization, an approach that will enable us to systematically study the pollination syndrome evolution in the monkeyflower system.

P.1543 Floral and genomic divergence identified at early stage of speciation in the Ophrys aveyronensis system

Anaïs Gibert[1], Joris A.M. Bertrand[1]

1 Laboratoire Génome et Développement des Plantes, Université de Perpignan, Perpignan, France.

Adaptive radiation in *Ophrys* orchids results in complex floral phenotypes characterized by variation in scent, color and shape. Using a newly developed pipeline for quantifying these complex phenotypes, this study investigates how trait divergence arises at early stages of speciation. Integrating trait network and quantitative genetics with reverse and forward genomic approaches and Genotyping-by-Sequencing data, we investigated in six populations of *Ophrys aveyronensis* experiencing recent allopatry: (i) multi-trait variation and integration, (ii) identification of phenotypic/genomic regions under divergent selection, and (iii) the genetic bases of trait variation. Potential signature of divergent selection on macular color and convergent selection (or canalisation) on floral morphology and odor were detected, using a PST-FST approach. A large genomic island associated with variation in alkane production was revealed using forward genetic approaches. A gene potentially associated with fatty acid biosynthesis, encoding enoyl-acyl carrier protein reductases, was pinpointed in this region. The system revealed standing genetic variation in color and odor, and potential pleiotropy. This study sheds light on early differentiation in *Ophrys*, providing a crucial genomic region and phenotypic traits for subsequent research, while highlighting the importance of a multifaceted approach to unraveling plant speciation in species with large genomes.

P.1544 Floral size and pollination visitation rate in polymorphic populations of Digitalis purpurea along an altitudinal gradient

Pamela Espinoza-Peñaloza[1], Mónica Móraes Ramírez[1], Sissi Lozada-Gobilard[1,2]

1 Instituto de Ecología, Unidad de Botánica (Herbario Nacional de Bolivia - LPB), Universidad Mayor de San Andrés, La Paz, Bolivia. 2 Department of Biology, Lund University, Lund, Sweden.

Flowers exhibit different traits that vary in scent, shape, color, and size to be more attractive to different pollinators. Floral color polymorphism occurs in some species due to abiotic and biotic agents. Within-population flower color variation are good models to understand microevolutionary processes. In this study we analyze flower size variation and pollinator visitation rate in polymorphic populations (white, pink, and violet) of *Digitalis purpurea* along an altitudinal gradient from 2,500 to 3,800 in Yungas of Bolivia. *Digitalis purpurea* is native to Western Europe, introduced to South America in different places through independent events. In Bolivia is rapidly expanding and probably competing for resources and pollinators with the native flora. Our aim is to understand how flower size and within-population flower color vary along the altitudinal gradient and how this affects pollinator visitation rate. We expect to find a decrease in flower size and visitation rate with altitude due to more difficult environments at high altitudes; as well as difference in size and visitation within populations between the different flower color morphs. We measured flower size and observed pollinators in six population of *D. purpurea* along the gradient. Preliminary results show that polymorphic populations (two or three morphs) occur in low altitudes only, and a variation in flower size between color morphs and altitude. We found violet flowers larger than white at higher altitudes (>3,000 m), while the opposite was found at lower altitudes (<3,000 m). Lower pollinator visitation rate was observed in white and pink flowers, but legitimate visits of mainly *Bombus* sp. in violet and pink morphs. We are currently quantifying fitness (fruit and seed set) to estimate phenotypic selection per site and color morph. Our results contribute to better understanding how *D. purpurea* reproduces and how is adapting in this new habitat.

P.1545 Molecular analysis for multiple functions about flavanone 3-hydroxylase from Cyclamen purpurascens

Riho Mikami[1], Yusuke Akita[1]

1 Graduate school of Engineering, Saitama Institute of technology, Saitama, Japan.

Fragrant wild cyclamen, *Cyclamen purpurascens* has pale-purple flowers, and attractive fragrance resembling rose, hyacinth, or lily of the valley. The flower of *C. purpurascens* contains a kind of anthocyanin, malvidin 3,5-diglucoside (Mv3,5dG) as main component of flower coloration and monoterpenes, sesquiterpenes, and aromatic compounds as fragrance component. Several enzyme genes involved in flavonoid biosynthesis have been isolated from *C. purpurascens*, however, flavanone 3-hydroxylase (F3H) has not been identified yet. F3H, belongs to the 2-oxoglutarate-dependent dioxygenase (2-ODD) family, is one of the key enzymes for flavonoid biosynthesis in plants. Moreover, some reports suggested that F3H had multiple functions not only for flavanone 3-hydroxylation but also flavonols synthesis or fragrance biosynthesis. To analyze the multiple functions of F3H in *C. purpurascens*, we isolated the complete open reading frame of the *F3H* gene (*CpurF3H*) from *C. purpurascens* and tried some experiment such as the expression analysis by qRT- PCR, in vitro enzyme assay, and functional analysis using *f3h* mutant in Arabidopsis (*tt6*). In this presentation, we will show about the function of CpurF3H for anthocyanin biosynthetic pathway and flower coloration. We will also discuss the functionality about CpurF3H for fragrance biosynthesis, and the relationship with CpurFLS2, previously isolated as flavonol synthase from *C. purpurascens*. Our results will provide new knowledge about interrelationship between anthocyanin and fragrance biosynthesis.

P.1546 Interplay between population mating system and temporal variation of pollination reliability in Dalechampia vines

Juan I. Moreira-Hernández[1], Cristina Rodríguez-Otero1, Øystein H. Opedal[1]

1 Speciation, Adaptation, and Co-evolution Research Group (SPACE), Department of Biology, Lund University, Sweden.

The ongoing worldwide decline of pollinators and the ecosystem services they provide raises the urgent need to understand how angiosperms respond evolutionarily to changing pollination environments. In plants with mixed mating systems, significant interpopulation variation in local mating system and the floral traits that mediate it has been revealed by several studies, but it remains unknown how such variation is related to temporal changes in pollination reliability and reproductive success. Using multiyear data from the tropical vine ***Dalechampia scandens***, we propose a framework to link interpopulation variation in local mating system with temporal changes in pollination reliability. Our results show that highly herkogamous (i.e. more outcrossing) populations experienced greater absolute change in pollination reliability between years than populations with low herkogamy and which are more prone to selfing. In contrast, proportional variation in pollination reliability was negatively correlated with herkogamy. Moreover, we found that high percent annual changes in reliability predict greater fitness losses for low herkogamous populations when outcross pollination is unreliable. However, these same conditions increase the reproductive assurance value of herkogamy and allow for the maintenance of selfing. Taken together, our results suggest that the locally adapted mating system of a population can reflect long-term patterns of pollination reliability, and that traits facilitating selfing can be especially advantageous for populations exposed to significant fitness losses due to high fluctuations in the pollination environment.

P.1547 Floral nectar and morphology differ in adaptive potential to novel pollination environments

Andrés Romero-Bravo[1], Maria C. Castellanos[1]

1 University of Sussex, Brighton, UK.

Pollinator changes can trigger rapid adaptive change in flowers. However, despite the integration between floral traits, different traits may respond differently to novel selection pressures. While corolla dimensions tend to be canalised in specialized systems to maintain pollination accuracy, nectar traits can be more sensitive to environmental factors. Studying the interactions between additive genetic variance, environmental sensitivity and genetic correlations across the floral phenotype remains a key issue to explain the patterns of flower evolution and adaptation to changes in pollinators. Introduced populations of *Digitalis purpurea* have experienced recent rapid evolution in floral morphology, but not in nectar traits, under novel pollination environments that include hummingbirds as effective pollinators. Here, we used this study system to compare phenotypic plasticity, heritability, evolvability and integration of floral morphology and nectar traits in a multi-population common garden with controlled crosses. Dimensions of the corolla presented higher heritable variation and lower plasticity than nectar traits, with nectar concentration being the most plastic trait. The proximal section of the corolla, which regulates access to nectar and has undergone convergent adaptive change in introduced populations, showed less integrated dimensions than the rest of the corolla. While the length of the proximal corolla was more evolvable than that of the rest of the corolla, nectar production rate was the most evolvable trait of the floral phenotype. Our results suggest that the different roles of the proximal and distal sections of the corolla of *D. purpurea* led to evolutionary autonomous intra-floral modules, allowing each section to respond differently to the novel selection pressures acting in the introduced populations. This is an example of how floral modularity plays a fundamental role in maintaining flower evolvability and enables quick adaptive responses in very short time scales.

S.174. USING GENOMIC DATA TO UNDERSTAND THE BIOLOGY AND EVOLUTION OF LICHENS

P.1548 Multiple colonization events of the intertidal and supralittoral zones by lichen-forming Verrucariaceae

Daniel Fernández-Costas[1], Luis González-Gallego[2-1], Ulf Schiefelbein[3], Cécile Gueidan[4], Allison Knight[5], Starri Heidmarsson[6], HolgerThüs[7], Asunción de los Ríos[8], Sergio Pérez-Ortega[1]

1 Real Jardín Botánico (CSIC), Madrid, Spain. 2 Universidad Pablo de Olavide, Sevilla, Spain. 3 Botanical Garden, University of Rostock, Rostock, Germany. 4 CSIRO Australian National Herbarium, Canberra, Australia. 5 Otago University, Dunedin, New Zealand. 6 Northwest Iceland Nature Research Centre, Saudarkrokur, Iceland. 7 State Museum of Natural History Stuttgart, Stuttgart, Germany. 8 Museo Nacional de Ciencias Naturales, CSIC, Madrid, Spain.

The lichen-forming fungal fungi family Verrucariaceae (Eurotiomycetes, Ascomycota) contains about 950 species in 43 genera, several of which are found in aquatic environments. Many of these species are known to have an exclusively marine distribution, in the intertidal and supralittoral zones of rocky coasts in temperate and cold regions, or even in the subtidal zone where they are always submerged under water (as is the case of *Verrucaria serpuloides*). Several genera of taxa growing in such environments have been described in recent years. Several studies have raised the question of whether all these lineages have the same origin or, on the contrary, represent several colonization events of this of environment. So far, the sampling of taxa in this group of organisms has prevented a clear answer to this question. We have now expanded the data on marine Verrucariaceae to include data new European species as well as data from species collected in different areas of the Southern Hemisphere, such as Antarctica and South America. We have used five genetic regions (nrITS, RPB1, nrLSU, Mcm7, nrSSU) and Bayesian and Maximum Likelihood inference to reconstruct the phylogenetic relationships among the marine genera described in the Verrucariaceae (*Hydropunctaria*, *Mastodia*, *Turgidosculum*, *Verrucaria* s.l., *Verrucariopsis* and *Wahlenbergiella*) and to analyse the number of independent colonizations of the marine environment.

P.1549 The marine Verrucariceae in Southern South America and maritime Antarctica

Daniel Fernández-Costas[1], Ulf Schiefelbein[2], Leopoldo G. Sancho[3], Asunción de los Ríos[4], SergioPérez-Ortega[1]

1 Real Jardín Botánico (CSIC), Madrid, Spain. 2 Botanical Garden, University of Rostock, Rostock, Germany. 3 Facultad de Farmacia, Universidad Complutense de Madrid, Spain. 4 Museo Nacional de Ciencias Naturales, CSIC, Madrid, Spain.

Verrucariaceae (Eurotiomycetes, Ascomycota) is a family of lichen-forming fungi with 43 genera and about 950 species. Interestingly, several lineages within the family have colonised the marine environment, particularly the intertidal and supralittoral zones of the temperate and cold rocky coasts of both hemispheres. Although the systematics of the group has recently been addressed and several new genera have been described in recent years, this research has mainly focused on the northern hemisphere and most of the molecularly studied species come from Europe. The diversity of marine Verrucariaceae in the Southern Hemisphere is known to be high, but their taxonomy has not been reviewed for decades, and never with modern molecular approaches. We investigated the diversity of marine Verrucariaceae in southern South America and maritime Antarctica using a modern integrative approach, including automated species delimitation using single locus-based algorithms (ASAP, GMYC, bPTP) and a robust phylogeny using five genomic regions (nrITS, RPB1, nrLSU, Mcm7, nrSSU). Our results show that the number of species in the group has been underestimated and we propose several new taxa for science. We also address the question of the relationship between the genus *Wahlenbergiella* and *Mastodia*, including a re-evaluation of the genus *Mastodia*.

P.1550 Disentangling the population structure of Cladonia carneola (Lecanorales, Ascomycota) in the Northern Hemisphere

Raquel Pino-Bodas[1], Troy McMullin[2], Miguel de Celis Rodríguez[3], Ana Rosa Burgaz[3]

1.Universidad Rey Juan Carlos, Móstoles, Spain. 2. Canadian Museum of Nature, Ottawa, Canada. 3. Universidad Complutense de Madrid, Madrid, Spain.

Genetic diversity and gene flow among populations are crucial for the survival of species and indicate their potential adaptation to environmental changes. We investigated the genetic diversity and population structure of *Cladonia carneola*, a bipolar species that grows mainly on stumps and decaying wood of conifers, sometimes on rich humus soils. It is a rare species, most abundant in the circumpolar area of the northern hemisphere. Its distribution in the Iberian Peninsula is limited, only a few populations are known, being the ones in the Sistema Central mountains the southernmost known in Europe. To achieve this aim, populations from different biogeographical regions of the Northern Hemisphere were sampled. Specimens were collected in Andorra, Canada, Finland, Norway, Spain and Switzerland. Population structure is assessed using the RadSeq approach. On the base of small population size and their geographical distance from the rest of the populations we hypothesise that populations from central Spain have low genetic diversity and are genetically isolated.

S.175. USING HIGHTHROUGHPUT SEQUENCING TO UNDERSTAND PLANT EVOLUTION ON ISLANDS IN A DATARICH ERA: NEW INSIGHTS FOR NEW CHALLENGES.

P.1552 Genomic study of endemic species of Helianthemum (Cistaceae) in the Canary Islands

Rafael G. Albadalejo[1], Sara Martín-Hernanz[1,2], María Olangua-Corral[3], Alfredo Reyes-Betancort[4], Arnoldo Santos-Guerra[4], Abelardo Aparicio[1]

1 Universidad de Sevilla, Seville, Spain. 2 Universidad Complutense de Madrid, Madrid, Spain. 3 Jardín Botánico Canario Viera y Clavijo, Las Palmas de Gran Canaria, Spain. 4 Jardín de Aclimatación de la Orotava, Santa Cruz de Tenerife, Spain.

The Canary Islands are considered one of the most appealing oceanic island systems worldwide, from both geological and biological perspectives. Their complex geological history has resulted in a wide range of habitats, which has led to rapid diversification in many lineages and an extremely rich biota with a high degree of endemicity. The colonization of the genus *Helianthemum* (Cistaceae) in the Canary Islands has resulted in a recent evolutionary radiation of 15 endemic species, most of them remarkably stenochorous and critically endangered. They constitute cradles of diversity as they are in an incipient process of diversification. However, taxonomic boundaries between species are unclear, and the levels of genetic variation have never been studied in most of them. Here, we analyse the genetic variation of c. 200 individuals from 20 populations and 11 species using genotyping-by-sequencing data to provide useful information for their conservation and management. The analysis of species delimitation, carried out using coalescence, recognizes all but two of the described species, *H. gonzalezferreri* and *H. bramwelliorum*. They inhabit the same island of Lanzarote and should be considered as a single species according with its low genetic divergence. Both, the phylogenetic network and the STRUCTURE analyses suggest that hybridization has had a limited impact on the evolutionary history of this lineage. Species-level genetic diversity is dramatically low, ranging from P.03 (e.g., *H. bramwelliorum* and *H. linii*) to P.36 (*H. tholiforme*). The demographic analyses are consistent with the low genetic diversity, supporting the existence of scenarios with strong bottlenecks associated to the origin of species and low current effective population sizes. These results have direct implications for conservation strategies and policies in the Canary Islands.

P.1553 Where to invade? Bioclimatic invasibility as a tool to predict invasion

Alberto de la Rosa Padilla[1], Victoria E. Martín Osorio[1], Wolf H. Wildpret Martín[2], Wolfredo Wildpret de la Torre[1]

1 Departamento de Botánica, Ecología y Fisiología Vegetal, Universidad de la Laguna, Tenerife, España. 2 Biodiversity, Macroecology & Biogeography Research Group. Faculty of Forest Sciences and Forest Ecology. University of Göttingen, Göttingen, Germany.

This study aims to determine the optimal invasion scenarios for invasive alien species in the evergreen cloudforest of the Anaga Rural Park (Biosphere Reserve), Tenerife, Canary Islands. To meet the objective, a total of 82 species have been inventoried using a geobotanical information system (GBOTIS), which are, according to the classification applied in the List of Wild Species of the Canary Islands (2019), 37 sure introduced invasive (from Spanish; ISI), 25 sure introduced non-invasive (ISN), 2 sure introduced albeit with missing data (ISF), 16 probably introduced (IP) and 2 are new alien taxa (NC). Nine IAS were identified, defined as having "greater impact" according to legislative, scientific and abundance/extension aspects of the taxon itself ***in situ***. The environmental variables of the potential range of the evergreen cloudforest of Anaga that can influence the invasion process were characterized, with altitude being the variable that has the greatest influence on the distribution of species. Data on the distribution of IAS in Anaga have been correlated with the bioclimatic belts and occupied vegetation belts and a new concept called Bioclimatic Invasibility is proposed to define the susceptibility of invasion of homogeneous bioclimatic zones based on thermoclimatic and ombroclimatic factors. The habitats with the greatest susceptibility to invasion are also determined at the level of Climactic Domain (Association) or Climactic Territory (Alliance). Bioindicative IAS of habitat invasion have been defined. The variation in the distribution of these species across bioclimatic parameters will serve to observe and predict trends of increasing temperatures and climate change in the Canary Islands. It is considered that knowledge about IAS populations and their chorology is very relevant to be able to establish a diachronic monitoring study in the evergreen cloud-forest of the Anaga Rural Park.

P.1554 Exploring floral trait adaptation to ornitophily and entomophily: A genomic examination of two Macaroneasian endemics

Lluis Garcia Mir[1], Dario Ojeda Alayon[2], Javier Fuertes Aguilar[1]

1 Departamento de Biodiversidad y Conservación, Real Jardín Botánico CSIC, Madrid, España. 2 Department of Forest Biodiversity, Norwegian Institute of Bioeconomy Research, Ås, Viken, Norway.

Across the Macaronesian islands, several lineages independently adapted their flower structures to bird pollination. In contrast with the genetic basis of adaptation to entomophilous pollination, this convergent adaptation of floral traits to interacting with non-specialist birds remains largely unexplored. Using comparative, functional and evolutionary genomics in three species of Malvaceae with contrasting pollination syndromes and a shared phylogenetic history, the Canarian endemics ornitophilous *Navaea phoenicea* and entomophilous *Malva canariensis*, and its mediterranean sister entomophilous *Malva wigandii*, we performed genome and transcriptome sequencing, assembly, annotation and analysis of gene sequence and expression to explore the genomic mechanisms by which pollinator shifts exert natural selection on floral traits. Genome sequencing with Illumina and PacBio reconstructed *de novo* draft assemblies highly fragmented but complete at gene space. Further, we assembled high coverage Illumina floral transcriptome data across five pre- and anthetic flower developmental stages. The results show that for most gene families involved in morphological, anatomical, biochemical and physiological traits examined, the gene content, sequence evolution and gene expression profiles are similar between ornitophilous and entomophilous species, yet, several candidate genes show unique features associated to each pollination syndrome, in each of the steps of advertisement, mechanical interaction and reward to pollinators, that eventually determine the fitness of pollination. In brief, the gene expression of entomophilous species is directed to produce a pale blue petal pigmentation and an epidermal surface mainly composed of sinuous cells, while *N. phoenicea* produces a salmon-like color pigment suite, and its transcriptional regulation of sinuous cell differentiation is also almost absent, leading petal epidermal surface be mainly composed of tabular cells. The higher expression of transcription factors related to floral nectary inception results in a bigger floral nectary area, and the higher production of parenchymatic carbohydrate biosynthesis machinery results in a higher outcome of secreted nectar.

P.1555 Resolving cryptogenic species within the Compositae across the Canary Islands using a generalized demographic-based approach

Louis S. Jay-García[1, 2], Yurena Arjona[1, 2], Raúl Orihuela-Rivero[1, 2], Guillermo Sicilia-Pasos[1, 2], Miguel A. Padrón-Mederos[3], J. Alfredo Reyes-Betancort[3], Marcos Salas-Pascual[4], Agustín Naranjo Cigala[4], Javier Morente-López[2], Sebastien Mirolo[1, 5], Juli Caujapé-Castells[6], Juan A. Calleja[7], Cherif Harrouni[8], Fouad Msanda[9], Stephan Scholz[10], Aurelio Acevedo[11], Carlos Cáceres Marrero[4] and Jairo Patiño[1, 2].

1 Universidad de La Laguna, San Cristóbal de La Laguna, Tenerife, Spain. 2 Instituto de Productos Naturales y Agrobiología (CSIC), San Cristóbal de La Laguna, Tenerife, Spain. 3 Jardín de Aclimatación de la Orotava - Instituto Canario de Investigaciones

Agrarias, Puerto de la Cruz, Tenerife, Spain. 4 Universidad de Las Palmas de Gran Canaria, Las Palmas de Gran Canaria, Spain. 5 University of Liège, Liège, Belgium. 6 Jardín Botánico Canario "Viera y Clavijo" - Unidad Asociada de I+D+i al CSIC, Cabildo de Gran Canaria, Spain. 7 Universidad Autónoma de Madrid, Madrid, Spain. 8 Hassan II Institute of Agronomy and Veterinary Sciences, Agadir, Morocco. 9- Ibn Zohr University, Agadir, Morocco. 10 Oasis Park Wildlife, Pájara, Fuerteventura, Spain. 11 Independent Researcher, El Paso, La Palma, Spain.

In the Canary Islands, about half of non-endemic native Asteraceae are under an uncertain category of origin. A species is classified as cryptogenic when there is no evidence that supports its native origin, and a (sub-)historic introduction cannot be discarded. Cryptogenic species in the Canary Islands are often native to adjacent areas in the Mediterranean basin and/or have long-distance dispersal traits. It is crucial to identify which cryptogenic species are exotic, particularly when they have been proven to be invasive elsewhere. A sound example of this is *Volutaria tubuliflora*, a thistle that is native to the north of Africa and introduced in mainland Spain but considered probably native to the Canarian archipelago. There are no general evidence-based criteria to assess cryptogenic species. We propose here the use of a genome-wide sequencing technique (ddRAD-seq) as an ideal approach to assess the cryptogenic status of 22 Canarian species from the three main subfamilies within Asteraceae. We aim to test which scenario best explains the spatial distribution of genomic variation between the continental and insular distribution range, and whether demographic pathways best fit single or recurrent human-mediated introductions or natural colonization events. Specifically, we have collected around 2700 samples from all 8 main islands and two adjacent continental areas (South Iberian Peninsula and the Macaronesian enclave of Morocco). The different demographic patterns that we have obtained allow us to hypothesize the native or exotic origin of the selected species. Our results help to improve oceanic island biodiversity conservation, particularly decision-making in exotic species management.

P.1556 Phylogenomics of Agave, biogeography and genome size evolution across the Caribbean

Karen Y. Ruiz Mondragón[1], José Ignacio Márquez-Corro[2], Sara Barrios[2], Marcella Corcoran[2], Paul Rees[2], Amy Barker[2], Stuart Cable[2], Bryan Naqqi Manco[3], Dodly Prosper[3], Junel Blaise[3], Erika Aguirre Planter[1], Abisaí J. García-Mendoza[4], Jorge Nieto Sotelo[4], Jesús Gutiérrez[4], Luis E Eguiarte[1], Ilia J. Leitch[2], Juan Viruel[2*]

*1 Instituto de Ecología, Universidad Nacional Autónoma de México, Mexico City, México. 2 Royal Botanic Gardens, Kew. Richmond, UK. 3 Department of Environment and Coastal Resources, National Environmental Centre, Lower Bight Road, Providenciales, Turks and Caicos Islands. 4 Jardín Botánico, Instituto de Biología, Universidad Nacional Autónoma de México, Mexico City, Mexico. *Contact: j.viruel@kew.org, juanviruel@gmail.com*

Agave *is a culturally important genus, with more than 70 traditional uses recorded in Mexico, highlighting the production of alcoholic beverages (pulque, mezcal and tequila). Some species (i.e.,* Agave tequilana, A. angustifolia, A. salmiana *etc.) have been described with a domestication gradient.* Agave*species have a monocarpic life cycle, with the often-large inflorescence arising from the terminal growing point of the plant, meaning the flowering head dies after flowering.* Agave*spp. have large haploid genomes, estimated between 2,940 and 4,100 Mbp (1Cx); and displaying various levels of ploidy (2x, 3x, 4x, 5x, 6x and 8x).It is a relatively young genus (8-10 Mya),currently containing 287 accepted species, with its center of diversity found in Mexico (ca. 80% of the species).*

However, scarce information about the evolutionary and biogeographic origin of the 50 *Agave* known species occurring across the Caribbean. In our project, we will test different hypothesis of colonization from Mesoamerica to the six sections described for Caribbean agaves. We have sequenced 279 samples belonging to 204 taxa with hundreds of nuclear genes using a target capture approach, which quadruple the number of species sequenced in previous phylogenetic studies based solely in a few Sanger-sequenced regions. We included 17 species representatives of the six sections of the genus described in the Caribbean. Using phylogenomic approaches, we reconstructed biogeographic patterns to discern if agaves dispersed across the Caribbean from a single or multiple colonization events. Additionally, we investigate the evolutionary patterns of genome size and polyploidy.

P.1557 Caribbean Zanthoxylum (Rutaceae): species delimitation, biogeography, and conservation genetics of endangered Z. thomasianum

Thomas Heller[1], Sara Barrios[1], Jeanine Vélez-Gavilán[2], José A. Sustache[3], Martin A. Hamilton[1,4], Omar A. Monsegur-Rivera[5], Nancy Woodfield-Pascoe[6], Steven Dodsworth[7], Rocio Pérez Barrales[7,8], Marc S. Appelhans[9], Juan Viruel[1*]

*1 Royal Botanic Gardens, Kew, UK. 2 University of Puerto Rico, Mayagüez, Puerto Rico. 3 Department of Natural and Environmental Resources, San Juan, Puerto Rico. 4 South Carolina Botanical Garden at Clemson University, USA. 5 US Fish and Wildlife Service, Caribbean Ecological Services Field Office, Puerto Rico. 6 National Parks Trust of the Virgin Islands, British Virgin Islands. 7 Portsmouth University, UK. 8 University of Granada, Granada, Spain. 9 Georg-August-Universität Göttingen, Germany. *Contact: j.viruel@kew.org, juanviruel@gmail.com*

Target capture enables the recovery of hundreds of nuclear genes from a broad range of materials, such as old herbarium specimens and recently collected plant tissue. These new tools are of great utility for answering evolutionary and conservation questions at a broad range of scales, from relationships among plants at the ordinal level down to infra-specific population structure. The genus *Zanthoxylum* (Rutaceae) in the Caribbean, with high diversity and many taxonomic uncertainties, as well as facing acute human-driven threats, presents many questions to which these new molecular tools are well suited to answering. In this research, DNA sequence data, using the universal target capture bait set Angiosperms353 in combination with custom baits optimised for the genus, have been generated for over 670 samples. This represents 41 taxa of *Zanthoxylum* from across the Caribbean, and hundreds of population-level samples of Endangered *Z. thomasianum*. These data are being used to advance knowledge in three ways: Systematics of *Zanthoxylum* Sect. *Tobinia*. In this poorly understood group, we seek to test competing classifications and clarify uncertain species delimitation. Combining phylogenetic and morphometric approaches, this work is urgently required for robust conservation prioritisation. Biogeography of *Zanthoxylum* in the Caribbean. Representing a case study in Caribbean biogeography, we aim to reconstruct the evolutionary history of the genus in the region. Phylogenetic approaches will be used to better understand the processes behind the high diversity of the Caribbean. Conservation genetics and ecology of the *Z. thomasianum*. Sequence data from population-level samples of this threatened tree species from the Virgin Islands and Puerto Rico will be analysed to better understand population genetic structure, diversity and inbreeding. Combined with ecological data collected in the field (variation in the reproductive ecology of populations), those data will be used to design a conservation plan for the species.

S.176. USING PLANTS FOR RESTORATION, CONSERVATION AND MANAGEMENT OF FRESHWATER HABITATS

P.1558 Inventory, assessment and monitoring of plant conservation in two emblematic Tunisian wetlands: Dar Fatma peat bog and Garâa Sejenan

Imtinen Ben Haj Jilani[1,2], Amina Daoud-Bouattour[2], Zeineb Ghrabi-Gammar[2,3], Imen Khemiri[4], Sami Dhouib[4], Serge D. Muller[5]

1 Institut National Agronomique de Tunisie, Université de Carthage, Tunis, Tunisie. 2 Biogéographie, Climatologie Appliquée et Dynamiques Environnementales, Faculté des Lettres, des Arts et Humanités de Manouba, Université de Manouba, Manouba, Tunisie. 3 Association la Recherche en Action, REACT, Cité des Sciences-Tunis, Tunis, Tunisie. 4 World Wildlife Fund North Africa, Tunis, Tunisie. 5 Institut des Sciences de l'Evolution, Université de Montpellier, Montpellier, France.

Dar Fatma peat bog and Garâa Sejenane are two emblematic wetlands in northern Tunisia. Dar Fatma is one of the few *Sphagnum* moss peat habitats in North Africa, with a unique hydrological functioning revealed by the presence of several tremblants. Home to several rare habitats and species, the bog has been a Nature Reserve since 1993 and a Ramsar site since 2007. However, over the last ten years or so, the site has come under serious threat and is in urgent need of new protection measures. Garâa Sejenane is a former lake of around 1,500 ha, drained since the late 1950s. The high anthropic pressure exerted on this wetland has profoundly altered it, leading to the local extinction of 11 species, 5 of which are extinct in Tunisia. However, the residual habitats are still of major conservation interest, hosting almost 80 wetland taxa, 1/3 of which are rare and/or threatened. *Rumex tunetanus*, a strict endemic of the site is assessed as Critically Endangered (CR), *Persicaria amphibia*, is extremely rare in Tunisia and found only in Garâa Sejenane, the Mediterranean endemic *Pilularia minuta* (CR) and *Elatine macropoda*, whose populations are respectively the largest in the world and North Africa. Having never benefited from protection, it was only in 2021 that Garâa Sejenane was listed as a private Ramsar site. Botanical surveys carried out regularly for over 15 years on both sites have enabled us to inventory, map and assess the flora, particularly the heritage taxa. Traditional protocols for monitoring the remarkable plants and habitats of these two sites have also been drawn up. Involving managers, farmers and civil society, they are an essential tool for effective conservation and management of the ecosystem as a whole. They will enable to intervene rapidly, if necessary, to prevent any degradation.

P.1559 New tools for the monitoring of Ruppia spiralis in a restored landscape

Jordi Bou[1,2], Nerina Gilbert[1], Adrià Casacuberta[1], Fiona Corominas[1], Diego Varga[1,2], Xavier D. Quintana[3]

1 LAGP, Institute of the Environment, University of Girona, Girona, Spain. 2 BioLand – Biodiversity and landscape research group, University of Girona, Girona, Spain. 3 GRECO, Institute of Aquatic Ecology, University of Girona, Girona, Spain.

Coastal wetlands provide a wide variety of ecosystem services. In the northern mediterranean basin, these ecosystems have been severely transformed by urbanization and tourism development. Restoration is needed to recover their biodiversity and ecosystems functions. Macrophytes that live in these environments are relevant, among others, for their role in water and nutrient cycles and habitat supply and are related to high ecological state. Specifically, in mediterranean coastal lagoons, the hydrophyte *Ruppia spiralis* can be found. Despite its ecological importance, there are few studies on the species due to the limitations of traditional sampling techniques. Currently, this issue can be solved with the use of unmanned aerial vehicles and high-resolution remote sensors that are able to calculate different vegetation indices. The main objective of this work is to study the cover of *R. spiralis* over time in a restored landscape and to assess if information provided by remote sensors can help in estimating macrophyte recovery. The study was conducted in the wetlands of Baix Ter (NE Iberian Peninsula), where different restoration projects have been developed since 1999 to recover natural ecosystems. Four coastal lagoons were selected and have been seasonally monitored since 2023. In each sampling campaign, vegetation transects to measure the cover of *R. spiralis* were carried out. Simultaneously, multispectral images of the lagoons were obtained with drone flights. Six different vegetation indices have been calculated with the images (e.g., NDVI). The results show that the distribution and coverage of *R. spiralis* vary along the lagoon system. Seasonality is not well-marked, which could be explained by the plant's biology and other environmental factors. Vegetation indices show limitations on the detection of *R. spiralis,* however GNDVI seems to be effective in winter when there is a poor algal development. Such findings should be taken into consideration for future monitoring programs.

P.1560 Macroinvertebrate and environmental responses to dredging and submerged macrophytes transplantation

Hong Fu[1,2]

1 State Key Laboratory of Freshwater Ecology and Biotechnology of China, Institute of Hydrobiology, Chinese Academy of Sciences, Wuhan, China. 2 School of Geography and water@leeds, University of Leeds, Leeds, UK.

Eutrophication of freshwater ecosystems is a global problem, but restoration can be difficult due to ongoing problems relating to water pollution, sedimentary nutrient stores, and altered aquatic biodiversity. Mitigation of Eutrophication is often conducted alongside transplantation of submerged macrophytes and dredging, but knowledge of ecosystem response to post-dredging transplantation of submerged macrophytes is limited. We report a long-term (2008-2018) in-situ monitoring study to evaluate the effects of different restoration measures: dredging only (Dredged) and dredged with post transplantation of submerged macrophytes (Dredged with macrophytes) conducted in five subtropical eutrophic lakes, Taihu basin. Water and sediment nutrients, bloom-forming algae Microcystis, and macroinvertebrate were monitored every two years for each treatment and compared with reference areas (Control) established in unrestored parts of the same lake. Dredging only decreased sediment nutrients (e.g., carbon, phosphorus) significantly, however, this effect diminished about five years later. Dredged with macrophytes had a stronger, longer-lasting positive effect on water quality than dredged alone. Disturbance caused by dredging (without macrophytes transplantation) decreased the biomass of Microcystis, while transplantation of macrophytes shortly after dredging did not contribute to the decreasing of Microcystis biomass. The biomass of Microcystis in Dredged with macrophytes areas was always similar with Control over the period of our monitoring. A positive effect of submerged macrophytes transplantation post-dredging was found for macroinvertebrate abundance and diversity: Dredged with macrophytes areas had significantly higher macroinvertebrate biomass and richness than Dredged areas after 9 years' recovery. Macroinvertebrate richness in Dredged with macrophytes areas nearly doubled compared to Control; while Dredged areas were just restored to Control levels. *Synthesis and applications*: Our study provides an long-term field monitoring with new findings about the benefits and caution of submerged macrophytes transplantation post-dredging and the effect of partial restoration, which could inform eutrophic waterbody restoration schemes.

P.1561 Impact and responses to kaolin mines restoration on Tagus river's macrophyte communities

Nadia Javandel1, María D. Bejarano[1]

1 Department of Natural Systems and Resources, Polytechnic University of Madrid, Madrid, Spain.

This study examines the impacts of kaolin mining restoration on macrophyte communities in the Tagus river's headwaters, within the Alto Tajo Natural Park. Through systematic sampling from 2020 to 2023, we analyzed species composition, coverage, substrate, and water depth across ten transects in seven river reaches, categorized as upstream (control), downstream (impacted), and further downstream (recovered). Despite restoration efforts in 2021, findings indicate a lower increase in macrophyte diversity in altered reaches compared to control sites. *Chara vulgaris* and *Riccia fluitans* emerged as dominant species across all reaches post-restoration. The consistent river substrate and water depth supported the observed macrophyte patterns, highlighting the mining's influence through increased fine sediment. The study reveals that while macrophyte diversity has increased, the restoration was insufficient for full ecological recovery within three years. It underscores the need for ongoing ecological monitoring to refine restoration strategies in industrial-impacted freshwater ecosystems.

P.1562 Nature-based solutions for wastewater reuse and storage capacity improvement of water infrastructures in agriculture

Raquel Marijuan Cuevas [1], Nuria Fernández Rico [1], Bárbara Díez Rodríguez [1], Raúl Sánchez Francés [1], Isabel Martín García [2], Khalid Fahd Draissi [2], Mª Pilar Flores Sáenz [2], Guillermo Solís Sastre [2], Jordi Serramia Ruiz [3], Natalia Gómez Mateu [3], Patricia Briega Martos [3], Hugo Riquelme Ortega[3]

1 CARTIF Technology Centre, Valladolid, Spain. 2 AMAYA Environment and Water Agency of Andalusia, Seville, Spain. 3 Singular Green, Alicante, Spain.

Nature-based Solutions (NbS) play a crucial role in the restoration, conservation and management of freshwater ecosystems. NbS build on natural processes to address environmental and social challenges, benefiting both people and nature. NbS can provide a range of water-related Ecosystem Services necessary for healthy ecosystems, such as water storage and purification, soil erosion reduction and flood control, and other water-dependent Ecosystem Services related to biodiversity conservation. Furthermore, maintaining healthy ecosystems has a direct effect on improving water availability. However, freshwater ecosystems face several threats. Overexploitation of water resources for agriculture is one of the main threats of water ecosystems and is the major cause of human pressure on natural waters systems and loss of aquatic ecosystems. Therefore, it is necessary to implement NbS that can contribute to increase the availability of water resources for agriculture, reducing the withdrawal of better-quality conventional resources for other uses. In the NATMed project, we design and develop NbS to 1) using treated wastewater for irrigation purposes, and 2) improve the storage capacity of water infrastructures. On one hand, we study the most optimal combination of several types of Constructed Wetlands (CW) or wastewater depuration, previous to reclamation treatment for reaching the EU Regulation (2020/741) for irrigation purposes. On the other hand, we design Floating Gardens to prevent water evaporation and microalgae growing and increase the capacity of water storage reservoirs. In addition, when adequately designed and managed, both approaches provide further benefits related to biodiversity conservation and management. We predict that the NbS implemented can set the basis not only for more sustainable water management practices able to integrate traditional treatment methods with new innovative technologies, but also contribute to attain biodiversity conservation and management goals.

P.1563 Habitat quality assessment using indicator species in Atlantic riverside forests

Eva Martínez-Veiga[1], Jaime Fagúndez[1,2]

1 Universidade da Coruña, Departamento de Bioloxía, A Coruña, Spain. 2 Universidade da Coruña, BIOCOST research group, Centro Interdisciplinar de Química e Bioloxía, A Coruña, Spain.

The European Atlantic alluvial forests dominated by alder (*Alnus glutinosa* (L.) Gaertn.) and ash (*Fraxinus excelsior* L.) are priority conservation habitats according to the European Union legislation, that provide essential ecosystem services. Despite their high conservation value, they are in decline due to factors such as land use changes to forestry, agriculture, changes in hydrological dynamics and the intrusion of invasive exotic species, which impacts the structure and functionality of this habitat. Using indicator species to address habitat quality or conservation status is a standard method that balances field work effort with reliable results. However, the main challenge lies in the selection of such species, which is generally done through literature with limited empirical assessment. In this study, we developed and tested a method to evaluate the quality of the riverside forest of the Barcés river (A Coruña, Galicia, Spain), based on indicator species richness. Firstly, we performed a floristic survey of the study area, obtaining a total species pool. Secondly, we selected a preliminary list of 72 herbaceous plant species that are considered indicators of good habitat quality, based on bibliographic references. We sampled at 28 sites distributed along the river where we recorded presence and cover of each indicator species at five 2x4 m plots. We also measured several environmental variables such as tree cover, trunk density or diversity and we created an index to classify each site according to its habitat quality. The final selection of indicator species, based on the highest correlation with the quality index, provides the minimum number of species that explains the highest resolution of the model. This method optimizes field work to assess habitat quality and is suitable for the rapid evaluation of riparian Atlantic forests.

P.1564 Morphological variability of Myriophyllum spicatum correlated with different physicochemical parameters of water

Danijela Nikolić[1], Irena Raca[1], Ivana Kostić Kokić[1], Miodrag Đorđević[1], Marina Jušković[1], Tatjana Anđelković[1], Dragana Jenačković Gocić[1]

1 Faculty of Sciences and Mathematics, Niš, Serbia.

The objective of this study was to establish correlations between the morphological variability of *Myriophyllum spicatum* L. and various physicochemical parameters of water. For this purpose, 353 individuals of *Myriophyllum spicatum* from 15 ponds, 14 rivers, and 7 lakes in Serbia were collected and analyzed. Number of leaves in the nodus, leaf length, leaf width, number of leaf lobe pairs, leaf lobe length, internode length, stem diameter, epidermis thickness, primary cortex thickness, central cylinder diameter, aerenchyma thickness, aerial cavity area and number of aerial cavities were characters selected for analysis. Spearman's coefficient of correlation was calculated between physicochemical parameters (pH, electroconductivity, concentrations of nitrite, nitrate, phosphate, sulfate, fluoride, bromide and chloride ions) and morpho-anatomical characters. Canonical Correspondence Analyses (CCA) based on raw data were used to explain the relationships between morphological traits and environmental variables. According to Spearman's coefficient of correlation pH, concentrations of nitrite, nitrate, fluoride, and bromide exhibited a moderate to high level of correlation with morphological characters. pH showed positive correlations with characters such as internode length, leaf width, leaf lobe length, stem diameter, primary cortex thickness, central cylinder diameter, aerenchyma thickness, aerial cavity area, and negative correlation with the number of leaf lobe pairs. Nitrate and nitrite were negatively correlated with stem characters including stem diameter, primary cortex thickness, aerial cavity area, and aerenchyma thickness. CCA revealed that 41% of the morphological characters-environment relationship was explained by the first two axes. The first axis was negatively defined by pH and positively with nitrates. The second axis was characterized positively with chlorides and sulfates. The CCA plot differentiated the three morphological groups of the population according to the first CCA axis. The study's findings underscored the considerable adaptability of *Myriophyllum spicatum* to diverse environmental conditions, shedding light on the invasive nature of this species in introduced regions.

P.1565 The relationship between morpho-anatomical traits of Ceratophyllum demersum and physicochemical parameters of water habitats

Irena Raca[1], Danijela Nikolić[1], Anastasija Jevtić[1], Ivana Kostić Kokić[1], Tatjana Anđelković[1], Miodrag Đorđević[1], Dragana Jenačković Gocić[1]

1 Faculty of Sciences and Mathematics, Niš, Serbia.

The research was designed to define the impact of physicochemical parameters of water (the pH value, electroconductivity, concentrations of chloride, nitrite, bromide, nitrate, phosphate, and sulfate ions) on morpho-anatomical features of *Ceratophyllum demersum*. The list of morpho-anatomical features analyzed per each of 350 individuals collected from 35 localities in Serbia was as follows: the internode length, leaf lobe, base length, complete leaf length, the total teeth number per leaf, the number of leaves without/with one/two/three/four dichotomies, and the total number of leaves in the fifth node; the leaf cross-section surface area, thickness, and diameter, the total number, average and total surface area of air cavities, the total surface area of mechanical tissue and epidermal layer thickness; the stem cross-section surface area, the number of air cavities in the cortex, epidermal, parenchyma, aerenchyma and cortex tissue thickness, the vascular cylinder surface area and the number of hydropotes. According to Spearman's Correlation Coefficient (p<P.1), the concentrations of chlorides, nitrates, and phosphates showed moderate (0.30-0.49), while bromides and sulfates expressed moderate to high levels of correlation (0.50-1.00) with particular morpho-anatomical traits. A positive correlation was revealed between the concentration of chlorides, bromides, sulfates and the leaf lobe on the one, and the concentration of phosphates and the number of leaves without dichotomies and bromides and the number of hydropotes on the other hand. The concentration of bromides was negatively correlated with the leaf diameter, its cross-section, and the average and total surface area of air cavities. The last mentioned two characters expressed a negative correlation with the concentration of sulfates. The negative correlation was confirmed for the concentration of nitrates and the epidermal layer thickness. Finally, the correlation examined becomes particularly important when observed in the context of the phytoremediation potential of *C. demersum*.

P.1566 Functional response of key plant species in ecological restoration of tropical dry forest (Huila, Colombia)

Alisson Dennis González-Cortes[1], Natalia Rodríguez-Jiménez[1], Yesid Alejandro Mariño-Macana[2], Mary Lee Berdugo-Lattke[3,4]

1 Semillero Tygua, Programa de Biología, Facultad de Ingeniería y Ciencias Básicas, Universidad Central, Fundación Natura Bogotá, Bogotá, Colombia. 2 Programa de Biología, Facultad de Ingeniería y Ciencias Básicas, Universidad Central, Bogotá, Colombia. 3 Grupo de investigación de agua y desarrollo sostenible, Semillero Tygua, Programa de Biología, Facultad de Ingeniería y Ciencias Básicas, Universidad Central, Bogotá, Colombia. 4 Grupo de investigación de biodiversidad y conservación, Instituto de Ciencias Naturales, Universidad Nacional de Colombia, Bogotá, Colombia.

In the process of propagating and managing key plant species for ecological restoration, it is necessary to detail their performance in the phases of acclimatization (nursery) and transplanting. In this research, the response of four plant species from the tropical dry forest (TDF) was studied under different soil water availability (WA) conditions: 100%, 79.6%, 65.9%, and permanent wilting point (PWP, without irrigation). Growth, survival, and variation of functional traits were analyzed in 480 individuals (120 per species) of *Ochroma pyramidale* (pioneer), *Senna spectabilis* (pioneer), *Tabebuia rosea* (intermediate-advanced), and *Astronium graveolens* (intermediate-advanced). The experiment included 30 individuals per treatment per specie, statistical analyses included linear mixed models for repeated measurements, principal component analysis, ANOVA, and correlations. We found that for pioneer species, the optimum growth rate is at 79.6% (WA), while for intermediate-advanced succession species, it is at 79.6% and 65.9% (WA). Regarding functional traits, differential relationships were observed related to species and treatment. However, it was common that the functional space was defined by the contribution of variance for stem traits (diameter and pore density), followed by the proportion of secondary roots (independence with ecological role). *Ochroma pyramidale* (pioneer) and *Tabebuia rosea* (intermediate-advanced) showed resistance to drought, *Astronium graveolens* (intermediate-advanced) showed tolerance to drought and *Senna spectabilis* (pioneer) showed avoidance of drought and requires more water availability. In conclusion, these key plant species for TDF ecological restoration require differential management of soil water availability to improve their response in growth, transplanting, and nursery survival. This can ensure greater success when they are planted in the areas to be restored.

S.177. WORLD FLORA ONLINE: DEVELOPING TAXONOMIC CONSENSUS FOR LAND PLANTS SUPPORTING SCIENCE, CONSERVATION AND SUSTAINABLE USE

P.1567 A new classification system and taxonomic synopsis for Malpighiaceae (Malpighiales, Rosids) based on molecular phylogenetics, morphology, palynology, and chemistry

Rafael Felipe de Almeida[1,2], Isa L. de Morais[1], Thais Alves Silva[1], Higor Antonio-Domingues[2], Marco Octávio de Oliveira Pellegrini[2]

1 Universidade Estadual de Goiás, campus Sudoeste, Quirinópolis, Goiás, Brazil. 2 Royal Botanical Gardens, Kew, Richmond, UK

Malpighiaceae has undergone unprecedented changes in its traditional classification in the past two decades due to several phylogenetic studies shedding light on the non-monophyly of all subfamilies and most tribes and genera. Even though morphological characters were used to reconstruct the last molecular generic phylogeny of Malpighiaceae, a new classification system has never been proposed for this family. Based on a comprehensive review of the last twenty years of published studies for this family, we propose a new classification system and provide a taxonomic synopsis for Malpighiaceae based on molecular phylogenetics, morphology, palynology, and chemistry as a baseline for the systematics, conservation, and taxonomy of this family worldwide. Malpighiaceae currently comprises two subfamilies (Byrsonimoideae and Malpighioideae), 12 tribes (Acmanthereae, Acridocarpeae *trib. nov.*, Barnebyeae *trib. nov.*, Bunchosieae *trib. nov.*, Byrsonimeae, Galphimieae, Gaudichaudieae, Hiptageae, Hiraeeae, Malpighieae, Mcvaughieae *trib. nov.*, and Ptilochaeteae *trib. nov.*), 72 genera (incl. *Mamedea gen. nov.*), and 1,495 accepted species (715 of which are currently under some kind of extinction threat). We present identification keys for all subfamilies, tribes, and genera, a full morphological description for the proposed new genus, the re-circumscription of ten genera alongside the needed new combinations, the proposition of several new synonyms, the typification of several names, and notes on the taxonomy, distribution, conservation, and ecology up to the genus rank. Morphological plates are also provided to illustrate the immense diversity of morphological traits used in the new classification and synopsis.

P.1568 Vascular plants of Azerbaijan: a nomenclatural checklist of nonflowering and flowering plants

Rashad A. Salimov[1],Valida Ali-zade[2], Naiba Mehdiyeva[3]

1 Faculty of Science, Sumgayit State University, Sumgayit, Azerbaijan. 2 Natural History Museum, .Baku, Azerbaijan. 3 Institute of Botany, Baku, Azerbaijan.

An updated checklist of plant species increases knowledge about flora available for a given area and are fundamental to the public awareness and conservation of plant diversity. These kinds of achievements are closely linked to the implementation of Global Strategy for Plant Conservation Target 1. In recent years, as part of the international projects “Caucasus Plant Biodiversity Initiative”, 2009-2019 and World Flora Online, botanists of Azerbaijan on the basis of ongoing systematic and an overview of nomenclature studies and an updated classification of dicot families, including genera and infrageneric taxa of the flora of Azerbaijan, are presented. As a result of the latest research, 57 families of bryophytes (152 genera and 504 taxa), 17 families of pteridophytes (30 genera and 97 taxa), 5 families of gymnosperms (20 genera and 17 taxa) and 27 families of monocotyledons (222 genera and 974 taxa) has been recorded for the flora of Azerbaijan. Currently, a systematic review and updated classification of the dicotyledonous families including the genera and infrageneric taxa of Azerbaijan flora is ongoing. Because of the systematic and nomenclatural research continues the total number of families, genera and species can be judged after the completion of the ongoing work on the checklist of the vascular plant species of Azerbaijan. It became necessary to provide an easy update taxonomic backbone of these plants by including all published names (both accepted names and their synonyms) and creating an electronic system. An up to date nomenclatural checklist will be a key text to develop e-flora of Azerbaijan and is necessary for future systematics, ecology, physiology, ethnobotany and phytochemistry in Azerbaijan.

P.1569 The development of an information database for the biodiversity studies of flora in Kazakhstan

Turuspekov Y.[1], Almerekova S.[1], Yermagambetova M.[1], Abugalieva S.[1]

1 Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan.

Kazakhstan, being a vast and diverse country with different climate zones, is home to a rich and varied flora. The country's flora comprises approximately 6,000 plant species, and about 10% are considered endemic. It is necessary to monitor, study constantly, and inventory wild flora using modern botany, molecular taxonomy, and bioinformatics methods. The research aimed to study the genetic diversity of the Kazakhstan flora and create an information database (DB). In the framework of Program 0237/PTF (2015-2017), the genetic diversity of endemic, rare, endangered, and wild-growing economically valuable plant species was started. In the framework of the grant (AP05131621), an open web resource with digitized data on the genetic diversity of flora in Kazakhstan was created. A database on the botanical description of the collected around 450 endemic, rare, endangered, and economically useful species belonging to 233 genera and 79 families of the Kazakhstan flora has been elaborated. Continuing these studies on the genetic diversity analysis of plant genera like *Juniperus*, *Tulipa*, and *Salsola* offers a promising avenue to gain crucial insights into their population structure, phylogenetic relationships, and potential conservation strategies. Within the scope of these studies, the first comparative analysis of chloroplast genomes in Kazakhstan has been initiated.

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P.1570 The flora of Cambodia project

Visotheary Ung[1]

1 Institut de Systématique, Évolution, Biodiversité, Muséum national d'Histoire naturelle, Centre National Recherche Scientifique, Sorbonne Université, Université des Antilles, Paris, France.

Cambodia, located in continental Southeast Asia, is a developing country and a biodiversity hotspot (Myers et al. 2000, Sodhi et al. 2010). France and Cambodia share a long history of relations and collaboration. The French presence in Cambodia dates back to 1863 when Cambodia became a French protectorate. It later became part of French Indochina in 1887, alongside other French colonies and protectorates. This French presence not only facilitated the "rediscovery" of Angkor Wat and Angkor Thom by Henri Mouhot, a French naturalist, botanist, and entomologist, but also contributed to the collection of Cambodia's biodiversity. The protectorate status for Cambodia ended in 1949, and it declared its independence in 1953.During the same period, the "*General Flora of Indo-China*" (Gagnepain et al. 1907) began its publication in 1907 and continued until 1951 by French editors. In 1960, this flora was reinitiated as the "*Flora of Cambodia, Laos, and Viêt-Nam*". Since 2013, it is jointly edited by the Museum National d'Histoire Naturelle in Paris and the Royal Botanic Garden of Edinburgh.The Flora of Cambodia project arose from a simple question: why is the flora still managed jointly with Laos and Viêt-Nam? The three countries have been independent since 1954, their respective floras should be separate and published independently. The project's initial phase involves compiling an up-to-date understanding of Cambodia's plant life, including an inventory of collections housed at the Museum National d'Histoire Naturelle in Paris and accessible Cambodian floristic data online through the Global Biodiversity Information Facility (GBIF) and other sources (Joyce et al. 2020).The ultimate goal is to produce a comprehensive flora of Cambodia.In the short term, the project aims to provide an open and curated checklist of vascular plants of Cambodia, in multiple languages, including Khmer.

S.178. XYLEM ANATOMY AS A CENTRAL HUB LINKING FLUID TRANSPORT PROCESSES FROM THE INDIVIDUAL PLANT LEVEL TO ECOSYSTEMS

P.1571 Isohydry and anisohydry of photosynthetic stems – a survey of desert ecosystems

Osedipo Adegbeyeni1, Eleinis Ávila-Lovera[1]

1 School of Biological Sciences, University of Utah, Salt Lake City, USA.

The way plants regulate their water use is of paramount importance for drought tolerance and survival, especially in desert species that face water limitation year-round. When there is a drought, plants can either close their stomata, limiting water loss and carbon gain but maintaining relatively constant water potentials (Ψ), or keep their stomata open and continue gaining carbon at the expense of losing water and reducing leaf and stem Ψ. This stomatal regulation of plant Ψ is known as the degree of iso-anisohydry. We studied 17 species from two desert sites in southern Utah to compare the stomatal regulation of leaves and photosynthetic stems, and whether they differ in sites with different mean annual temperature (MAT) and precipitation (MAP). Rio Mesa is located in the Colorado Plateau (MAT: 13.8 °C, MAP: 240 mm), and Beaver Dam is located in the Mojave Desert (MAT: 15.1 °C, MAP: 264.9 mm). We did not find differences in the degree of iso-anisohydry between leaves and photosynthetic stems; however, we found more isohydric behavior in species from Beaver Dam, the relatively warmer and wetter site. We also found that stem instantaneous water-use efficiency (WUE_{ins}) was higher in Beaver Dam, which was attributed to a lower stomatal conductance (supporting the isohydric behavior) instead of a greater photosynthetic rate. However, there were no differences in leaf WUE_{ins} between sites or in any other gas exchange trait between organs and sites. The stricter stomatal regulation in Beaver Dam may be related to the lower (more negative) predawn and midday Ψ experienced by plants despite its higher MAP. Higher MAT in Beaver Dam, and potentially greater vapor pressure deficit, may be modulating these responses. We conclude that climate has a stronger effect on the degree of iso-anisohydry of desert plants than the identity of the organ.

P.1572 Gelatinous fibretracheids as an escape mechanism for the physiological drought phenomenon

Cátia H. Callado[1]; Gabriel U. C. A. Santos[2]; Cláudia F. Barros[3]; Fábio R. Scarano[4], Cecilia G. Costa[3]

1 Laboratório de Anatomia Vegetal, Departamento de Biologia Vegetal, Instituto de Biologia Roberto Alcantara Gomes, Universidade do Estado do Rio de Janeiro – UERJ, Rio de Janeiro, Brazil. 2 Colégio Pedro II, Duque de Caxias, Brazil. 3 Instituto de Pesquisas Jardim Botânico do Rio de Janeiro, Rio de Janeiro, Brazil. 4 Departamento de Ecologia, Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil.

Alchornea sidifolia is a tree species used in the regeneration of degraded forest environments and which grows in both non-flooded and flooded soils. We compared the wood anatomy of trees growing under both conditions in Atlantic Forest remnants in the state of Rio de Janeiro, Brazil, to understand intraspecific aspects of the adaptation of tropical woody species to these conditions. Trees from permanently flooded soils showed wider, shorter, and less frequent vessel elements; wider fibretracheids, with a greater proportion of the gelatinous type; and a lower frequency of radial parenchyma, but with longer strands of axial parenchyma. These results indicate that *A. sidifolia* trees growing in permanently flooded sites do not show water deficit and that the species is capable of maximizing water use in this growth condition. This conclusion may be directly related to the greater proportion of gelatinous fibretracheids in flooded trees and is contrary to what was expected for wood anatomy of trees under physiological drought.

P.1573 The relevance of the successional group on xylem embolism resistance is size dependent

Debora Coelho-Silva[1], Marciel J. Ferreira[2], Guilherme S. Modolo[2], Diego S. Podadera[1], Carmen R. Marcati[1]

1 São Paulo State University, Botucatu, Brazil. 2 Federal University of Amazonas, Manaus, Brazil.

Numerous studies have identified plant height as a key determinant of greater xylem embolism resistance (*P50*); however, in tropical forests, this relationship appears less straightforward. Here, we investigate whether xylem resistance to embolism is influenced by the successional group while controlling for two growth variables: diameter and height. Our study was conducted in a 17-hectare area located in the Amazonas region of Brazil (2°38° S, 60°03° W), comprising a 5-year-old enrichment plantation within a 25-year-old secondary forest. The experimental design employed randomized blocks with five replications. Non-pioneer species examined were *Bertholletia excelsa* (Bonpl.), *Carapa guianensis* (Aubl.), and *Hymenaea courbaril* (L.); pioneer species included *Cedrela fissilis* (Vell.) and *Tabebuia rosea* (Bertol.) Bertero ex A.D.C. Basal stem diameter and total height measurements were collected bimonthly, with relative growth rates (RGR) calculated using the formula: $RGRX = \ln(X2) – \ln(X1) / (T2 – T1)$. *P50* measurements were conducted during the rainy season of 2022, with one branch per individual per species assessed under three light conditions across five blocks, utilizing a semi-automatic pneumatic method. Our results indicate a significant effect of the successional group on *P50*, even after adjusting for relative growth (ANCOVA: diameter F= 5.59, P < P.5; height: F= 8.73, P < P.1). Contrary to expectations, non-pioneer species exhibited greater embolism resistance only at higher RGR, suggesting that larger individuals in terms of height and diameter within these species are more adept at coping with water stress. Pioneer species, conversely, maintained consistently low *P50* values across relative growth rates. This study underscores the necessity of considering successional groups in investigations of xylem resistance to embolism within tropical regions, where forest structure is intricately shaped by these dynamics.

P.1574 Predicting branch-scale hydraulic capacitance across European trees

Sonia Hernando[1,2], Oliver J. Binks[1], Jordi Martínez-Vilalta[1,2], Maurizio Mencuccini[1,3]

1 CREAF, Bellaterra, Spain. 2 Autonomous University of Barcelona, Bellaterra, Spain. 3 ICREA, Barcelona, Spain.

Water storage capacity gives a reservoir of water that can be used during periods of high transpiration and during stressful conditions, avoiding dehydration of precious organs and reducing the impacts on their functionality. Capacitance has importance in plant ecology because it is related to the capacity for water storage, at scales varying from individual leaves to branches or even ecosystems. Despite, capacitance is a poorly defined trait, partly because it is not clear on what bases (or units), it should be expressed. To eliminate size-dependency, it is generally normalised by mass, leaf area or water content. However, the impacts of these different definitions have not been systematically investigated. In this study, the main objective was to predict whole-branch capacitance and capacity to detect the relative impacts of allometric scaling versus the functional traits of the individual tissues. For that determination, we measured whole-branch capacitance and total dry mass, its distribution among different tissues (leaves, bark and wood) and functional traits such as leaf turgor loss point (as a measure of maintenance of cell turgor pressure), wood density (as an anatomical trait related to wood water storage) and P50 (as a measure of xylem hydraulic conductivity). All these measurements were performed at about sixty sites across Europe on four tree species (*Populus nigra, Fagus sylvatica, Pinus sylvestris* and *Pinus pinaster*). We will present results showing how the allometry of tissue distribution of each species influences branch-level capacitance and consequently its water use. Total biomass was the most important explanatory variable for predicting capacitance and capacity, compared to the studied traits. The units on which capacitance is expressed may affect the proper upscaling of tissue-level properties to whole trees. Extensive properties indicate a strong allometric dependence and intensive properties can still be allometrically dependent on biomass.

P.1575 Stem anatomy of species of Cereinae (Cactoideae, Cactaceae) and ancestral state reconstruction

Mariana R. Fantinati[1], Alice Calvente[2], Patricia Soffiatti[3]

1 Botanical Museum "Frederico Carlos Hoehne", Unesp, Assis, Brazil. 2 Department of Botany and Zoology, UFRN, Natal, Brazil. 3 Department of Botany, UFPR, Curitiba, Brazil.

Species of Cereinae have a remarkable occurrence in arid and semiarid regions of eastern Brazil. However, there is a lack of anatomical studies on the group. The aim of this study was to investigate the existence potential diagnostic and phylogenetic anatomical traits of the dermal system and part of the fundamental system of representatives of 11 genera of Cereinae. Qualitative and quantitative traits of the stem of 30 species belonging to the subtribe and two species of Trichocereinae and Rebutiinae were studied in surface view and cross sections. The evolutionary patterns showed in ancestral character state reconstruction analysis demonstrated that most of the anatomical features analysed are homoplastic, but some of them corroborate clades representing genera, or combined genera. The species present skin features informative for some groups within the subtribe such as the markedly plicate cell outline shared by all *Melocactus* species, the abundant prismatic crystals in the epidermal cells shared by all species of *Arrojadoa* and *Stephanocereus*, the presence of druses with the rounded-oval-shape outline in the spongy parenchyma shared by all species of *Cereus* and *Cipocereus*, and the combination of druses with the rounded-oval-shape outline and in concretions in the spongy parenchyma shared by *Cereus* species. These groups emerge as clades strongly supported by Bayesian analyses in a recent phylogeny for Cereinae, demonstrating the relevance of anatomical characters in taxonomy. Our results showed some anatomical novelties for Cereinae species as a basis for further and more detailed anatomical studies in a systematic framework.

P.1576 Quantitative wood anatomy of treeline tree seedlings taking into account eccentricity and compression wood

Eunice Romero[1], Edgar J González[2], Václav Treml[1]

1 Department of Physical Geography and Geoecology, Faculty of Science, Charles University, Czech Republic. 2 Department of Ecology and Natural Resources, Faculty of Sciences, National Autonomous University of Mexico, Mexico.

Treelines are forests growing at their altitudinal limit, where low temperature affects their growth. Treeline seedlings are key to understanding treeline dynamics because they are particularly sensitive to environmental conditions; they are exposed to summer droughts, winter freezing temperatures and mechanical forces such as snowpacks. Their wood traits determine hydraulic and mechanical functions, ultimately having impacts on their growth. Mechanical forces applied to seedling stems can generate eccentric growth and the formation of compression wood; this wood is different from unaffected wood in certain attributes that may modify the functions and growth of the seedlings. In this study we analysed the quantitative wood anatomy considering the eccentric growth of *Picea abies* seedlings collected in European treelines. We calculated compression wood plus latewood proportion per cross section. We measured manually, in transects, per ring, the earlywood and latewood tracheid lumen diameter and width, in tangential and radial directions, and wall thickness. We constructed generalized linear mixed-effects models to estimate and compare means of the afore mentioned variables between wide (containing high proportion of compression wood) and narrow transects of the cross sections. We also estimated and compared variability through standard deviations. In both cases we considered the height of each seedling and the sample pseudoreplication. We found unexpected results in variables related with hydraulic and mechanical functions: a greater mean tracheid lumen diameter in the wider transects of the cross sections, which contain less compression wood; and we found no significant differences in mean tracheid wall thickness although mean was greater in wide transects. Analysing wood anatomical traits taking into consideration the eccentric growth and the proportion of compression wood in the stem of treeline tree seedlings is important to understand their hydraulic and mechanical functions, and therefore their ecological performance at the treeline.

P.1577 Mineral crystals and secretory structures in the wood and bark of Indian Sundarbans' mangroves and their systematic potential

Sreya R. Parbat[1], Subir Bera[1]

1 Department of Botany, Ballygunge Science College, University of Calcutta, Kolkata, India.

In the present study, the distribution patterns, morphology, cellular location, chemical composition of mineral (excluding silica bodies) and organic inclusions in the wood and bark of the true mangroves and their associate taxa from the Indian Sundarbans were investigated by using Light Microscopy, Scanning Electron Microscopy and Energy-Dispersive X-ray Analysis. Restricted occurrence of such inclusions in wood and bark is found to be delimiting certain mangrove taxa. These inclusions are calcium oxalate crystals which can occur in a wide range of structural forms- prismatic, druses, raphides, acicular, styloid, spherical, cubic, crystal sand etc and based on their availability certain mangrove genera could be recognized e.g., styloid in *Avicennia*, Rhomboids in Sonneratia etc. Moreover, the cells accommodating such inclusions are found to be diagnostic at certain taxonomic levels viz, chambered crystalliferous parenchyma and fibres in *Dalbergia*, idioblast in *Aegiceras* etc. Different hypotheses have been proposed about possible function of such crystals in plants, which are: defence against herbivory, cellular ion balance, tissue rigidity and support, detoxification of oxalic acid and/or heavy metals, light gathering and reflection and bulk calcium regulation. As the mangroves are resistant to breakage during strong waves, high wind speed and other natural calamities and also surviving in harsh coastal environment, these crystals may provide additional support along with other mechanical tissues and may help in lowering water potential for better water uptake in physiologically dry condition. The present study also includes the distribution of laticifers and tannin cells in bark and woods of different mangrove taxa and their potential in distinguishing them at different taxonomic levels.

OTHERS

P.1579 Endemic diversity and distribution of the Altai Mountain vascular flora across biodiversity hotspots, conservation gap and global

Shukherdorj Baasanmunkh[1p], Andrey Erst[2], Batlai Oyuntsetseg[3], Hyeok Jae Choi[1]

1 Department of Biology and Chemistry, Changwon National University, Changwon, South Korea. 2 Central Siberian Botanical Garden, Novosibirsk, Russia. 3 Department of Biology, National University of Mongolia, Ulaanbaatar, Mongolia.

The Altai Mountains of Central and North Asia are biologically rich and comprise a wide range of ecosystems and phytogeographical regions. According to the latest checklist, a total of 321 endemic vascular plant species, including 217 endemic and 104 subendemic taxa, have been recognized in the Altai Mountain Country (AMC). Among these, over 60% of the total endemic species were successfully barcoded with at least one of three common DNA barcoding loci. In this study, we conducted species risk assessment, distribution evaluation and conservation gap analysis for the endemic vascular flora of the AMC. The conservation status of 217 endemic species was assessed at the global level using the ConR package. As a result, 197 species were evaluated as potentially threatened, and 20 species were evaluated as not threatened. The AMC was divided into 350 grid cells, with a grid cell size of 50 × 50 km^2, for the spatial assessments of the endemic vascular plants. A total of 2,657 unique georeferenced occurrences of endemic species were found and analyzed with three endemism indices, species richness (SR), weighted endemism (WE), and corrected weighted endemism (CWE), to quantify geographic patterns and centers of endemism across the whole AMC. The results showed that the endemic species are spread across 186 grid cells and distributed unevenly within the AMC. According to the conservation gap analysis, the main hotspots of endemism (*i.e.*, SR and WE indices) were found at high elevations in the Russian Altai, while the CWE points to the Kazakh Altai as a hotspot, and many such hotspots are currently afforded no formal protections. Finally, we have established that the Baitag Bogd Mountain is deemed an important plant area, considering the diversity of threatened and endemic species across the AMC.

P.1580 Comparative study on habitat loss impact on two narrow-distributed species’ reproductive strategies: from flowers to seedlings

Joshua Borràs1, Amparo Lázaro[2,3], Miquel Capó[4], Joana Cursach[1]

1 Research Group on Plant Biology under Mediterranean Conditions, Department of Biology, University of Balearic Islands, Palma, Spain. 2 Global Change Research Group, Mediterranean Institute for Advanced Studies (UIB-CSIC), Esporles, Spain. 3 Area of Ecology, Department of Biology, University of Balearic Islands, Palma, Spain. 4 Plant & Animal Ecology Lab. Centro para la Conservación de la Biodiversidad y el Desarrollo Sostenible, Universidad Politécnica de Madrid, Madrid, Spain.

Natural habitat loss is a major threat to biodiversity worldwide. This is particularly pronounced in insular ecosystems, which are often biodiversity hotspots and home to a multitude of endemic species. However, few studies have analyzed how the complete reproductive cycle of plants, from flowering to seedling survival, is affected by habitat loss in islands. Here, we studied two co-occurring species with contrasting reproductive strategies: *Centaurium bianoris* (Gentianaceae), an annual herbaceous plant, and *Teucrium capitatum* subsp. *majoricum* (Lamiaceae), a perennial shrub. For that, we selected six sites in Mallorca (Balearic Islands, Spain) with varying degrees of natural habitat loss, measured as the percentage of natural habitat within a 2km radius. At each site, we conducted focal observations of pollinator visits and performed pollen exclusion experiments. Then, we recorded fruit set, seed set, pre-dispersal predation, and seedling recruitment. Our findings revealed fascinating differences between the two species. Despite the high capability for self-pollination and the abundant fruit and seed production of *C. bianoris*, the species showed a low seedling emergence and survival. Otherwise, *T. capitatum* subsp. *majoricum* relies heavily on pollinators and produces fewer fruits and seeds that are dispersed by ants. Interestingly, *T. capitatum* subsp. *majoricum* attracted more pollinators in sites with greater habitat loss, leading to increased fruit production. However, these populations were more sparse and with smaller individuals, indicating potential recruitment and survival challenges. Our study underscores the importance of examining the complete plant reproductive cycle when assessing the impact of habitat loss. This comprehensive approach allows us to better understand the intricate interplay between plants and their environment, ultimately contributing to more effective conservation strategies. Furthermore, our research highlights the need for further exploration of plant reproduction response to global change. We hope this work will inspire further studies and contribute to innovative conservation approaches.

P.1581 Carbohydrates reserves and pollen viability in European hazelnut (Corylus avellana L.): a defense strategy against changing climatic conditions.

Claudio Brandoli[1], Elisabetta Sgarbi[1,2]

1 BIOGEST-SITEIA, University of Modena and Reggio Emilia, Reggio Emilia, Italy. 2 Department of Life Sciences, University of Modena and Reggio Emilia, Reggio Emilia, Italy.

The outcome of a pollination event is constrained by the formation of a mature gametophyte, which depends on the availability of nutrients during its development. A low intake of carbohydrates, due to drought or impoverishment of the soil can cause pollen sterility. In this study we propose a correlation between sucrose content, viability and germinability in the European hazelnut. The analysis was performed on pollen samples of four wild type (WT) hazelnut accessions, from field collections in the Northern and Central Italy. All samples reported high levels of viability - between 80 and 96%, showing a completely accession-specific trend. When subjected to forced dehydration, all accessions lowered their levels of viability down to 90%, and then recovered the initial values once appropriate rehydration occurred. Carbohydrates analysis revealed that glucose and fructose were almost absent in hazelnut pollen and starch was not detectable. On the contrary, the sucrose analysis revealed that concentration followed the trend of pollen viability and germinability throughout the dispersal phases. The reaction of pollen to dehydration and rehydration indicates an acquired ability of hazelnut pollen to bypass extreme dry climatic conditions and then recover full viability once right conditions have been re-established. These data suggest a direct involvement of sucrose in the protection of plasma membranes from dehydration, in the maintenance of pollen viability and promoting germinability. The influence of climatic condition on phenology in hazelnut trees was confirmed by the correlation between the beginning of flowering and the variations in temperature and RH found at a regional level.

P.1583 Paleontological heritage of the state of Veracruz, Mexico and paleobiological collection of the Universidad Veracruzana

Gustavo Carmona-Díaz[1,2,*], Alfredo Delgado-Calderón[2], Saúl Hernández-Carmona[3], Alejandro Retureta-Aponte[1]

*1Faculty of Agricultural Production Systems Engineering, Universidad Veracruzana, Acayucan, Mexico. 2 Museum of Anthropology and History of the Universidad Veracruzana, Xalapa, Mexico. 3 Institute of Neuroethology, Universidad Veracruzana. Xalapa, Mexico. *gcarmona@uv.mx*

The state of Veracruz, located in the coastal area of the Gulf of Mexico, has many fossil remains present in various geological formations ranging from the Jurassic to the Pleistocene. But from the time of the Spanish conquest to the present day, the fossils of Veracruz have been subject to looting, sale, deterioration and destruction, or at the very least, they are kept in private confinement. Since 2001, the Universidad Veracruzana through the Museum of Anthropology and History (MAX) has had the objective of investigating, collecting, recording and making known the important paleontological heritage of the state of Veracruz. Until a few years ago, Veracruz did not figure among the states of the country as an important area for Paleontology. Paleobotanic findings in Veracruz have shown the opposite, but no one had done paleobiological research in a systematic way and with an academic purpose. The fossils found in Veracruz range roots, stipites, trunks, leaves, flowers and fruits of a great variety of angiosperms, ferns and Cycadales. Among some new fossil records from Veracruz are *Juglans veracrucensis* and the first fossil record of trunks of a Cicadaceae genus *Dioon*, show the rich paleontological heritage of Veracruz, Mexico. This fossil material will form the scientific collection of the Universidad Veracruzana that will be exhibited at the MAX.

P.1584 Diversity of weeds and associated entomofauna in the incidence of Diaphorina citri in an organic and a conventional orchard in Veracruz

Carlos Castillejos[1], Salvador Garibay[2], Sonia Rojas[1], Carolina Rojas[1]

1 Universidad Nacional Autónoma de México, Ciudad de México, Mexico. 2 Instituto de Investigaciones para la Agricultura, Frick, Switzerland.

During the three-year period of Valencia orange production, the diversity of weeds and associated insects was compared on the incidence and abundance of *Diaphorina citri*. In two orchards, one with organic management and the other with conventional management. The developed methodology consisted of sampling flora and entomofauna during the sprouting periods of the orange trees and the four seasons of the year. Likewise, the number of *D. citri* organisms was counted in their different stages of egg-nymph-adult development. The richness of weeds and associated entomofauna was evaluated. In addition, the Shannon-Weiner diversity index was calculated for weeds and insects in each orchard and the diversity present in the orchards was compared using the Jaccard index. The Pearson correlation index was also calculated between the aforementioned parameters. The organic garden presented a richness of 144 species, highlighting Asteraceae (30), Poaceae (16), Fabaceae (13) and Euphorbiaceae (6). In the conventional orchard the richness was 70 species, Asteraceae (17), Poaceae (13), Fabaceae (6) and Euphorbiaceae (5) stand out. The Shannon-Wiener diversity index of the orchards was 3.478 for the organic and 2.846 for the conventional. It was estimated that the treatments present a similarity of 35%. For the entomofauna, richness was determined in 13,450 individuals of 18 orders for the organic and 5,132 for the conventional, the Shannon-Wiener diversity indices were 2,051 organic and 1,889 conventional. The population density of *D. citri* was 680 individuals in the organic and 5907 for the conventional, with an incidence concentrated in the budding season of the trees in winter, late February and early March. A 700% reduction in the amount of *D. citri* in the organic garden was evaluated.

P.1585 MircoRNA regulation of hormone- and flavonoid-signalling during floral and fiber development in cotton (Gossypium)

Bhupendra Chaudhary1, Sakshi Arora[2]

1 School of Life Sciences, Jawaharlal Nehru University, New Delhi, India. 2 School of Biotechnology, Gautam Buddha University, Greater Noida, India.

Various plant development activities and stress responses are tightly regulated by various microRNAs (miRNA) and their target genes, or transcription factors in a spatiotemporal manner. Here, to exemplify how flowering-associated regulatory miRNAs synchronize their expression dynamics during floral and fiber development in cotton, constitutive expression diminution transgenic lines of auxin-signaling regulatory Gh-miR167 (35S-MIM167) were developed through target mimicry approach. '*Moderate*' (58% to 80%)- and '*high*' (>80%)- Gh-miR167 diminution mimic lines showed dosage-dependent developmental deformities in anther development, pollen maturation, and fruit (=boll) formation. Cross pollination of 35S-MIM167 lines with wild type (WT) plant partially restored boll formation and emergence of fiber initials on the ovule surface in 'moderate'-diminution lines. Gh-miR167 diminution favored organ-specific transcription biases in miR159, miR166 as well as miR160, miR164, and miR172 with their target genes during anther and petal development, respectively. Similarly, accumulative effect of percent Gh-miR167 diminution, cross regulation of its target ARF6/8, and temporal mis-expression of hormone signaling- and flavonoid biosynthesis-associated regulatory miRNAs at early fiber initiation stage caused irregular fiber formation. Spatial and temporal transcription proportions of regulatory miRNAs were also found crucial for the execution of hormone- and flavonoid-dependent progression of floral and fiber development. These observations discover how assorted regulatory genetic circuits get organized in response to Gh-miR167 diminution and converge upon ensuing episodes of floral and fiber development in cotton.

P.1586 Comparative RNAseq analysis of style response to heterospecific pollen across a spectrum of genetic distance

Rachel Cohen[1], Deren Eaton[1]

1 Department of Ecology, Evolution, and Environmental Biology, Columbia University, New York, USA.

Heterospecific pollen transfer negatively affects both male and female reproductive fitness in plants and a number of floral traits are hypothesized to have evolved to limit foreign pollen receipt and effects. One hypothesis for the decrease in maternal reproductive success (*e.g.*, seedset) following heterospecific pollen receipt is the physical clogging of the stigma and/or style by heterospecific pollen tubes, blocking the normal growth of conspecific pollen tubes in the style. If heterospecific pollen can germinate pollen tubes that penetrate stigmas, we may expect some form of molecular-level recognition of heterospecific vs. conspecific pollen tubes, perhaps to suspend pollen tube growth somewhere in the stigma or style and prevent fitness costs. Whereas the genetic underpinnings of pollen tube growth have been studied extensively in a conspecific context, the genes that underlie heterospecific pollen tube growth and recognition have not yet been identified. I collected RNA from stigmas and styles following pollination with conspecific, within-genus heterospecific, and between genus heterospecific pollen using species in *Pedicularis* and *Mimulus.* Using a comparative transcriptomic framework, I evaluated differences in the transcriptomic profiles of each cross-type. I additionally identified candidate genes that could have particularly impactful roles in recognition. Preliminary results show that more genes are up-regulated during conspecific relative to heterospecific crosses, suggesting that plants may not be recognizing heterospecific pollen tubes at the molecular level. These results indicate that reproductive barriers to reproduction may not broadly include suspension of heterospecific pollen tubes within the stigma and style. Instead, pre-pollination barriers, differences in pollen tube growth rates, and post-zygotic barriers are likely more significant.

P.1587 Chromosome evolution on Narcissus sect. Bulbocodii (Amaryllidaceae): reproductive and environmental correlates

J. Cuscó-Borràs[1], M. Escudero[1], V. Simón-Porcar[1], J. Arroyo[1]

1 Universidad de Sevilla, Sevilla, Spain.

Narcissus sect. *Bulbocodii* is probably one of the largest sections in the genus. Although most of the species in the section have 2n = 14 or 2n = 28, there is a great complexity of chromosome variation including polyploid series, dysploidy and hybridization. Our aim is to understand the relationship between phylogeography, chromosome evolution and reproductive traits (incompatibility system and floral architecture), hybridization patterns, climate niche and pollinators. Our framework hypotheses are: 1) polyploids are related to selfing syndrome through self-compatibility, have generalist pollinators and frequently have hybrid origin; and 2) chromosome rearrangements contribute to climate niche shifts and genetic isolation. To test these hypotheses, we studied all the species of sect. *Bulbocodii* across the whole geographical range. We run experiments to determine the incompatibility system with self and cross hand pollination treatments. The pollinators were ascertained in each species using direct observations and video camera recording in at least one population per species. We also run phylogeographic analyses with RADseq. Using the fine phylogeographical information of the populations we were able to map reproductive traits and chromosome numbers, to understand hybridization patterns and the role of chromosome evolution on genetic differentiation processes.

P.1588 Silica nanoparticles – a promising source of silica for plants

Jaqueline Santos[1,2], Ricardo Azevedo[2], Elizabete Carmo-Silva[1]

1 Lancaster University, United Kingdom. 2 University of Sao Paulo, Brazil.

Silica (Si) is a beneficial element for plants, acting as a protector against various types of environmental stress and pests. Si in the form of silicon dioxide (SiO_2) is one of the most abundant elements in the Earth’s crust, but it is rarely found in isolation, it is aggregated in minerals such as granite, quartz, sand, etc. And for plants, the bioavailable form of Si is its soluble form as monosilic acid (H_4SiO_4). Si nanoparticles (Si-NPs), due to their small size, diversity of shapes, and high surface area, can reportedly enter plant tissues through pores. Therefore, they are a promising source of Si for agriculture. This work hypothesizes that Si-NP when compared to traditional silica (Si-CV), offers superior results in photosynthesis and growth parameters of soybean and cowpea plants. Simultaneous experiments with soybean (Williams 82) and cowpea (IT97K-499-35) plants were conducted for 22 days. The treatments were 200 mg of silica/kg of substrate for Si-NPs and Si-CV, in addition to the controls without silica, each treatment had 12 plants. The climatic conditions of the greenhouses were temperature 30/18 °C day/night (cowpea) or 24/18 °C day/night (soybean), photoperiod 16h, and light intensity above 500 W/m2. The results showed that the estimated leaf area and plant weight were greater in plants that received Si-NPs when compared to control plants, whereas diferences between control plants and plants grown with Si-CV were less significant. A lower transpiration rate was also observed for soybean plants grown in the presence of Si-NPs. Therefore, through our results we can conclude that Si-NPs offer superior results when compared to Si-CV, showing themselves to be a promising source of silica for plants.

P.1589 Ontogeny of Tillandsioideae stigmas

Sanny Siqueira[1], Andrea da Costa[2], Karen de Toni[1]

1 Rio de Janeiro Botanical Garden, Rio de Janeiro, Brazil. 2 National Museum, Universidade Federal do Rio de Janeiro, Brazil.

Tillandsioideae is the Bromeliaceae subfamily with the greatest taxonomic and morphological diversity, reflected in the controversial classification of genera, subgenera, and species. Floral morphology stands out as the most important characteristic for the group's systematics and taxonomy. In this context, stigma morphology provides important data on generic limits and morphologically related species. Bromeliaceae exhibits different types of stigmas, which are highly diverse in Tillandsioideae. Therefore, this study aimed to detail the morphology and ontogeny of stigmas in the subfamily, in order to understand the diversification of stigmas and their phylogenetic relationships based on ontogenetic sequences. Samples of 17 genera and 60 species of Bromeliaceae, focusing on Tillandsioideae, were collected at different stages of development, and stigmas were observed using standard scanning electron microscopy protocols. Analyzing stigma ontogeny from early stages to flower anthesis, nine stigma types were identified: simple-erect, simple-truncate, spiral-conduplicate, convolute blade I, II, and III, lobate blade, coralliform, and conduplicate-erect. Two new types are described here for the first time. Results revealed significant variations among taxa, such as differences in the degree of folding of stigma lobes in convolute blade and stigma lobes with and without twists in simple-erect stigmas. Homologies between different stigma types were also revealed, as stigmas exhibited identical development in early stages but diverged into three ontogenetic sequences establishing homologous stigmas: simple-erect (sequence I: erect and free stigma lobes; simple-truncate and simple-erect), convolute blade (sequence II: slightly recurved stigma lobes; convolute blade I, II, III, lobate blade, coralliform, and conduplicate-erect), and spiral-conduplicate (sequence III: conduplicate and spiralized stigma lobes; lax and congested spiral-conduplicate). In summary, Tillandsioideae presented all mentioned stigma types, confirming the high morphological diversity within the subfamily and the potential of stigmas as taxonomic markers at the genus and species levels.

P.1590 Ameliorating effect of the cyanobacteria Nostoc commune on the moss Tortella squarrosa growing on heavy metal-polluted soil

Isabel Domarco Sagra[1], Belén Estébanez Pérez[1]

1 Faculty of Science, Universidad Autónoma de Madrid, Madrid, Spain.

The escalating soil pollution with heavy metals drives research into its consequences on various organisms and into feasible remediation methods. Through an experimental study of artificial soil contamination, we have studied the damage to the moss *Tortella squarrosa* caused by soil contamination with lead, copper, and both metals in synergy, as well as the potential mitigation effects of the cyanobacterium *Nostoc commune*. Both species are common in Mediterranean biological crusts. We grew in greenhouse plants of *T. squarrosa*, with and without fragments of *N. commune* colonies, on seedbeds with soil polluted with different doses of copper and/or lead. After 11 weeks, we analyzed the metal bioavailability in the soils using TXRF, assessed the moss damage through semi-quantitative macroscopic observations, and investigated the metal presence in moss tissues using histochemical tests and SEM-EDX. We observed low metal bioavailability in soil, especially for lead, but it was further reduced with the addition of *N. commune* (capturing up to 100% of the bioavailable metal). The moss showed greater sensitivity to copper, alone or in synergy with lead. Also, copper was more frequently detected in moss tissues, especially in basal parts, than lead in histochemical tests and EDX analysis.

The addition of fragments of *Nostoc* colonies to the soil also reduces the metal detected in the moss tissues and improves the survival ability and condition of the plants, especially in treatments with lead, a metal that the cyanobacteria is capable of retaining more effectively. The phytoremediation potential of both organisms (*Tortella*, absorbing copper in its basal parts, and *Nostoc*, absorbing both metals, especially lead) should be further confirmed in studies aimed at utilizing them in soil recovery programs.

P.1591 Calcium influx through peizo-channels at pollen tube tip membrane

Rajiv Dutta[1]

1 School of Biological Engineering and Life Sciences, Shobhit Institute of Engineering and Technology, Modipuram, Meerut, India and School of Biological Engineering and Sciences, Shobhit University, Gangoh, Saharanpur, India.

The growing pollen tube needs higher calcium concentration inside pollen tube near tip. This result a continuous influx of calcium from the pollen tube tip region is essential for its polarized growth. The pulsating growth of pollen tube oscillates with the calcium and potassium ions transport though the pollen tube membrane. The various kind of spontaneous and pressure sensitive ion channels have been identified from the pollen grain membranes. These ion channels were specifically for calcium and potassium transportation. The spontaneous potassium channel at pollen grain having conductance of 67 and 72 pS at different external potassium concentrations and reversal potential was found to be -40mV and -120 mV, respectively. Whereas the pressure activated potassium channel on pollen grain membrane is found to be activated when membrane was provided pressure of 10 kPa. The conductance of these channels was found to be 33 pS. The pressure activated voltage gated calcium channels with conductance of 15 pS were also found on pollen grain membrane. Both these stretched activated channels were blocked in presence of gadolinium chloride ($GdCl_2$) and 1,000-fold diluted crude venom from *Grammostola spatulata*. It was also observed that these membrane-based channels were activated by positive as well as negative pressure exerted on the membrane.

P.1592 eBryoSoil: a citizen science application to monitor changes in soil ecosystems

André Mira[1,2], Joaquín Hortal[1,3], Ana Paula Portela[4,5,6], Belén Albertos[7], Belén Estébanez Pérez[2], Cristina Branquinho[3], Cristiana Vieira[8], Helena Hespanhol[4,6], Isabel Draper[2,9], Joana Marques[8], Juliana Monteiro[3], María Leo Montes[10], Paula Matos[3], Pilar H. Aragüés[11,12], Raúl Ochoa-Hueso[13], Zulema Varela[14], Nagore G. Medina[2,9]

1 Dept. Biogeography and Global Change, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain. 2 Dept de Biología, Universidad Autónoma de Madrid, Madrid, Spain. 3 Centre for Ecology, Evolution and Environmental Changes & Global Change and Sustainability Institute, Faculty of Sciences, University of Lisbon, Lisbon, Portugal. 4 CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal. 5 Dept. de Biologia, Faculdade de Ciências, Universidade do Porto, Porto, Portugal. 6 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal. 7 Dept. de Botànica i Geologia. Universitat de València, Burjassot. Spain. 8 Museu de História Natural e da Ciência da Universidade do Porto, Porto, Portugal. 9 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain. 10 Dept. Soil, Plant and Environmental Quality, Instituto de Ciencias Agrarias (CSIC), Madrid, Spain. 11 Biodiversity and Conservation Area, Rey Juan Carlos University, Madrid, Spain. 12 DIFAR, University of Genoa, Genoa, Italy. 13 Dept. of Biology, IVAGRO, University of Cádiz, Campus de Excelencia Internacional Agroalimentario, Campus del Rio San Pedro, Puerto Real, Cádiz, Spain. 14 CRETUS, Ecology Unit, Department of Functional Biology, Universidade de Santiago de Compostela, Santiago de Compostela, A Coruña, Spain.

Biological soil covers (BSCs) are vital for ecosystem health and functionality, playing a key role in enhancing soil stability, mediating nutrient cycling, and influencing soil hydrology. These BSCs are commonly found in the Iberian landscapes, underscoring their importance in these ecosystems. Common throughout the Iberian Peninsula, they are integral to the ecological health and diversity of the region's ecosystems. However, there is limited information regarding their abundance and distribution across the Iberian Peninsula. Here we present the results obtained from the contributions of the citizen scientists between November 2019 and December 2020 with EbryoSoil, an app that allows citizens to participate in mapping the BSCs communities across the Iberian Peninsula. Our results highlight the importance of the habitat as a mediator of the influence of climate. Thus, conservation efforts targeted at preserving diverse habitats are essential to ensure the continued presence of lichen and moss communities. Despite challenges posed by the SARS-CoV-2 outbreak, the citizen science project demonstrated success in utilizing a specifically tailored app to gather valuable information on BSC communities, providing insights into their vulnerability to climate change. This program serves as an illustrative example of how citizen science can effectively identify and study vulnerable habitats, offering a blueprint for future studies focused on understudied organisms.

P.1594 Trait-environment relationships in Mediterranean alpine grasslands.

Jorge García Fernández[1], Manuel J. Macía[1,2], David S. Pescador[3, 4], Julia Chacón-Labella[1]

1 Departamento de Biología, Área de Botánica, Universidad Autónoma de Madrid, Madrid, Spain. 2 Centro de Investigación en Biodiversidad y Cambio Global, Universidad Autónoma de Madrid, Madrid, Spain. 3 Departamento de Farmacología, Farmacognosia y Botánica, Facultad de Farmacia, Universidad Complutense de Madrid, Madrid, Spain. 4 Departamento de Biología y Geología, Física y Química Inorgánica, Universidad Rey Juan Carlos, Móstoles, Spain.

A fundamental goal of trait-based ecology is to generalize predictions across spatial scales, linking the phenotypes with the demography, community dynamics, and environmental variation. Indeed, a fundamental assumption in trait-based ecology is that relationships between traits and environmental conditions are globally consistent. These relationships are generally consistent when studied along large environmental gradients. We used field-measured microclimate and detailed trait data to explore if trait-environment relationships are consistent across spatial scales. We collected community data from 15 plots and nine species, along an altitudinal gradient in alpine Mediterranean grassland in Sierra de Guadarrama, Madrid (Spain). We combined these plant data with locally measured traits: height, specific leaf area (SLA), and leaf dry matter content (LDMC), along with recordings of microclimatic conditions such as soil temperature and soil moisture. Our aim was to relate local plant community trait composition (described by the abundance-weighted central moments of the traits such as the mean and variance) to in-situ recordings of soil moisture, soil temperature and soil surface temperature. Results showed that higher temperatures and low water availability have a negative and significant effect on height mean and variance but showed a non-significant effect on LDMC and SLA mean and variance. Our results suggest that warmer and drier conditions may act as an environmental filter on height values, which tend to be lower and more homogeneous among locations (less dispersed). Although general relationships between SLA and LDMC and environmental variables are well supported in the literature when studied at large environmental gradients, those relationships might not be directly transferable to the fine scale, even when accounting for microclimate variation. Our results suggest that other drivers beyond microclimate (i.e., species interactions) might be driving trait variation at the fine-scale in Mediterranean alpine grasslands.

P.1595 Floral inception patterns of two native Mexican acacias (Leguminosae: Caesalpinioideae: mimosoid clade)

Jassiel Raúl Núñez Rodríguez[1], Beatriz Benítez Cabrera[1], Sandra Luz Gómez Acevedo[1]

1 Facultad de Estudios Superiores Iztacala, Universidad Nacional Autónoma de México. Estado de México, Mexico.

The formation of a flower occurs in three main stages, insertion, elongation and maturation, of which the first provides evidence of the pattern by which each organ within a whorl is formed. This information is relevant in systematic studies, and in this work a study of floral development is used to highlight the differences in the insertion patterns that occur between two genera (*Senegalia* and *Vachellia*) that were previously grouped into one (*Acacia* s.l.). The species studied are *Senegalia acatlensis* and *Vachellia constricta*, two species characteristics of arid Mexican areas, whose flowers in the mature stage share particular characteristics such as the presence of glandular anthers. Both species have pentamerous and multistaminate flowers. Perianth merosity can be variable in the early stages of development. They present differences in the insertion patterns of the perianth, but not in the insertion pattern of the androecium (meristematic ring) and gynoecium (early appearance). The anther gland begins to form in intermediate stages of development, once the anthers have elongated and differentiated into thecae and filaments. The floral insertion pattern of *V. constricta* is consistent with that of other *Vachellia* species, while *S. acatlensis* differs from the pattern reported for other species from Se*negalia.*

P.1596 Study of the populations of Himantoglossum metlesicsianum in the Canary Islands

Rocío González Negrín[1], Victoria Eugenia Martín Osorio[1], Priscila Rodríguez Rodríguez[2], Wolf H. Wildpret Martín[3], Wolfredo Wildpret de la Torre[1]

1 Universidad de La Laguna, Tenerife, Spain. 2 Universidad de Las Palmas de Gran Canaria. Las Palmas de Gran Canaria, Spain. 3 Georg-August-Universität Göttingen, Göttingen, Germany.

The results obtained in this study of the population, chorological and molecular analysis of *Himantoglossum metlesicsianum* (W.P. Teschner) P.Delforge in the Canary Archipelago are presented. This orchid is classified as Endangered, according to the Spanish Catalogue of Threatened Species, Royal Decree 139/2011, of February 4, and the Law 4/2010, of June 4, of the Canary Islands Catalogue of Protected Species. Endemic to the Canary Islands, it is found on the islands of Tenerife, La Palma, Gran Canaria and El Hierro. The potential vegetation surrounding the populations on the four islands studied consists of pine forests dominated by *Pinus canariensis*, characteristic of dry-humid Thermo-Mesomediterranean climates with rainfall between 450-600 mm per year and average annual temperatures of 10-15°C. Occasional frosts and snow in winter occur, distributed between 900 and 1,400 m.a.s.l. Natural risks present on all the islands sampled include those associated with prolonged droughts resulting from the current trend of climate change. However, the main threat to the species is anthropogenic intervention, particularly the collection of specimens by amateurs and professionals for the illegal trade in endangered species. The study of the population dynamics, dispersal and reproductive systems of the species, as well as the genetic connections between populations, are key aspects that have helped us to know and understand the conservation status of the taxon. This knowledge makes it possible to establish the conservation measures necessary to guarantee the survival of the species.

P.1597 Plants used in the Guancasco ceremony in San Francisco de Opalaca, Honduras.

Eydi Yanina Guerrero Medina[1]

1 Department of Biology, School of Biology, Faculty of Sciences, National Autonomous University of Honduras.

Societies maintain collective memories, including experiences that are part of the oral tradition of people, such as rituals, legends, fables, stories, anecdotes, songs, myths, sayings and ceremonies. In this research, the “Guancasco” ritual forms the intangible heritage of the people that, due to generational circumstances, is deposited in adults that takes root throughout their lives and is transmitted orally to the next generation. The present project arises with the purpose of knowing the plants that are used and have been used in the ritual that has survived in the indigenous peoples called “Guancasco”, which has been celebrated for more than 500 years, in this case we will analyze what It takes place in the community of San Francisco de Opalaca, a Lenca village located in the department of Intibucá, in western Honduras. The Guancasco is a ritual of peace among indigenous peoples, at the same time it serves as a cultural and mythological expression that transmits knowledge and teaches the importance of subsistence. Rescuing and preserving valuable ancestral knowledge linked to the use of plants in rituals such as the Guancasco in Opalaca is a crucial task. A deep knowledge of the plant species used in these ritual practices is sought, analyzing whether they are in any risk category, and then proposing concrete actions that favor their conservation. In this context, by highlighting the exceptional botanical wealth present in the region, recognizing the cultural, medicinal and ecological importance of these plants, the awareness of the population is achieved, which must acquire a fundamental role, since it seeks to create a wake up. about the urgent need to conserve medicinal plants and preserve the unique biodiversity that the region has.

P.1598 Plant DNA identification with Angiosperm353: A computational and targeted sequencing approach

Nan Hu[1], Madison Bullock[1], Courtney Miller[1], Elizabeth Hunter[2], Sara Handy[2], Matthew G. Johnson[1]

1 Texas Tech University, Department of Biological Sciences, Lubbock, USA. 2 U.S. Food and Drug Administration, Center for Food Safety and Nutrition, Washington DC, USA.

The identification of plant species from mixed samples is crucial in various fields, including ecological surveys, medical diagnostics, and food and drug safety. Traditional methods face challenges due to the high costs of DNA sequencing, inefficiencies in computational workflows, and incomplete sequence databases. This study introduces a novel approach using the Angiosperm353 target sequencing kit for efficient identification of angiosperm DNA in mixed samples. Our method assembles short paired-end reads using existing workflows to assemble contigs from enriched DNA (HybPiper) for each mixed sample. Using a reference database of exemplar Angiosperms353 sequences from 700 taxa, assembled from the Kew PAFTOL Tree Explorer, we apply phylogenetic inference to categorize contigs and variance in phylogenetic distance across genes to identify likely taxa present. We demonstrate a high precision in identifying unknown taxa from a diverse set of mixed samples including in-silico mixes of reads, and libraries constructed from known mixed DNA. We further demonstrate our workflow using environmental DNA extracted from a soil seed bank, positively identifying species whose seeds are known to be present in the soil. Our research not only showcases the effectiveness of the Angiosperms353 and HybPiper assembly in sorting mixed plant DNA samples but also suggests their potential in scientific and practical applications.

P.1599 Floral ecology and in vitro cultivation of Tripleurospermum ziganaense (Asteraceae): a critically endangered stenoendemic species

Huseyin Inceer[1]*, Mustafa Cuce[2], Umit Incekara[3], Rabia Sagan[1]

*1 Department of Biology, Faculty of Sciences, Karadeniz Technical University, Trabzon, Turkey. 2 Department of Food Technology, Şebinkarahisar School of Applied Sciences, Giresun University, Giresun, Turkey. 3 Department of Biology, Faculty of Sciences, Atatürk University, Erzurum, Turkey. *inceer@ktu.edu.tr.*

Tripleurospermum ziganaense (Asteraceae) is a critically endangered (CR) stenoendemic species in Türkiye and is facing high risk of extinction. Little is known about the ecology or the life history of the species that could be used to inform conservation or management decisions. In this study, flower morphology, reproductive phenology (flowering and fruiting), microclimatic condition (air temperature and relative humidity), floral visitors and **in vitro** cultivation were presented. Reproductive season lasted from May to June. Flowering peaked from late May to early June, while fruiting peaked mid-June. The average temperature and relative humidity in the reproductive season of the species were detected as 16.47±6.61oC and 70.57±21.19%, respectively. The high insect visitors were observed in the groups of Coleoptera. The survival rate of plantules obtained from **in vitro** achene germination on Murashige & Skoog basal medium (MS) was 98% in botanical garden. After 30 days in the botanical garden, the plants developed new leaves and grew considerably. **Acknowledgments:** This study was partly supported by the Scientific and Technological Research Council of Türkiye (TUBITAK, project no.122Z845) in the frame of 2519-COST

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P.1600 rDNA transcription and processing of ribosomal RNA in A. thaliana

Sara A. Neumann[1,2], Jacinthe Azevedo-Favory[1,2], Anne de Bures[1,2], Christine Gaspin[3,4], Virginie Marchand[5], Iouri Motorin[5], Julio Sáez-Vásquez[1,2]

1 CNRS, Laboratoire Génome et Développement des Plantes, Perpignan, France. 2 Univ. Perpignan, Perpignan, France. 3 Université de Toulouse, INRAE, Castanet-Tolosan, France. 4 Université de Toulouse, INRAE, Touluse, France. 5 Université de Lorraine, CNRS, Nancy, France. 6 Université de Lorraine, CNRS, Nancy, France.

Ribosomal RNAs (rRNAs) are the structural and functional building blocks of ribosomes. In the nucleolus, rRNA 18S, 5.8S and 25S (28S in mammals) are transcribed by RNA polymerase I (Pol I) as polycistronic 35S, 45S or 47S pre-rRNAs respectively in yeast, plant and mammals. Therefore, these pre-rRNAs must be processed into mature 18S, 5.8S, and 25S/28S rRNAs. Processing consists of exo- and endonucleolytic cleavages to remove internal (ITS) and external (ETS) transcribed spacer sequences and sugar and base modifications of rRNA. The most abundant rRNA modifications are 2’-*O*-methylation (2’-*O*-Me) and pseudouridylation (Psi); guided respectively by C/D- and H/ACA-box snoRNPs. While these processes are severely impacted by stress conditions in multiple species, we lack information about the molecular mechanisms allowing sessile organisms without a temperature-control system, like plants, to cope with such circumstances. We performed Illumina-based RiboMethSeq approach for mapping rRNA 2’-*O*-Me sites in *A. thaliana* plants. We detected novel C/D snoRNA-guided rRNA 2’-*O*-Me positions and also some orphan sites without a matching C/D snoRNA. Immunoprecipitation of fibrillarin (FIB2), the methyltranfersase of the C/D snoRNP, identified and demonstrated expression of snoRNAs corresponding to the majority of mapped rRNA sites and also detected new ones. Furthermore, we demonstrated that disruption of nucleolin 1 (NUC1) expression, a major nucleolar protein, induces nucleolus disruption and decreases rRNA 2’-*O*-Me. Interestingly, cleavages of pre-rRNA is nearly unaffected, indicating uncoupling of pre-rRNA cleavages and rRNA 2’-*O*-Me in *nuc1* mutant plants (Azevedo-Favory ***et al.*** 2021). Little is known on how these rRNA modifications affects growth, development or the response to environmental conditions for an entire eukaryotic organism. We tackle this subject in the plant model *Arabidopsis thaliana* during seedling development and upon heat stress conditions.

Reference: Azevedo-Favory ***et al.*** RNA Biol 2021.

P.1601 The role of phytoglobin-nitric oxide cycle in anaerobic germination and submergence tolerance of deepwater rice

Aprajita Kumari[1], Pooja Singh[1], Vemula Chandra Kaladhar[1], Manbir, Pradeep Kumar Pathak[1], Kapuganti Jagadis Gupta[1]

1 National Institute for Plant Genome Research, New Delhi India.

Plant encounter low oxygen stress due to flooding/waterlogging or during development of various organs of plants such as seeds. In the environment vast numbers of plant species are prone to flooding. In contrast, plants such as deepwater rice can withstand flooding and submergence. An important and interesting feature of rice is that it can germinate under anoxic conditions. Though several biochemical adaptive mechanisms play an important role in anaerobic germination of rice but the role of phytoglobin-nitric oxide cycle and mitochondrial alternative oxidase pathway is not known. Recently investigated the role of these pathways in anaerobic germination. Under anoxic conditions deepwater rice germinated significantly higher and rapidly than aerobic condition and the anaerobic germination and growth was much higher in the presence of nitrite which is intermediate of nitrate reduction reaction mediated by nitrate reductase. Addition of nitrite to germinating seeds stimulated NR activity and NO production. Important components of phytoglobin-NO cycle such as methaemoglobin reductase activity, expression of *Phytoglobin1, NIA1* and the promoters of these genes were elevated under anaerobic conditions in the presence of nitrite. The operation of phytoglobin-NO cycle also accelerated anaerobic ATP generation and fermentation metabolites such as lactic acid production and activity of ADH. Interestingly nitrite significantly reduced ROS production and lipid peroxidation. The reduction of ROS was accompanied by enhanced expression of mitochondrial alternative oxidase protein and its capacity. Application of AOX inhibitor SHAM inhibited the anoxic growth mediated by nitrite. In addition, nitrite improved the submergence tolerance of seedlings. Our study revealed that nitrite driven phytoglobin-NO cycle and AOX are important players in anaerobic germination and submergence tolerance of deepwater rice.

P.1602 A prickly diversification: the rapid and recent radiation of tribe Opuntieae (Cactaceae)

Matias Köhler[1], Raul Puente-Martinez[2], Tatiana T. Souza-Chies[1], Lucas C. Majure[3]

1 Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil. 2 Department of Research and Conservation, Desert Botanical Garden, Phoenix, USA. 3 University of Florida Herbarium (FLAS), University of Florida, Gainesville, USA.

Evolutionary radiations are a fundamental topic in the understanding of life diversity. Cacti are one of the most fascinating New World's succulent plant radiations, but some of its major clades still lack detailed investigations about their patterns and processes of diversification. In this study, we explored a chloroplast genome dataset to investigate the major clade relationships within tribe Opuntieae, the celebrated prickly-pear cacti, to assess its morphological evolution, time divergence, historical biogeography, and macroevolutionary dynamics. Our analyses strongly supported Opuntieae as monophyletic with four major clades – 1) *Consolea*, 2) *Brasiliopuntia* + *Tacinga*, 3) *Miqueliopuntia* + *Salmonopuntia* + *Tunilla*, and 4) *Opuntia* – but contentious relationships between some clades were recovered comparing whole plastome and just genes data. Within *Opuntia*, the most diverse clade of Opuntieae, eight major well-supported clades were recovered. Our analyses suggested that Opuntieae has undergone a rapid and recent evolutionary radiation during the last ~5 Mya, in which the clade have exhibited long-distance dispersal events that resulted in currently occupying all major arid and semi-arid regions of the Americas. These events have occurred accompanied by phenotypic disparity with the evolution of several homoplasious characters within Opuntieae members, and a prickly history of diversification with no one key feature detected single explaining it across lineages. This study provides the first chloroplast genome phylogenetic framework within a satisfactory taxon sampling of tribe Opuntieae, promoting new lights regarding hypotheses on the evolutionary history of cacti.

P.1603 Assessing marks of introgression on the Pilosocereus cacti evolutionary radiation

Matias Köhler[1], Monique Romeiro-Brito[1,2], Milena C. Telhe[1], Daniela C. Zappi[3], Nigel P. Taylor[1], Gerardus Olsthoorn[4], Fernando F. Franco[1], Evandro M. Moraes[1]

1 Departamento de Biologia, Universidade Federal de São Carlos (UFSCar), São Paulo, Brazil. 2 Department of Natural History, University of Florida, Florida, USA. 3 Programa de Pós-Graduação em Botânica, Universidade de Brasília (UNB), Brasília, DF, Brazil. 4 Olsthoorn Cactus, Holambra, São Paulo, Brazil.

Understanding the mechanisms driving the origin of a large number of disparate species in a short time frame, aka evolutionary radiations, is crucial for unraveling the biodiversity origin and formulating effective conservation strategies. The 'facheiro' cacti (*Pilosocereus* spp.) represent an intriguing lineage of ca. 60 species that have putatively originated within the last 2 Myr. These cacti are distributed across the major arid and semi-arid regions of Central and South America, with the bulk of diversity in eastern Brazil. In this study, we use a nuclear dataset derived through target-enrichment sequencing of Cactaceae591 with a comprehensive sampling of species diversity to delve into the evolutionary history of the facheiro cacti. Our primary objective is to investigate the potential imprints of introgression on the diversification of the clade. By utilizing integrative methods grounded in phylogenetic and phylonetwork inferences, coupled with D statistics, we aim to quantify the significance of deep and shallow hybridization events in shaping the genomic landscape of *Pilosocereus* spp. Our work intends to shed light on the putative intricate patterns of introgression within the 'Facheiro' cacti, providing valuable insights into the mechanisms that have facilitated their rapid diversification. Additionally, our findings aim to contribute to a deeper understanding of the broader implications of hybridization in plant biodiversity evolution.

P.1604 Floral structure of Leea rubra (Leeaceae) and its systematic implication for Vitaceae

Huaicheng Li[1], Julien B. Bachelier[1]

1 Institute of Biology/Dahlem Center of Plant Sciences, Freie Universität Berlin, Berlin, Germany.

The genus *Leea* comprises 34 species of trees, shrubs, scramblers or herbs, widespread in tropical and subtropical Asia. It was commonly placed in its own family Leeaceae, closely related to Vitaceae. But in APG IV, both families are ranked as subfamilies in Vitaceae *sensu lato*. However, flower structural studies have mostly concentrated on members of Vitoideae because of its economic value, and only a few focused on or integrated species of *Leea*. Using light and scanning electron microscopy, microtome section series, we studied flower structure and development of *L. rubra* with the special focus on its floral disc and gynoecium. The flowers of *L. rubra* are arranged in a thyrse. The flowers are bisexual and protandrous. They are polysymmetric and whorled, with a pentamerous perianth and haplostemonous androecium surrounding a trimerous gynoecium. The sepals are basally connate and form a floral cup encompassing the semi-inferior ovary, surrounded by valvate petals and antepetalous stamens, and a distinct tubular intrastaminal disc. However, the filaments are hooked over the disc and the anthers, which are laterally connivent, forming a caducous “unit” to expose the slender style and discoid stigma after the male phase. The ovary is syncarpous and entirely symplicate with two crassinucellate and bitegmic anatropous ovules per locule separated by a secondary septum, and thus appears as having 6 univolutate chambers. The present study is the first detailed analysis of the floral structure of *Leea rubra* and shows that like in other species of *Leea*, flowers of *Leea* are essentially similar and share several potential apomophies not found in Vitoideae. Depending on the weight given to the abscission of all postgenitally united anthers as a unit, a distinct intrastaminal floral disc, and a gynoecium with no synascidiate zone, the genus could thus be recognized as a distinct family or not.

P.1605 Seedling survival drives the population dynamics of Abies religiosa (Kunth) Schltdl. & Cham. in a high mountain forest of Mexico

Lauro López-Mata[1], Gabriel Arroyo-Cosultchi[1]

1 Posgrado en Botánica, Colegio de Postgraduados, Texcoco Estado de México, Mexico.

The fir or oyamel, *Abies religiosa*, is a dominant conifer of the temperate high mountain forests of Mexico whose wood, uses and environmental services are widely appreciated. However, these forests are subject to anthropogenic disturbances that cause fragmentation, reduce their connectivity and could put their population viability at risk. Our objective was to project the population dynamics of this fir species by calibrating integral projection models (IPM) and explore the impact of different survival rates of its seedlings on the population growth rate (λ). Understandably, these analyzes will allow us to search for whether fir populations are stable, growing or decreasing demographically, and explain the importance of vital rates: survival, growth and reproduction on λ. In 2021, we established 3 plots of 50m × 50m at 3 altitudinal levels (22,500 m^2) in which all fir trees with a diameter at breast height (DBH) ≥ 1 cm were measured and numbered. We photographed the crowns of reproductive trees to evaluate their cone production, seeds and individual fecundity. In 2022, we did a re-census to record changes in individual DBH, dead trees and reproductive trees. MPIs calibrated based on a variable seedling survival rate from 17.9% to 30.9% yielded λ values of 1.0797 to 1.0553 for the forest. However, the maximum and minimum values of λ fluctuated between altitudinal levels: λ_{upper} (1.1019-1.0754), λ_{lower} (1.0932-1.0681), and λ_{middle} (0.9936-0.9880). The results suggest that fir populations are growing, or close to demographic stability. It is apparent that the population viability of *A. religiosa* is not threatened and that seedling survival rates are the critical state driving its population dynamics.

P.1606 Bioreceptivity of engraved schists in the Côa Valley Archaeological Park

Joana Marques[1,2,3], Sara Gutierrez-Patricio[4], Thierry Aubry[5], Beatriz Cubero[4], Ana Briga-Sá[6], Heather A. Viles[7], Ana T. Caldeira[8], Ana Z. Miller[4,8]

1 Museu de História Natural e da Ciência da Universidade do Porto, Porto, Portugal. 2 Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal. 3 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal. 4 Instituto de Recursos Naturales y Agrobiologia, IRNAS-CSIC, Sevilla, Spain 5 Fundação Côa Parque, Vila Nova de Foz Côa, Portugal. 6 Centre of Chemistry of Vila Real and School of Science and Technology, University of Trás-os-Montes e Alto Douro, Vila Real, Portugal. 7 School of Geography and the Environment, University of Oxford, Oxford, United Kingdom. 8 HERCULES Laboratory, Évora University, Évora, Portugal.

The Côa Valley, a UNESCO-designated site in Northeast Portugal's Upper Douro region, is renowned for its prehistoric open-air rock art. Dark biofilms composed of phototrophic microorganisms, such as cyanobacteria and green algae, are among the first colonisers of these exposed rock surfaces, paving the way for other organisms to follow, thereby contributing to the deterioration of rock art. In the ROCKinBIO project, we are assessing all levels of bioreceptivity of these schists, and shedding light on the relationship between stone properties and biological colonisation. Schist probes, acquired from the nearby quarries of Poio, where traditional exploitation continues, were subjected to accelerated ageing and different engraving techniques, thereby replicating the rock art of the Côa. A laboratory-based stone bioreceptivity experiment was conducted to understand the stone properties influencing microbial growth and biodeterioration processes. The engraved schists were inoculated with a multi-species phototrophic culture. The inoculated surfaces were then placed in an incubation cabinet for 3 months maintaining controlled temperature, humidity, and photosynthesis-inducing light cycles. The development of photosynthetic biofilms was monitored, quantified, and characterized every month. Chlorophyll-*a* quantification methods and digital image analysis were employed to quantify photosynthetic biomass and determine the stone surface areas covered by the biofilms, respectively. Microscopy, geochemical and geophysical analyses were conducted to quantify the impact of biological colonisation on the different sets of engraved schists. Spatial variation in rock surface bioreceptivity will soon be addressed using proxy indexes, and incorporated into biodeterioration models as a critical driver of biological impact on rock surfaces and open-air rock art. This research not only contributes to our understanding of the bioreceptivity of schists in the Côa Valley, but also serves as a methodological exploration for replicating and studying rock art in controlled environments, with broader implications for the preservation and management of other cultural heritage sites.

P.1607 Towards a biodeterioration model to predict biological impact on exposed rock surfaces and open-air rock art

Joana Marques[1,2,3], Cândida G. Vale[1,2], João Gonçalves[1,2], Helena Hespanhol[1,2,3], Ana Z. Miller[4,5], Heather A. Viles[6]

1 CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, InBIO Laboratório Associado, Campus de Vairão, Universidade do Porto, Vairão, Portugal. 2 BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal. 3 Museu de História Natural e da Ciência da Universidade do Porto, Porto, Portugal. 4 Instituto de Recursos Naturales y Agrobiologia, IRNAS-CSIC, Sevilla, Spain. 5 HERCULES Laboratory, Evora University, Évora, Portugal. 6 School of Geography and the Environment, University of Oxford, Oxford, United Kingdom.

The Côa rock art (UNESCO) is preserved on numerous rock surfaces along the steep slopes of the Côa river valley in the Upper Douro region (NE Portugal). These surfaces, and associated art, are continuously exposed to and shaped by the synergistic impacts of several biotic and abiotic agents operating at different temporal and spatial scales. Yet, these impacts remain understudied. To start addressing such complex interactions, we propose that an ecological and structural similarity between rock surface features and landscape features exists, and that each individual rock surface that may bear rock art can be viewed as a miniature landscape where the same fundamental processes that shape the land surface operate on a smaller scale. Following this rationale, we argue that the ecological concepts and tools used to analyse the spatiotemporal distribution patterns of vegetation and ecosystem functioning at the landscape level can be applied to model and predict the distribution patterns and impact of biological colonisation on exposed rock surfaces and associated rock art, provided that meaningful fine resolution environmental data is available. In the ROCKinBIO project we have been applying ecological tools to: i) characterise rock-colonising communities, their abundance, indicator traits and distribution patterns, linking biodiversity to function; ii) characterise the multi-scalar environmental drivers of rock colonisation dynamics; and iii) quantify the geochemical and geophysical impact of rock-colonising communities on exposed rock surfaces. The final goal is to develop a predictive biodeterioration model that allows to diagnose current interactions between biological colonisation and colonised rock surfaces, and anticipate future impact of biodeterioration processes on open-air rock art.

P.1608 Sexual size dimorphism of gynodioecious Lycopus lucidus (Lamiaceae) from Korean natural populations

Hye-Kyoung Moon[1]

1 Kyung Hee University, Seoul, South Korea.

Sexual size dimorphism is an integrative topic in evolutionary biology. Similar to animals, the sexual size dimorphism of angiosperms could be highly related to the separation of sexes. Certain sexual systems from dicliny show general syndrome as system specifically, gynodioecy is one of them. In gynodioecious populations hermaphroditic flowers are generally known to be larger than female flowers in most floral parts. Flower size may have positively correlated with number of fertile stamens especially in Lamiaceae, which have relatively more gynodioecious species. However, little has been studied about sexual size dimorphism, which can occur at the species level, regardless of individual or population differences. To confirm the existence of sexual size dimorphism of gynodioecious population, the Korean natural populations of *Lycopus lucidus* were observed. Two sexual morphs, hermaphrodite and female, were identified at the individual levels. To address the following questions, I measured fully mature flowers in 20 different individuals from six populations. 1) Do sexual morphs exhibit specific floral size variation within and between populations? 2) Can sexual size dimorphism overcome individual and population level differences? 3) Do size variation between populations provide further evidence confirming the status of gynodioecy?

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P.1609 Plant natural products to treat Chagas disease

Nora H. Oleas[1], Jaume Bastida[2]

1 Centro de Investigación de Biodiversidad y Cambio Climático, Universidad Tecnológica Indoamérica, Quito, Ecuador. 2 Universitat de Barcelona, Barcelona, Spain.

Chagas disease, caused by the protozoan parasite *Trypanosoma cruzi*, poses a significant global health threat, particularly in endemic regions of Latin America. According to WHO, around 7 million people are affected with this disease. It is a persistent infection that causes a chronic disease characterized by progressive damage to the cardiac and/or digestive tissues. Despite advances in treatment, including antiparasitic drugs, challenges such as drug resistance and toxicity persist, requiring the search for novel therapeutic agents. Natural products derived from plants have historically served as invaluable sources of bioactive compounds, offering diverse chemical scaffolds and modes of action. This poster presents an overview of recent research efforts aimed at identifying natural products with anti-*T. cruzi* activity. Through the use of bibliometric techniques to generate a general perspective of the accumulated research, we report a revision of the current literature on pharmacological studies using natural plant products for Chagas treatment. This poster underscores the importance of harnessing the rich biodiversity of natural products in the ongoing fight against Chagas disease and emphasizes the need for continued exploration and innovation in this field.

P.1610 Recovery and/or rescue of the Dioon edule L. to counteract its extinction in Veracruz, Mexico

Retureta-Aponte, Alejandro[1], Carmona-Diaz, Gustavo[1], Hernández Romero, Ángel Héctor[1]

1 Universidad Veracruzana, Acayucan, Veracruz México.

Cycads are threatened plants largely due to their high potential as ornamental species. The species *Dioon edule* L. has been extracted from its natural habitat through clandestine practices, without adequate management of natural populations as non-timber forest resources, which has led to its disappearance in territories where it is found naturally. This justifies the establishment of an Environmental Management Unit (UMA) for its management and production, to cope with the high demand and thus contribute to its conservation in a legal manner. Although this species is highly recommended for breeding in ornamental plant nurseries, there is very little information on physiological, productive, or commercial aspects of the plants for sale in nurseries. Likewise, there are no studies on their ecological, cultural, and economic value. This study addresses management aspects for the recovery and/or rescue to halt or reverse the decline of the species.

P.1611 Spatial phylogenetics of the genus Solanum (Solanaceae) in Mexico

Geraldine Murillo-Pérez[1,2], Guadalupe Munguía-Lino[1,2], Aarón Rodríguez[1,2]

1 Herbario Luz María Villarreal de Puga, Instituto de Botánica, Zapopan, Mexico. 2 Laboratorio Nacional de Identificación y Caracterización Vegetal, Zapopan, Mexico.

Solanum (Solanaceae) is one of the 10 richest genera of flowering plants with half of the Solanaceae species. It includes 1,228 species distributed unevenly across the globe in all major temperate and tropical regions. Higher diversity and endemism locate in the Neotropics, but the greater diversification rates were observed in Africa and Australia. In Mexico, we founded 134 species of which 43 were endemics. The evaluation of the spatial distribution of the species richness and endemism of *Solanum* showed that the main mountainous chains in Mexico, the Mexican Transition Zone (MTZ), hosted the highest species richness and endemism. There, we found 114 species and 39 endemics. The grid cell analysis uncovered the richest cell at the southernmost end of the MTZ, the Chiapas Highlands (CH), at the boundary with Guatemala with 32 species. Likewise, the Weighted Endemism (WE) analysis recovered four centers of endemism in the MTZ. The Transmexican Volcanic Belt (TVB) and the Sierra Madre Oriental were the biogeographical provinces with the highest WE. The Corrected Weighted Endemism (CWE) analysis recovered a different pattern. Four cells were identified as microendemic sites. These cells occurred in the MTZ in the Sierra Madre Occidental and the TVB provinces as well as the Neotropical Zone in the Pacific Lowlands province. The spatial phylogenetics showed the same pattern, were the specific endemism, phylogenetic diversity and phylogenetic endemism were in the CH, TVB and the Sierra Madre del Sur. Spatial phylogenetics of *Solanum* supports the relevance of the MZT in the diversification of Mexican flora.

P.1612 Species diversity, species richness distribution and endemism of the genus Bletia (Orchidaceae)

Brandon E. Gutiérrez-Rodríguez[1], Guadalupe Munguía-Lino[2,3], Aarón Rodríguez[2,3]

1 Instituto de Ecología A. C., Xalapa, Mexico. 2 Herbario Luz María Villarreal de Puga, Instituto de Botánica, Zapopan, Mexico. 3 Laboratorio Nacional de Identificación y Caracterización Vegetal, Zapopan, Mexico.

Within the tropics, plant species richness concentrates along the mountains. There, topographic heterogeneity promotes speciation and persistence. The genus *Bletia* (Orchidaceae) groups geophytes with corms, plicated and deciduous leaves. Additionally, it includes myco-heterotrophic species. Phylogenetic evidence suggests that terrestrialization and seasonality helped the diversification of the group in Mexico with further dispersal elsewhere. We used *Bletia* to evaluate the concentration of the latitudinal diversity gradient on the tropical mountains. The database and species distribution maps were elaborated using the presence records of *Bletia* held at CHAP, CHAPA, ENCB, FCME, HUAP, IBUG, IEB, INEGI, INIF, MEXU, QMEX, SLPM, and XAL herbaria. Additionally, the digital herbaria CAS, K, MO, and US, as well as the information available in the Global Biodiversity Information Facility (GBIF), the Southwest Environmental Information Network and the Sistema Nacional de Información sobre Biodiversidad de México (CONABIO) were compiled and curated. To confirm the taxonomic identity of the digital records, only specimens with images were examined. Specimens without geographical data were georeferenced using Google Earth Pro and the Mapa Digital de México. Specimens with ambiguous information were excluded. Species richness distribution and endemism were quantified by 1) political divisions, 2) ecoregion, 3) biogeographical province 4) elevation and latitude, and 5) 1.0° × 1.0°grid cell. The data base had 3599 entries and 51 species of *Bletia*. Its geographical range goes form Southwestern USA through Florida, Mexico, the Caribean Islands to Brazil and northern Argentina. The geographic range follows the Tropical Dry Forest in the Americas but species richness and endemism concentrates on the oak-pine forest along the Trans-Mexican Volcanic Belt, Mexico.

P.1613 The roles of florivory and herbivory in maintaining intra-population flower color variation in Anemone coronaria

Norah Saabna[1,2], Tamar Keasar[3], Yuval Sapir[1]

1 School of Plant Sciences and Food Security, Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv, Israel. 2 Department of Evolutionary and Environmental Biology, University of Haifa, Haifa, Israel. 3 Department Biology and the Environment, University of Haifa - Oranim, Tivon, Israel.

Flowers of most plant species are color monomorphic. The relatively rare within-population flower color variation can be the hallmark of balancing selection, which drives polymorphism. Plant interactions with mutualist and antagonist selection agents may equalize the fitness of different color morphs and maintain polymorphism. We explored the relationship between flower color and biotic antagonistic interactions in *Anemone coronaria* (Ranunculaceae), a winter-flowering Mediterranean geophyte. Some *A. coronaria* populations bloom in red, while others comprise both red and non-red flowers. Petals of red flowers contained higher concentrations of anthocyanin pigments, potential herbivore repellents, than petals of non-red flowers. We evaluated leaf (herbivory) and flower (florivory) damage by micro-herbivores, and the corresponding maternal fitness, in three color-polymorphic anemone populations over two flowering seasons. Red flowers experienced higher leaf and petal damage, yet both color morphs had similar fitness. Increased herbivory and florivory levels were not associated with reduced fitness in the surveyed plants, and experimentally induced petal damage did not reduce visits by potential pollinators in field assays. Scratch marks, attributed to damage by beetles, were more common in red flowers, while bite marks, assigned to damage by caterpillars or grasshoppers, were more common in non-red flowers. As glaphyrid beetles are the major pollinators of red anemone flowers, we suggest that their service to red flowers as mutualists (pollinators) outweighs their disservice as antagonists (florivores). These pollinators, and possibly additional selection agents that favor red flowers, may compensate for the higher herbivory suffered by the red morph, thereby promoting color-polymorphism.

P.1614 Flower evolution in Ericales: A total-evidence approach including extant and fossil flowers

Julian Herting[1], Jürg Schönenberger[2], Hervé Sauquet[1,3,4]

1 Botanic Gardens of Sydney, Mount Annan, Australia. 2 University of Vienna, Vienna, Austria. 3 University of New South Wales, Sydney, Australia. 4 University of Sydney, Sydney, Australia.

The inclusion of fossil flowers into ancestral state reconstructions is critical for understanding flower evolution and promises new insights by capturing past morphological diversity. The asterid order Ericales is characterized by highly diverse floral structures and a rich fossil record, making it well-suited for a study on flower evolution integrating the fossil record. We used a Bayesian tip-dating approach with a total-evidence dataset and the fossilised birth-death model to jointly infer the position of the 13 fossils among 413 extant species of Ericales, considering both morphology and age. We reconstructed ancestral states for 38 floral characters using Bayesian and maximum likelihood methods, for 21 of the 22 families currently recognised in the order as well as six well-supported supra-familial clades. Accounting for uncertainty of fossil position influences the reconstructed ancestral states, generally introducing more uncertainty in reconstructed states. We show that the ancestral flower of Ericales exhibits both typical characteristics of its sister group, the large clade comprising lamiids and campanulids (e.g. fused petals), and plesiomorphic features (e.g. actinomorphic perianth) inherited from their Pentapetalae ancestor. In combining a quantitative approach to infer fossil phylogenetic relationships with multiple approaches to reconstruct ancestral states, we facilitate a deeper understanding of flower evolution of Ericales.

P.1615 Promoting IAPT through social media

Gustavo H. Shimizu[1]

1 Unicamp, Campinas, Brazil.

IAPT (International Association for Plant Taxonomy) is a global association of taxonomists and systematists, founded in 1950, at the Seventh International Botanical Congress, in Stockholm, Sweden. The main goals are to promote and support taxonomic and systematic research on algae, fungi, and plants, facilitate the governance and maintenance of the International Code of Nomenclature for algae, fungi, and plants, publish relevant contributions to the field through the official journal Taxon and the Regnum Vegetabile book series, and connect and support its collaborative community of members spread around the world. Like other scientific associations, IAPT also started new communication channels (Facebook, Instagram, and X/Twitter) to connect and expand its audience, sharing taxonomic and systematic news, grant calls, and promoting new issues of Taxon, webinars, workshops and symposia. Lena Struwe created these accounts in 2018, and was followed by Timothy Hammer, who served as the Social Media manager from 2019 to 2021. Currently we have 4,073 followers on Facebook, 1,325 on Instagram, and 3,990 on X/Twitter. The top countries on Facebook are India, Brazil, and United States, and on Instagram are Brazil, United States, and Argentina. Usually the most commented, liked, or shared posts are related to the research and small collections grants, but also in recent years those related to the XX International Botanical Congress, in Madrid, Spain. Interactions with authors of Taxon articles, especially via Instagram and X/Twitter are also remarkable. The next steps include interacting more using the available resources of each channel (e.g. reels, stories, polls) and trying to raise awareness of the general public to the importance of algae, fungi, and plants.

P.1616 Systematic studies on family Convolvulaceae of India: present status and challenges

Vinod B. Shimpale[1]

1 Laboratory of Angiosperm Systematics, Department of Botany, The New College, Kolhapur, Maharashtra, India.

The biological diversity of the Indian subcontinent is one of the richest in the world because of its outstanding vast geographic area, varied topography and climatic conditions. Because of its richness in overall species diversity, it is recognized as one of the 12 mega-diversity centres of the world. The family Convolvulaceae (commonly recognized as a bindweed or morning glory family) represents one of the larger and more diverse families of angiosperms in India. Worldwide it comprises more than 1,840 species, belongs to 59 genera. The members of Convolvulaceae have worldwide distribution, but the species richness occurs in the tropics. Although previous reports suggest that in India family Convolvulaceae is represented by *ca.* 20 genera and 180 species (Santapau & Henry, 1973), afterwards many nomenclatural alterations took place in various genera and many species added to Indian flora. Although the members of family Convolvulaceae are most diverse in morphology, widely distributed in India, till date there is no revisionary type of work carried out (except Hooker, 1887). But there are few fragmented publications are available on the family including Biju (1997) and Johari (1983), including few publications in the form of regional floras (district or state flora) etc. So, there is a need of comprehensive revisionary studies on the family of India to understand the present status of the family. In connection with all above points, author have taken a task to revise family Convolvulaceae and till date three genera are revised (*Argyreia* Lour.: 37 spp.; *Ipomoea* L.:60 taxa; *Distimake* Raf.:10 spp.) and revision of tribe Convolvuleae, Cuscuteae and Merremieae is in progress. Till date author has documented total 170 taxa of the family from India. In present communication author have discussed the current taxonomic status of Indian Convolvulaceae and highlighted challenges in the present study.

P.1617 A bird's eye view of the systematics of Convolvulaceae: novel insights from nuclear genomic data

Ana Rita G. Simões[1], Lauren A. Eserman[2], Alexandre R. Zuntini[1], Lars W. Chatrou[3], Timothy M. A. Utteridge[1], Olivier Maurin[1], Saba Rokni[1], Shyamali Roy[1], Felix Forest[1], William J. Baker[1], Saša Stefanovic[4]

1 Royal Botanic Gardens, Kew, United Kingdom. 2 Conservation & Research Department, Atlanta Bo-

tanical Garden, Atlanta, United States. 3 Systematic and Evolutionary Botany Lab, University of Ghent, Ghent, Belgium. 4 University of Toronto Mississauga, Mississauga, Canada.

Convolvulaceae is a family of c. 2,000 species, distributed across 60 currently recognized genera. It includes species of high economic importance, such as the crop sweet potato (*Ipomoea batatas* L.), the ornamental morning glories (*Ipomoea* L.), bindweeds (*Convolvulus* L.), and dodders, the parasitic vines (*Cuscuta* L.). Earlier phylogenetic studies, based predominantly on chloroplast markers or a single nuclear region, have provided a framework for systematic studies of the family, but uncertainty remains at the level of the relationships among subfamilies, tribes, and genera, hindering evolutionary inferences and taxonomic advances. One of the enduring enigmas has been the relationship of *Cuscuta* to the rest of Convolvulaceae. Other examples of unresolved issues include the monophyly and relationships within Merremieae, the "bifidstyle" clade (Dicranostyloideae), as well as the relative positions of *Erycibe* Roxb. and Cardiochlamyeae. In this study, we explore a large dataset of nuclear genes generated using Angiosperms 353 kit, as a contribution to resolving some of these remaining phylogenetic uncertainties within Convolvulaceae. For the first time, a strongly supported backbone of the family is provided. *Cuscuta* is confirmed to belong within family Convolvulaceae. "Merremieae," in their former tribal circumscription, are recovered as non-monophyletic, with the unexpected placement of *Distimake* Raf. as sister to the clade that contains Ipomoeeae and *Decalobanthus* Ooststr., and Convolvuleae nested within the remaining "Merremieae." The monophyly of Dicranostyloideae, including *Jacquemontia* Choisy, is strongly supported, albeit novel relationships between genera are hypothesized, challenging the current tribal delimitation. The exact placements of *Erycibe* and *Cuscuta* remain uncertain, requiring further investigation. Our study explores the benefits and limitations of increasing sequence data in resolving higher-level relationships within Convolvulaceae, and highlights the need for expanded taxonomic sampling, to facilitate a much-needed revised classification of the family.

P.1618 The transcriptome data reveals the synthesis pathways and regulatory networks of the active components of Cibotium barometz

Zhang Yuli[1], Wang Zhen[1], Li Minghui[1], Wang Ting[2], Su Yingjuan[1]

1 School of Life Sciences, Sun Yat-sen University, Guangzhou, China. 2 College of Life Sciences, South China Agricultural University, Guangzhou, China.

Cibotium barometz is widely used as a medicinal herb. However, previous research mainly focused on breeding techniques and the extraction and identification of components, with a lack of high-quality molecular resources and in-depth exploration into the biosynthesis process of bioactive components. Given its endangered status and medicinal value, the fern is an important material for theoretical research and practical application to investigate the biosynthesis and regulatory mechanisms of bioactive components. In this study, we first determined the differences in polysaccharide and flavonoid content among different organs. Secondly, we conducted the transcriptome analysis of three organs of *C. barometz* using Illumina and PacBio sequencing technology, and identified the pathways and genes involved in the biosynthesis of bioactive components. The main results are as follows: There are differences in polysaccharide and flavonoids content among different organs. The content of polysaccharide in root is the highest, while the least in pinna. The content of flavonoids in pinna is significantly higher than that in the root and rachis. The differentially expressed genes in the pinna were mainly enriched in photosynthesis. Nevertheless, differentially expressed genes in root and rachis were enriched in plant secondary metabolic pathways. The content of total polysaccharide was positively correlated with the expression pattern of UDP-arabinose 4-epimerase, but negatively correlated with the expression patterns of phosphoglucomutase and 3,5-epimerase/4-reductase. The conserved plant secondary product glycosyltransferase motif was identified in UDP-glycosyltransferases. The expression of genes involved in flavonoids biosynthesis in the pinna is significantly higher than that of the other organs. The content of flavonoids was negatively correlated with the expression patterns of chalcone synthase. We identified several key genes and pathways associated with the biosynthesis of bioactive components. The results create the link between polysaccharides and flavonoids biosynthesis and gene expression It also provides molecular resource for further pharmaceutical research.

P.1619 Gene expression underlying floral epidermal specialization in Aristolochia fimbriata (Aristolochiaceae)

Harold Suárez-Baron[1,2], Juan F. Alzate[3], Barbara A. Ambrose[4], Soraya Pelaz[5,6], Favio González[7], Natalia Pabón-Mora[2]

1 Department of Natural Sciences and Mathematics, Pontificia Universidad Javeriana Cali, Cali, Colombia. 2 Instituto de Biología, Universidad de Antioquia, Medellín, Colombia. 3 Centro Nacional de Secuenciación Genómica, Facultad de Medicina, Universidad de Antioquia, Medellín, Colombia. 4 The New York Botanical Garden, Bronx, USA. 5 Centre for Research in Agricultural Genomics, Bellaterra, Spain. 6 Institució Catalana de Recerca i Estudis Avançats, Barcelona, Spain. 7 Universidad Nacional de Colombia, Facultad de Ciencias, Instituto de Ciencias Naturales, Bogotá, Colombia.

The species of *Aristolochia* possess a petaloid perianth, which is derived from the fusion of sepals to form a unique and convolute structure. This perianth exhibits distinctive characteristics, including various types of trichomes and other epidermal cells that facilitate pollination. Most genes responsible for trichome development have been identified in unicellular trichomes found on the leaves of the model species *Arabidopsis*. However, information on the genetic basis controlling the differentiation of epidermal cells in early diverging angiosperms is scarce, and poor studied on the flower. In this study, we investigated the morphoanatomical and molecular bases underlying perianth development in *A. fimbriata*, aiming to characterize the floral epidermis and identify the gene regulatory network (GRN) related to the development of multicellular trichomes. Transcriptomic profiles of the perianth in this species allowed the identification of differentially expressed genes (DEGs). Additionally, spatial-temporal expression patterns of canonical gene homologs were assessed through *in situ* hybridization. We re-evaluate the core genetic network shaping trichome fate in flowers of an early-divergent angiosperm lineage and show a morphologically diverse output with a simpler genetic mechanism in place when compared to the models *A. thaliana* and *Cucumis sativus*. These analyses revealed that genes involved in trichome development in *A. fimbriata* vary depending on the organ in which they form. The results suggest modifications in the genetic complement, expression, and putative functions compared to those reported in model species. Furthermore, the obtained results allowed us to propose the first hypothetical gene regulatory network underlying the development of floral multicellular trichomes in *Aristolochia* species. Our findings constitute the first comprehensive study of floral epidermis development in early diverging angiosperms and serve as a reference to identify genes involved in the specialized development of floral trichomes in non-model species.

P.1620 Biodiversity in Morocco: State of knowledge and efforts deployed for its conservation and sustainable management

Taleb Mohammed Sghir[1]

1 Institut Scientifique, Mohammed V University in Rabat, Rabat, Morocco.

Located at the northwest corner of the African continent between 21 ° and 36 ° north latitude and between the 1st and the 17th degree of west longitude, Morocco with a total area of 715,000 km2 enjoys a privileged position with a coastline of 3,446 km long opening to the Mediterranean and the Atlantic Ocean. Its privileged location with a double coastline and its diverse mountain with four major mountain ranges: the Rif, Middle Atlas, High Atlas and Anti Atlas with altitudes exceeding 2,000 m in the Rif, ,3000 m in the Middle Atlas and 4,000 m in the High Atlas. The Moroccan mountains are characterized by an important forest genetic diversity represented by a rich and varied flora and many ecosystems: forest, preforest, presteppe, steppe, Sahara that spans a range of bioclimatic zones: arid, semiarid, subhumid and humid. The vascular flora of Morocco has 3,913 species and subspecies in 1,298 (including 426 sub-species types), distributed among 155 families and 981 genera. The number of endemic species amounted to 640 (16%) and 280 subspecies (32%). The rare or endangered flora species is estimated to be 463 and 1,284 subspecies. However, this diversity is subjected to many natural pressures (climate change, parasitic attacks…) and anthropic pressures (clearing, overgrazing etc.). Conscious of the risks that weigh on biodiversity, Morocco set a strategy of biodiversity management that focus on programs of in-situ conservation and more 154 protected areas in Morocco are proposed for a management of their natural resources This presentation is focused on research conducted in Morocco in terms of ecology, flora, ecosystem of Morocco while focusing on the major threats and conservation strategies developed by Morocco to reverse negative trends.

P.1621 Fergana Valley IPA network: Implications for transboundary conservation strategies in Central Asia

Tojibaev Sh. Komil[1], Lazkov A. Georgi[2], Gil Heeyoung[3], Hyeok Jae Choi[4]

1 Institute of Botany, Uzbekistan Academy of Sciences, Uzbekistan. 2 Institute of Biology, National Academy of Sciences, Kyrgyzstan. 3 Korea National Arboretum, Korea. 4 Changwon National University, Korea.

Central Asia (CA) is estimated as one of the eight centers of cultivated plants origin. Its flora consists of about 10,000 species of vascular plants. More than 2,000 species and 60 genera are strongly endemic to this region. All CA countries inherited the Soviet system of environmental practices. National biodiversity strategies and protected area management are very similar, and the basic approaches to developing plant conservation strategies and their implementation remain the same. The Important Plant Area (IPA) program is one of the new directions of botanical research in CA. The first steps in this direction were taken in 2018. Scientists from CA and Korea have begun IPA research in the Fergana Valley (FV), which can be treated as the most densely populated region of CA with rich plant diversity. Over the past time, two transboundary IPA sites (between Uzbekistan, Kyrgyzstan, and Tajikistan) and one inside of Uzbekistan have been identified (Tojibaev & al., 2022, 2023). The IPA study in FV demonstrated the effectiveness of the core principles of IPA in mountainous Central Asia and our research was completed considering the main principles of Plantlife International. This was a very important step in the creation of a regional database of threatened species and critical habitats, as well as the Red List of the CA region, which can serve to focus conservation action at the transboundary level. The best available data in CA by an international team of scientists was used to IPA sites with high concentrations of endemic and threatened plant species and critical habitats. Also, the research objectives correspond to (a) area-based approaches that dominate biodiversity conservation, reinforced by the Kunming-Montreal Global Biodiversity Framework and (b) IPAs are the leading approach for plants and fungi, supporting targets of the Global Strategy for Plant Conservation.

P.1622 Diet analysis of spotted deer (Axis axis Erxleben) based on meta-barcodes to understand the grazing patterns in Tamil Nadu, India

Rajendran Harani[1], Gnanasekar Swetha[1], James J. Amuldoss[1], Umapathy Senthilkumar[1]

1 Division of DNA Barcoding Laboratory, Department of Botany, Madras Christian College (Autonomous), East Tambaram, Chennai, India.

DNA barcoding, a tool that obtains species-specific DNA signatures based on the simple premise within small stretches of the organism’s genome. It can provide a ‘’biological barcode’’ to identify any organism at the species level. It is believed that DNA barcoding, will provide a “universal key” that will allow the identification of a species by running unknown DNA sequences through a DNA barcode database such as BOLD, NCBI etc… Further, “barcoding”, has helped clarify taxonomic position of an ‘Apparent species complex’ by revealing several cryptic species within a ‘single’ species described through conventional taxonomy. This study aims to understand the grazing preferences of Spotted Deer within the Madras Christian College campus by analysing the pellets using a Meta-barcoding approach. DNA markers have greater fidelity to unravel the diets even if the plant materials have been processed through the gut. This study has been identified the niches (foraging grounds) for spotted deer, hence the demarcation can be derived to avoid niche overlaps and animal conflicts within the campus. Thus, this study can be established further as a model to implement the methods and protocols for the first time in India to understand such patterns amongst other herbivores such as endemic-Nilgiri Tahr, Asian Elephants, Blackbuck deer, etc. towards the conservation and restoration of the foraging grounds.

P.1623 Nothofagus antarctica, a South American species with medicinal properties. Anatomical and morphological characterisation.

Bilbao Marco[1], Aguayo Paula[1], Pedreros Alberto[1], Silva Gonzalo[1], Pastene Edgar[2], Urbina Angélica[1]

1 Facultad de Agronomía, Universidad de Concepción, Chillán, Chile. 2 Departamento de Ciencias Básicas, Universidad del Biobío, Chillán, Chile.

Nothofagus antarctica, commonly known as ñire or ñirre, is a deciduous tree species, attracting attention especially in autumn for its beautiful reddish colouring before falling. In Chile, present in the forests of the Andes Mountains, it is distributed between the regions of O'Higgins and Magallanes. In Argentina, from Neuquén to Tierra del Fuego. It is a very interesting species, due to its medicinal properties. Recent research has demonstrated the presence of antioxidants in its aromatic leaves, with which Ñirre tea has been prepared and consumed for generations. *Nothofagus antarctica* has inspired artists because of its beautiful autumn colouring, as well as being very interesting from an ornamental point of view. The aim of this research was to describe the anatomy of its leaves and seeds obtained in Los Ñirres sector, Cordillera de los Andes, Ñuble region, Chile, using techniques of fixation, dehydration, critical point drying and metallisation with 450 Å thick gold vapours, to be observed in SEM of the Electron Microscopy Laboratory of the Universidad de Concepción. The results will be presented in sequential images of sheets and seeds in a poster.

Note: This abstract was translated with AI.

P.1624 Repetitive sequences, chromosome affinities and genome evolution in the grass genus Paspalum (Poaceae)

Magdalena Vaio[1], Renata Carvalho[1], Francisco Ruiz-Ruano[2], Andrea Pedrosa-Harand[3], Paola Gaiero[1], Gabriel Rua[4], Pablo Speranza[1]

1 Facultad de Agronomía, Universidad de la República, Montevideo, Uruguay. 2 Center for Molecular Biodiversity Research (ZMB), Bonn, Germany. 3 Centro de Biociências, Universidade Federal de Pernambuco, Recife, Brazil. 4 Facultad de Agronomía, Universidad de Buenos Aires, Buenos Aires, Argentina.

Paspalum L., with ~350 species, is one of the most diverse genera in the Poaceae, with most of its species distributed in tropical and subtropical areas of the Americas. Species in the genus have small genomes (mean 1C = 600 Mbp) and a basic chromosome number of x=10. Genome formulae (subgenomes I, J, N, D and X) have been proposed for some species based on chromosome pairing during meiosis in hybrids. However, phylogenetic analyses are not congruent with chromosome pairing affinities in some groups. Repetitive elements have multiple roles in chromosome organization including the recognition of homologous chromosomes at early meiosis. Recently, repetitive sequence abundances have been reported to also provide a phylogenetic signal in other plant genus. We used genome skimming, sequence clustering, phylogenetic analyses and fluorescent in situ hybridization to compare the repetitive sequences of 21 diploid *Paspalum* species. We searched for correlation among repeat proportion, species phylogeny and chromosome affinities. Our results showed that repetitive sequences constitute from 30 up to 50% of the genomes of the species. The most abundant repeats are the LTR-retrotransposons (18-41%), but several species are also enriched in satellite DNAs (1.8-21%). Two variants of a putative centromeric satellite DNA were identified with monomer sizes of 156 and 157. Phylogenetic analyses with consensus sequences of the centromeric satellite showed relative congruence with a previous well supported chloroplast phylogeny. However, presence/absence of satellite DNAs and abundance of transposable elements grouped the JJ species and notably several non-monophyletic

II subgenome species in another clade. Altogether, our data indicates that *Paspalum* genome evolution is driven by diversification of different repetitive sequences. Although these signals are not always congruent with phylogenetic relationships, their diversification is congruent to subgenome assignment, and thus probably related to chromosome pairing during meiosis.

P.1625 Why do oaks (Quercus spp.) have lobed leaves?

Kristel van Zuijlen[1], Thomas Denk[1]

1 Swedish Museum of Natural History, Stockholm, Sweden.

Lobed leaves are a characteristic feature of oak trees (*Quercus* L., Fagaceae) although only a subset of the more than 400 species do possess such leaves. Oaks became abundant in the northern hemisphere during the early Eocene (*ca.* 50 Mya.) but the first records of deeply lobed leaves are only known from Oligocene deposits, at least 15 Myr later. Lobed leaves started to radiate during the Eocene-Oligocene transition (EOT, *ca.* 34 Mya.), which denotes the most dramatic global drop in temperature during the past 65 Myr. We aim to assess how lobed leaves and other leaf characteristics are distributed across the global oak phylogeny and how their distribution is constrained by climate. To do this, we compiled leaf traits and climate envelopes for all modern oak species. We then used the extensive leaf fossil record and past climate reconstructions to trace the origin of lobed oak leaves.

P.1626 What does the floral morphology of the holoparasitic family Mitrastemonaceae (Ericales) tell us about its systematic position?

Maria von Balthazar[1], Stefan Löfstrand[1], Diego da Silva Graciano[2], Sandra Maria Carmello-Guerreiro[2], Margarita Lachmayer[1], Silvia Ulrich[1], Kenji Suetsugu[3], Jürg Schönenberger[1]

1 University of Vienna, Vienna, Austria. 2 University of Campinas, Campinas, Brazil. 3 Kobe University, Kobe, Japan.

Mitrastemonaceae are a small angiosperm family comprising only one genus of two species with a disjunct distribution: *Mitrastemon matudae* Yamam. occurs from Mexico across Central America to Colombia and *M. yamamotoi* Makino is known from India across Southeast Asia to Japan. They are holoparasites on roots of Fagaceae and as endophytes, they only become visible outside the host tissue and above ground when flowering. They produce cream-yellow- to whitish-pink-coloured flowers from the third or fourth year on after the initial host penetration and are reported to be pollinated by a wide range of insects and a bird species. The genus *Mitrastemon* was traditionally thought to be related to Rafflesiaceae (now placed in Malpighiales) based on their holoparasitic and endophytic life form. A phylogenetic placement within Ericales has only relatively recently been suggested based on molecular data. However, the phylogenetic position among Ericalean lineages remains largely elusive. A possible sister-group relationship with Lecythidaceae was recently proposed but received only weak statistical support. For this study, we conducted a detailed investigation of the floral structure of both species of Mitrastemonaceae using modern techniques including scanning electron microscopy, microtome sectioning, and X-ray computed tomography and re-evaluated the floral morphological literature on the family. We compare and discuss our findings with respect to floral morphological diversity observed in other ericalean lineages and provide a morphology-based hypothesis for the systematic position of Mitrastemonaceae within the order.

P.1627 Niche separation and mating system variation between ploidy types of Vaccinium vitis-idaea in Japan

Akimi Wakui[1], Gaku Kudo[2]

1 Arboretum and Garden Section, Botanic Gardens of Toyama, Toyama, Japan. 2 Faculty of Environmental Earth Science, Hokkaido University, Sapporo, Japan.

The Japanese archipelago includes southern distribution margins of many plant species originated from arctic regions. Thus, it is an important area for the studies on the migration and evolution history of northern plants. Although arctic-originated species commonly grow in alpine habitats at mid-latitudes, some populations of these species exist also in some specific habitats below the treeline. However, comparative studies between alpine and low-elevation populations are scarce. We aimed to reveal the ecological and genetic variations of *Vaccinium vitis-idaea* populations in Japan, by comparing 36 populations growing at different latitudes, elevations, and environments. Genetic diversity and selfing rate of individual populations and genetic differentiation among populations were calculated using microsatellite markers. We also analyzed the ploidy level of individual populations by the flow-cytometry technique. Pollination experiments were conducted at 12 populations to reveal the mating system variation across populations. All of the alpine populations were diploid, while the low-elevation populations were mostly tetraploid. In the genetic analysis, the diploid populations in northern and central Japan were estimated to be different lineages, as reported in many other arctic-alpine species growing in Japan. Additionally, the tetraploid populations were a specific lineage distinct from two diploid lineages. Diploids were self-incompatible consistently, while tetraploids showed a moderate level of selfing ability. Our results suggest that *V. vitis-idaea* growing at low elevations has a different origin from the alpine populations. Selfing ability of tetraploids may be suited to persistence in isolated situations at low-elevation habitat. Two ploidy types in *V. vitis-idaea* may be maintained by the niche separation in Japan. This study demonstrates the biological importance of small and isolated populations at the edges of species distribution.

P.1628 Trimerous flowers with a unique set of floral and pollen traits from the Late Cretaceous of Southern Bohemia (Czech Republic)

Xieting Wu[1], Maria von Balthazar[1], Friðgeir Grímsson[1], Zuzana Heřmanová[2], Jiří Kvaček[2], Jürg Schönenberger[1]

1 Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria. 2 National Museum, Prague, Czech Republic.

New, exceptionally well-preserved charcoalified flower fossils from the Late Cretaceous of Southern Bohemia, Czech Republic, were examined in detail using scanning electron microscopy and high-resolution X-ray computed tomography. The numerous specimens exhibit a unique combination of floral traits. Flowers are small, bisexual or female, trimerous, and actinomorphic. In bisexual flowers, the perianth is clearly differentiated into two types of organs. The calyx consists of three free and broadly triangular sepals with valvate aestivation. While in most flowers, the corolla comprises one or two whorls of three free, scale-like petals each, petals are absent in a few specimens and are apparently replaced by stamens. The androecium comprises one to three whorls of three stamens each. Filaments are narrow and very short; the basifixed anthers are slightly longer than the filaments and have four pollen sacs each. Each pollen sac contains a single spherical polyad comprising 32 pollen grains. The gynoecium is tricarpellate-syncarpous with a semi-inferior ovary. The three styles are short and apparently free from each other but place the wet stigmas in close proximity likely forming an extragynoecial compitum. The superior carpel surfaces are densely covered by glandular hairs. The ovary is trilocular and each locule contains at least three ovules inserted on axile placentae. One of the specimens represents a female flower, which is similar in size to the bisexual flowers and has three sepals, six scale-like petals, and six carpels. The numerous specimens found so far, clearly all belong to the same taxon based on the structure of their individual organs. However, the specimens differ not only in the number of perianth organs, stamens, and carpels (at least five morphotypes) but also in their sexual system (bisexual vs. unisexual). We discuss systematic affinities based on a detailed comparative investigation of floral morphology and an angiosperm-wide phylogenetic analysis.

P.1629 Hybridization of mountain-growing Hydrangea serrata (Hydrangeaceae) and island-growing H. macrophylla in peninsular regions

Kaoru Yamamoto1, Satoshi Kakishima[2], Chie Tsutsumi[3]

1 Yokosuka City Museum, Yokosuka, Japan. 2 Showa University, Fujiyoshida, Japan. 3 National Museum of Nature and Science, Tsukuba, Japan.

Peninsular regions possess unique plant diversity that differs from that of island or mountain regions. However, the plant diversity of peninsular regions has been less explored compared to island regions. The aim of this study was to elucidate the origin of this diversity and the uniqueness of plants in the peninsula region. We proposed that the plant diversity in the peninsular regions is a result of hybridization between mountain and island plants. In this study, we examined the hybridization between *Hydrangea serrata*, a mountain plant and *Hydrangea macrophylla*, an island plant. Using the MIG-seq method for 54 individuals, our network and STRUCTURE analyses estimated that 7 individuals were likely hybrids. These putative hybrids were identified in three geographically distinct locations, suggesting independent occurrences. The putative hybrids exhibited intermediate characteristics between *H. serrata* and *H. macrophylla*. Currently, the putative hybrids are growing in the same area as *H. serrata*. However, because of their separation from *H. macrophylla*, further hybridization is unlikely. In future studies, we plan to investigate the possibility that hybridization between *H. serrata* and *H. macrophylla* occurred during periods of rising sea levels (post-last glacial maximum).

P.1630 Direct regeneration of Drosera rotundifolia L. in vitro conditions

Yaroshko Olha[1]

1 Genetic engineering Department, Institute of Cell biology and Genetic engineering NAS, UA.

Drosera rotundifolia L. belongs to the *Droseraceae* family. *Drosera rotundifolia* is widespread species throughout the territory Holarctic (territory of America and Europe) (Wolf *et al.,* 2006).). In Ukraine there are 2 species of *Drosera*: *D. anglica* Huds., *D. intermedia* Hayne (https://redbook-ua.org/ru/item/drosera-intermedia-hayne/). They have the status of “vulnerable” and are listed in the Red Data Book of Ukraine. In previous years, there were mentioned 37 locations of *D. rotundifolia* in Ukraine (https://ukrbin.com/index.php?id=109939&action=map; Rak et al., 2022). Now *D. rotundifolia* was proposed to be included into Red data book of Ukraine into the category of “vulnerable plants” on the territory of Ukraine (Rak et al., 2022). One of the promising ways to preserve rare and endangered plants is to grow and multiply them *in vitro* conditions and then transfer them to the places of their natural growth. Our aim was to establish effective culture medium for the regeneration of *Drosera rotundifolia* for further micropropagation and obtaining of adult plants from regenerants *in vitro* conditions. The biotechnological methods were used in the work. After conducting a series of experiments, effective culture media for the regeneration of *Drosera rotundifolia* were established. The most effective media for shoot regeneration from leaf explants was 1/4 MS (Murashige & Skoog, 1962) + P.1mg/l NAA (1-Naphthaleneacetic acid) + P.3mg/l BAP (6-Benzylaminopurine). The obtained regenerants were separated from the explants and were transferred on the medium 1/4 MS with 0.1 mg/l of BAP for elongation. After two months of cultivation on medium 1/4 MS or ½ MS were successfully received adult plants.

P.1631 Integrative species delimitation of Xanthium sect. Acanthoxanthium based on herbarium specimens and type material

Eleonora Manzo[1], Justus Müller-Kiefer[1], Sebastian Nillies[1], Diego G. Gutiérrez[2], Salvatore Tomasello[1]

1 Georg-August University Göttingen, Germany. 2. Argentine Museum of Natural Sciences, Buenos Aires, Argentina.

Xanthium is a peculiar genus of the Asteraceae family, identifiable by its spiny female capitula (burs) and wind-pollination. Features of the burs are the primary morphological characteristics used for identifying taxa within the genus. The high degree of their morphological variability has led to inconsistent taxonomic treatment in the past, resulting in numerous names given by different authors. The genus can be divided into two sections: sect. *Xanthium*, which includes all taxa with unarmed stems; and sect. *Acantoxanthium* comprising plants with stems with trifurcate spines. The taxa of sect. *Acanthoxanthium* are native of South America, but due to human-mediated dispersal, some of its lineages have now reached a cosmopolitan distribution. Apart from the widespread *X. spinosum*, several other taxa have been described within this section. The aim of the present study is to determine species boundaries in *Xanthium* sect. *Acanthoxanthium*. The study employed phylogenomics, including target enrichment of hundreds of nuclear loci and complete plastomes, and geometric morphometrics, alongside coalescent-based species delimitation approaches. To ensure a comprehensive range of morphological variations in the section, including types and original material for some taxa, we surveyed key herbaria such as P, B, WU, and BA. Analysis of herbarium specimens that are nearly 200 years old, comprising type material, along with modern extraction techniques and integrative taxonomy analyses, have enabled us to identify distinct evolutionary lineages within the section. This further confirms the existence of two previously acknowledged species, *X. spinosum* and *X. ambrosioides* (Tomasello 2018). Two further independent lineages are inferred as species, the neglected *X. argentum*, initially described by Widder (1923) based on a single herbarium voucher from the province of "Nubles" in Chile and nowadays probably extremely rare; and *X. catharticum*, differentiated from *X. spinosum,* is its vicariant in the high-altitude environments of the Andes.

P.1632 Assessing the ecological impacts of invasive alien plants of France using adapted protocols of EICAT and EICAT+

Thomas de Solan[1], Aurélien Caillon[1], Guillaume Fried[2], Yohann Soubeyran3, Arnaud Albert[4]

1 Conservatoire Botanique National Sud Atlantique, Audenge, France. 2 Anses, Laboratoire de la Santé des Végétaux, Unité entomologie et botanique, Montferrier-sur-Lez, France. 3 French committee of the International Union for Conservation of Nature, Montpellier, France. 4 French Biodiversity Agency, Research and Scientific Support Department, Nantes, France.

The creation of prioritized checklists ranking alien taxa depending on their risk for biodiversity is an essential step for an effective management of invasive alien species (IAS). In France, such lists for alien plants are drawn up by different structures at regional and national scales using various risk assessment methods. This lack of homogenization in assessment methods limits the implementation of the French national strategy on IAS. To address this problem, we investigated if two recent frameworks, EICAT and EICAT+, have the potential to become standards for assessing the ecological impacts of alien plants in France. We first identified the needs and constraints associated with the use of these two protocols, and proposed several modifications. We then assessed with the modified EICAT/EICAT+ (i) the regional impacts of 100 alien plants naturalized in a French region, and (ii) the national impacts of the 230 plants identified as invasive in France. Modifying EICAT and EICAT+ is tricky, as too many changes would compromise the standardization feature of these methods and limit comparison with assessments from other regions. Firstly, we propose criteria to better define some concepts (e.g. local population), which were difficult to handle with plants in a continental context. Sourced impact data are required in both methods but are either non-existent or fragmentary for most species at a regional scale, leading to a high number of "data deficient" species. Therefore, we include local knowledge from botanists and wildlife specialists, in addition to literature review. Finally, we propose a key for translating field observations into impact levels, because local knowledge is usually related to species behaviour and often cannot be translated into EICAT(+) impact. This work provides the most comprehensive assessment to date of the current ecological impacts in France of 280 alien plants on a local and/or national scale.

P.1633 Stratification length, the key to breaking deep dormancy of Rhynchospora fusca (L.) W.T. Aiton

Ana Irene García del Bao [1], Maddi Otamendi-Urbiztondo[1], Mikel Etxeberria-Okariz[1], Pablo Tejero[2], Maialen Arrieta-Aseginolaza[1].

1Aranzadi Science Society. Donostia, Spain, 2 Instituto Pirenaico de Ecología (IPE – CSIC). Jaca, Spain

Rhynchospora fusca is a pioneer amphiatlantic species of acid peatlands which has in the Iberian Peninsula a southern distributioin limit, specifically in the Atlantic valleys and transition mountains of the Cantabrian Coast. Currently only 3 populations are known throughout the Iberian Peninsula, and therefore the taxon is placed in the category of Critically Endangered in both the autonomous level (CAPV, Navarra and Asturias) and state level (Spain).The most relevant populations is found in Izki (CAPV) in which different conservation measures have been carried out in the past years: population monitoring, germplasm collection and conservation, germination test, production of new individuals and population reinforcements. Until now, the germination rates obtained were very low compromising the effectiveness of some conservation actions. In this study, we compared several germination protocols with the objective of increasing the germination rate of R. fusca and reducing the germination time. We carried out six protocols with different periods of cold stratification from 2 to 12 weeks. Each protocol consisted of three cycles of stratification (6°C) of the corresponding length followed each cold cycle by a germination period of 28 days (30/20°C and photoperiod 12/12h). Preliminary results indicate, first, that the longer the stratification time is, the higher the germination rate will be; and, second, the results highlight the need to perform protocols with even longer cold stratification periods, until reaching the maximum germination rate (despite that extends the duration of the protocol) or the trade-off between time and germination rate.

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